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ME

## STIC-Biotech/ChemLib

188 888

From: Yu, Misook  
Sent: Friday, May 05, 2006 9:57 AM  
To: STIC-Biotech/ChemLib  
Subject: 09/870,216

Pls search SEQ ID NOs 3, 5, 7, 9, 11.

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\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 02:05:23 ; Search time 98.4 Seconds  
(without alignments)  
40.187 Million cell updates/sec

Title: US-09-870-216C-3

Perfect score: 44

Sequence: 1 FLQLMEPV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A\_Geneseq\_21.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003as.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	5	ABR08361 Synthetic
2	44	100.0	9	7	ABR82213 Human ant
3	44	100.0	352	5	ABB08366 Human can
4	35	79.5	67	4	AU022301 Human car
5	35	79.5	67	7	ADK46269 Human car
6	35	79.5	67	8	ADJ07687 Human car
7	35	79.5	329	5	ABR99785 Amino aci
8	34	77.3	307	5	ABP53033 C. elegan
9	34	77.3	307	9	ADV89954 Nematode
10	34	77.3	307	9	ADY56909 C. elegan
11	34	77.3	318	2	AYG5935 S. pneumo
12	34	77.3	318	5	ABG61495 Iron upta
13	34	77.3	318	6	ABU02362 S. pneumo
14	34	77.3	318	8	ADK46461 Streptoco
15	34	77.3	336	8	ADR96441 Novel S.
16	34	77.3	336	9	AEA60311 Streptoco
17	34	77.3	504	8	ADK76583 Plant ful
18	34	77.3	759	7	ABM87623 Rice abio
19	34	77.3	2785	3	AAV57148 Human dow
20	33	75.0	117	5	ABP34618 Human ORF
21	33	75.0	236	3	AAG44343 Arabidops
22	33	75.0	305	4	AAG82085 S. epider
23	33	75.0	318	6	ABM72286 Staphyloc
24	33	75.0	324	5	ABP40680 Staphyloc

25	33	75.0	324	8	ADS07952
26	33	75.0	345	3	AAG44342 Arabidops
27	33	75.0	368	3	AAV71459 Maize Rad
28	33	75.0	368	3	AAG44341 Arabidops
29	33	75.0	409	2	AAW75700 Vpr prote
30	33	75.0	409	2	AAW68186
31	33	75.0	409	6	ABU07460 Protein d
32	33	75.0	409	8	ADN03716 Antipsori
33	33	75.0	409	8	ADQ65876 Novel hum
34	33	75.0	409	9	ADM08718 Human pro
35	33	75.0	409	9	ADY14438 PRO polyp
36	33	75.0	416	5	ABB57171 Mouse isc
37	33	75.0	2764	4	ABB66967 Drosophil
38	33	75.0	2802	4	AAE05485 Drosophil
39	33	75.0	2802	4	ABB63789 Drosophil
40	33	75.0	2802	5	ABB08077
41	32	72.7	107	6	ADA34524 Acinetoba
42	32	72.7	195	7	ADH86453 Enterococ
43	32	72.7	272	8	ADX90400 Plant ful
44	32	72.7	290	8	ADR21275 Mosquito
45	32	72.7	316	2	AAV42689 His6-preg
46	32	72.7	316	5	AAW50626 His6-tag
47	32	72.7	322	9	ADW68625 Human tra
48	32	72.7	323	7	ADC95833
49	32	72.7	329	5	AAU78295 Human Pre
50	32	72.7	362	8	ADT59178 Plant pol
51	32	72.7	414	2	AAV42691 Human pre
52	32	72.7	434	2	AAV15931 A human i
53	32	72.7	434	2	AAV21799 Human ete
54	32	72.7	434	4	AAE84417 Amino aci
55	32	72.7	434	5	AAU78294 Human Pre
56	32	72.7	434	5	AAW50624 Human pre
57	32	72.7	434	6	AAE31708 Human Ste
58	32	72.7	434	6	ABB99786 Amino aci
59	32	72.7	434	7	ABO23618 Human orp
60	32	72.7	434	7	ABO23620 Human orp
61	32	72.7	434	8	ADK14081 SXR polyp
62	32	72.7	434	8	ADL65395 Monkey pr
63	32	72.7	434	8	ADP05761 Human nuc
64	32	72.7	437	2	AAV09515 Human vit
65	32	72.7	457	2	AAV15932 A human i
66	32	72.7	457	2	AAV16035 A human i
67	32	72.7	464	6	ABU62929 Human ste
68	32	72.7	466	2	AAV25410 Human nNr
69	32	72.7	473	2	AAV25411 Human nNr
70	32	72.7	473	2	AAV15936 A human i
71	32	72.7	473	2	AAV15933 A human i
72	32	72.7	473	2	AAV09516 Human vit
73	32	72.7	536	5	ABB90968 Herbicida
74	32	72.7	624	6	ADA48308 Rice prot
75	32	72.7	624	7	ABM86535 Rice prot
76	32	72.7	630	6	ADA48670 Rice prot
77	32	72.7	630	7	ABM90195 Rice abio
78	32	72.7	643	3	AAV77457 Rodent pr
79	32	72.7	3183	8	ADP84803 HIV-1 hyb
80	31	70.5	56	3	AAG60425 Arabidops
81	31	70.5	109	7	ADH87069 Human pan
82	31	70.5	109	7	ADH87070 Human pan
83	31	70.5	112	4	AAU17431 Novel sig
84	31	70.5	112	7	ADP94139 Human nov
85	31	70.5	142	1	AAV94151 Fish gona
86	31	70.5	181	8	ADK16705 Nanoarcha
87	31	70.5	270	8	ADK90701 Plant ful
88	31	70.5	270	8	ADK90671 Plant ful
89	31	70.5	291	4	AAU17333 Novel sig
90	31	70.5	291	7	ADB94041 Human nov
91	31	70.5	296	4	AAW25391 Human pro
92	31	70.5	307	3	AAG45206 Arabidops
93	31	70.5	307	3	AAG19976 Arabidops
94	31	70.5	335	3	AAG45205 Arabidops
95	31	70.5	335	3	AAG19975 Arabidops
96	31	70.5	354	3	AAG25005 Arabidops
97	31	70.5	375	2	AAV33843 Amino aci

98	31	70.5	375	2	AAY33938	Aay33938	Amino aci	171	30	68.2	526	7	ADH62319	Adh62319	Arabidops
99	31	70.5	375	2	AAY31194	Aay31194	Turkey GD	172	30	68.2	540	7	ABO69559	AbO69559	Pseudomon
100	31	70.5	375	5	AAY75628	Aay75628	Turkey pr	173	30	68.2	541	3	AAV71245	Aay71245	Arabidops
101	31	70.5	375	5	AAE18667	Aae18667	Meleagris	174	30	68.2	541	5	ABE90805	AbE90805	Herbicida
102	31	70.5	375	6	ABG73566	Abg73566	Turkey pr	175	30	68.2	541	7	ADH62372	AdH62372	Arabidops
103	31	70.5	375	6	ADA28703	Ada28703	Turkey my	176	30	68.2	561	5	ABP73404	AbP73404	Candida a
104	31	70.5	376	2	AAW69890	Aaw69890	Turkey gr	177	30	68.2	572	6	ADA55589	Ada55589	Human pro
105	31	70.5	378	3	AAW19974	Aaw19974	Arabidops	178	30	68.2	576	5	ABG60949	AbG60949	Cyclic nu
106	31	70.5	378	3	AAW45204	Aaw45204	Arabidops	179	30	68.2	614	7	ADJ27930	AdJ27930	Human hCO
107	31	70.5	378	8	ADN72849	Adn72849	Thale cre	180	30	68.2	685	4	AAE96519	Aae96519	Putative
108	31	70.5	382	6	ABU33229	Abu33229	Protein e	181	30	68.2	685	8	ADS43237	AdS43237	Bacterial
109	31	70.5	382	9	AEB39539	Aeb39539	L. pneumo	182	30	68.2	728	2	AAW44851	Aaw44851	Hereditar
110	31	70.5	395	9	AEB36116	Aeb36116	L. pneumo	183	30	68.2	728	6	ABG74453	AbG74453	Human exo
111	31	70.5	425	8	ADK92052	Adk92052	Plant ful	184	30	68.2	754	8	ABM82174	AbM82174	Tumour-as
112	31	70.5	433	8	ADX76210	Adx76210	Plant ful	185	30	68.2	754	8	ABM8328	AbM8328	Human pro
113	31	70.5	498	4	ABB62089	Abb62089	Drosophil	186	30	68.2	793	7	ADJ70948	AdJ70948	Human hea
114	31	70.5	539	5	ABB93022	Abb93022	Herbicida	187	30	68.2	828	8	ADS42230	AdS42230	Bacterial
115	31	70.5	544	7	ADJ92317	Adj92317	Mouse hai	188	30	68.2	843	4	AAE94326	Aae94326	Human pro
116	31	70.5	725	8	ADU01150	Adu01150	Human pro	189	30	68.2	857	7	ABE59992	AbE59992	Rat Prote
117	31	70.5	725	8	ADU15532	Adu15532	Novel hum	190	30	68.2	857	7	ABE60000	AbE60000	Rat Prote
118	31	70.5	969	8	ABM84650	Abm84650	Human dia	191	30	68.2	857	7	ABE59994	AbE59994	Human Pro
119	31	70.5	969	8	ABM84649	Abm84649	Human dia	192	30	68.2	857	7	ADD45756	AdD45756	Rat Prote
120	31	70.5	1000	5	AAW50353	Aaw50353	Human cal	193	30	68.2	857	7	ADD45758	AdD45758	Human Pro
121	31	70.5	1000	7	ABO53353	AbO53353	Human cal	194	30	68.2	857	7	ABE59998	AbE59998	Human Pro
122	31	70.5	1000	9	ADW11218	Adw11218	Human cal	195	30	68.2	857	7	ABE60002	AbE60002	Human Pro
123	31	70.5	1016	4	AAE90609	Aae90609	C glutami	196	30	68.2	857	7	ABE59996	AbE59996	Rat Prote
124	31	70.5	1019	6	ADJ13329	Adj13329	Human int	197	30	68.2	857	7	ABE59988	AbE59988	Rat Prote
125	31	70.5	1039	7	ADJ70453	Adj70453	Human hea	198	30	68.2	857	7	ABE59990	AbE59990	Human Pro
126	31	70.5	1098	7	ABE60625	AbE60625	Rat Prote	199	30	68.2	858	1	AAE70099	Aae70099	Sequence
127	31	70.5	1126	6	ABU70708	Abu70708	Human adi	200	30	68.2	858	1	AAE70100	Aae70100	Elongatio
128	31	70.5	1126	8	ABM80766	Abm80766	Tumour-as	201	30	68.2	858	4	AAW80193	Aaw80193	Human pro
129	31	70.5	1126	8	ABM80767	Abm80767	Tumour-as	202	30	68.2	858	4	AAW79209	Aaw79209	Human pro
130	31	70.5	1132	7	ADK60627	Adk60627	Human pro	203	30	68.2	858	7	ADD47661	AdD47661	Rat Prote
131	31	70.5	1132	7	ADK60623	Adk60623	Human Pro	204	30	68.2	858	7	ADD47663	AdD47663	Rat Prote
132	31	70.5	1132	8	ABM80765	Abm80765	Tumour-as	205	30	68.2	858	8	ABM82008	AbM82008	Tumour-as
133	31	70.5	1253	2	AAW10038	Aaw10038	Mad bindi	206	30	68.2	858	8	ADK67297	AdK67297	Human bla
134	31	70.5	1261	2	AAW10040	Aaw10040	Mad bindi	207	30	68.2	858	8	ADU60271	AdU60271	Housekeep
135	31	70.5	2250	9	ADY27516	Ady27516	HCoV-NL63	208	30	68.2	865	6	ABU23104	AbU23104	Protein e
136	31	70.5	4055	9	AEA06399	Aea06399	EMCR coro	209	30	68.2	911	2	AAE15355	Aae15355	Human ery
137	31	70.5	4060	9	ADY27513	Ady27513	Amino aci	210	30	68.2	911	2	AAW90263	Aaw90263	A. tigrin
138	31	70.5	6738	9	ADY27514	Ady27514	Amino aci	211	30	68.2	911	4	AAE29343	Aae29343	Human ery
139	31	70.5	6738	9	ADY27515	Ady27515	Amino aci	212	30	68.2	911	5	AAE29344	Aae29344	Human Ban
140	30	68.2	51	5	ABG60970	Abg60970	Cyclic nu	213	30	68.2	911	5	AAE29344	Aae29344	Human Pro
141	30	68.2	99	4	AAO13234	Aao13234	Human pol	214	30	68.2	911	7	ADE56706	AdE56706	Human hea
142	30	68.2	103	2	AYJ27219	Ayj27219	Amino aci	215	30	68.2	911	7	ADJ68197	AdJ68197	Human hea
143	30	68.2	116	7	ABO80969	AbO80969	Pseudomon	216	30	68.2	911	8	ADL06510	AdL06510	Human tum
144	30	68.2	141	8	ADY23478	Ady23478	Plant ful	217	30	68.2	911	8	ADL06510	AdL06510	Human tum
145	30	68.2	144	5	ABG60981	Abg60981	Cyclic nu	218	30	68.2	911	9	ADY69051	AdY69051	Human ani
146	30	68.2	144	5	ABG60986	Abg60986	Cyclic nu	219	30	68.2	911	9	ADZ26469	AdZ26469	Human sol
147	30	68.2	147	5	AAO1944	Aao1944	Human pol	220	30	68.2	911	9	ADZ80348	AdZ80348	Human sol
148	30	68.2	147	5	ABG60985	Abg60985	Cyclic nu	221	30	68.2	915	5	ABE97337	AbE97337	Novel hum
149	30	68.2	155	9	ADY80725	Ady80725	sanU prot	222	30	68.2	927	7	ADE56704	AdE56704	Rat Prote
150	30	68.2	180	4	ABG60980	Abg60980	Cyclic nu	223	30	68.2	933	8	ABM84084	AbM84084	Human dia
151	30	68.2	180	4	AAU29443	Aau29443	Human G p	224	30	68.2	962	4	AAU30825	Aau30825	Novel hum
152	30	68.2	180	5	ABG60731	Abg60731	Novel G p	225	30	68.2	1004	8	ADR86066	AdR86066	Aspergill
153	30	68.2	187	5	ABP41251	Abp41251	Human ova	226	30	68.2	1090	3	AAE10946	Aae10946	L. mexica
154	30	68.2	200	5	ADK34801	Adk34801	Novel hum	227	30	68.2	1229	8	ADN47425	AdN47425	Thermoco
155	30	68.2	232	4	AAW88054	Aaw88054	Human imm	228	30	68.2	1332	7	ABO77026	AbO77026	Pseudomon
156	30	68.2	244	5	ABG60984	Abg60984	Cyclic nu	229	30	68.2	1450	6	ADA89491	Ada89491	Staphyloc
157	30	68.2	299	3	AAE17379	Aae17379	Arabidops	230	30	68.2	1491	4	AAU34072	Aau34072	Staphyloc
158	30	68.2	327	7	ABO84321	AbO84321	Pseudomon	231	30	68.2	1499	6	ABU16457	AbU16457	Protein e
159	30	68.2	336	3	AAE53479	Aae53479	Arabidops	232	30	68.2	1501	4	AAE82878	Aae82878	S. epide
160	30	68.2	336	4	ABG00916	Abg00916	Novel hum	233	30	68.2	1502	4	AAU36569	Aau36569	Staphyloc
161	30	68.2	342	4	AAE96643	Aae96643	Putative	234	30	68.2	1502	6	ABM71608	AbM71608	Staphyloc
162	30	68.2	348	3	AAE17378	Aae17378	Arabidops	235	30	68.2	1509	6	ABU43942	AbU43942	Protein e
163	30	68.2	365	8	ADT60341	Adt60341	Plant pol	236	30	68.2	1529	5	ABP39100	AbP39100	Staphyloc
164	30	68.2	371	3	AAE17377	Aae17377	Arabidops	237	30	68.2	1529	8	ADS07312	AdS07312	Staphyloc
165	30	68.2	420	3	AAE53478	Aae53478	Arabidops	238	30	68.2	1614	4	ABE62664	AbE62664	Drosophil
166	30	68.2	442	8	ADS23239	AdS23239	Bacterial	239	29	65.9	11	4	AAE07185	Aae07185	Colostrin
167	30	68.2	498	3	AAE53477	Aae53477	Arabidops	240	29	65.9	12	4	AAE07195	Aae07195	Colostrin
168	30	68.2	515	3	AAE71249	Aae71249	Arabidops	241	29	65.9	17	4	AAE72501	Aae72501	Colostrin
169	30	68.2	515	7	ADH62380	Adh62380	Arabidops	242	29	65.9	17	4	AAE59310	Aae59310	Ewe colos
170	30	68.2	526	3	AAV71242	Aay71242	Arabidops	243	29	65.9	17	4	AAE72247	Aae72247	Colostrin

171	30	68.2	526	7	ADH62319	Adh62319	Arabidops
172	30	68.2	540	7	ABO69559	AbO69559	Pseudomon
173	30	68.2	541	3	AAV71245	Aay71245	Arabidops
174	30	68.2	541	5	ABE90805	AbB90805	Herbicida
175	30	68.2	541	7	ADH62372	Adh62372	Arabidops
176	30	68.2	561	5	ABP73404	Abp73404	Candida a
177	30	68.2	572	6	ADA55589	Ada55589	Human pro
178	30	68.2	576	5	ABG60949	Abg60949	Cyclic nu
179	30	68.2	614	7	ADD27930	Add27930	Human hCO
180	30	68.2	685	4	AAE96519	Aae96519	Putative
181	30	68.2	685	8	ADS43237	AdS43237	Bacterial
182	30	68.2	728	2	AAW44851	Aaw44851	Hereditar
183	30	68.2	728	6	ABG74453	Abg74453	Human exo
184	30	68.2	754	8	ABM82174	Abm82174	Tumour-as
185	30	68.2	754	8	ABM8328	Abm8328	Human pro
186	30	68.2	793	7	ADJ70948	Adj70948	Human hea
187	30	68.2	828	8	ADS42230	AdS42230	Bacterial
188	30	68.2	843	4	AAE94326	Aae94326	Human pro
189	30	68.2	857	7	ABE59992	AbE59992	Rat Prote
190	30	68.2	857	7	ABE60000	AbE60000	Rat Prote
191	30	68.2	857	7	ABE59994	AbE59994	Human Pro
192	30	68.2	857	7	ADD45756	AdD45756	Rat Prote
193	30	68.2	857	7	ADD45758	AdD45758	Human Pro
194	30	68.2	857	7	ABE59998	AbE59998	Human Pro
195	30	68.2	857	7	ABE60002	AbE60002	Human Pro
196	30	68.2	857	7	ABE59996	AbE59996	Rat Prote
197	30	68.2	857	7	ABE59988	AbE59988	Rat Prote
198	30	68.2	857	7	ABE59990	AbE59990	Human Pro
199	30	68.2	858	1	AAFP70099	Aap70099	Sequence
200	30	68.2	858	1	AAFP70100	Aap70100	Elongatio
201	30	68.2	858	4	AAW80193	Aam80193	Human pro
202	30	68.2	858	4	AAW79209	Aam79209	Human pro
203	30	68.2	858	7	ADD47661	Add47661	Rat Prote
204	30	68.2	858	7	ADD47663	Add47663	Rat Prote
205	30	68.2	858	8	ABM82008	Abm82008	Tumour-as
206	30	68.2	858	8	ABM82008	Abm82008	Tumour-as
207	30	68.2	858	8	ADU60271	AdU60271	Human bla
208	30	68.2	858	8	ADU60271	AdU60271	Housekeep
209	30	68.2	858	6	ABU23104	AbU23104	Protein e
210	30	68.2	911	2	AAW90263	Aaw90263	A. tigrin
211	30	68.2	911	4	AAW90263	Aaw90263	A. tigrin
212	30	68.2	911	5	AAE46914	Aab46914	Human ery
213	30	68.2	911	5	AAE29343	Aae29343	Human Ban
214	30	68.2	911	5	AAE29344	Aae29344	Human Ban
215	30	68.2	911	7	ADSE6706	AdE56706	Human Pro
216	30	68.2	911	7	ADJ68197	Adj68197	Human hea
217	30	68.2	911	8	ADU68510	AdU68510	Human hea
218	30	68.2	911	9	ADY69051	Ady69051	Human tum
219	30	68.2	911	9	ADY69051	Ady69051	Human ani
220	30	68.2	911	9	ADZ26469	AdZ26469	Human sol
221	30	68.2	915	5	ABB97337	AbB97337	Novel hum
222	30	68.2	927	7	ADP56704	AdP56704	Rat Prote
223	30	68.2	932	8	ABM84084	Abm84084	Human dia
224	30	68.2	962	4	AAU30825	Aau30825	Novel hum
225	30	68.2	1004	3	ABR86066	AbR86066	Aspergill
226	30	68.2	1090	3	AAE10946	Aab10946	L. mexica
227	30	68.2	1229	8	ADN47425	Adn47425	Thermococ
228	30	68.2	1332	7	ABO77026	AbO77026	Pseudomon
229	30	68.2	1450	6	ABD89491	Ada89491	Staphyloc
230	30	68.2	1491	4	AAU34072	Aau34072	Staphyloc
231	30	68.2	1499	6	ABU16457	AbU16457	Protein e
232	30	68.2	1501	4	AAE82878	AgE82878	S. epider
233	30	68.2	1502	4	AAU36569	Aau36569	Staphyloc
234	30	68.2	1502	6	ABM71608	Abm71608	Staphyloc
235	30	68.2	1509	6	ABU43942	Abu43942	Protein e
236	30	68.2	1529	5	ABP39100	Abp39100	Staphyloc
237	30	68.2	1529	8	ADSO7312	AdS07312	Staphyloc
238	30	68.2	3614	4	ABE62664	AbB62664	Drosophi
239	29	65.9	11	4	AAE07185	Aae07185	Colostrin
240	29	65.9	12	4	AAE07195	Aae07195	Medif
241	29	65.9	17	4	AAE59310	Aab59310	Ewe colos
242	29	65.9	17	4	AAE59310	Aab59310	Ewe colos
243	29	65.9	17	4	AAE72247	Aab72247	Colostrin

244	29	65.9	17	4	AAB72533	Aab72533 Colostrin	317	29	65.9	221	7	ADG06428	Ade06428 Human PRO
245	29	65.9	17	5	AAO14578	Aao14578 Neural ce	318	29	65.9	221	7	ADG38203	Adg38203 Human PRO
246	29	65.9	17	5	AAO15037	Aao15037 Colostrin	319	29	65.9	221	7	ADG88319	Adg88319 Human PRO
247	29	65.9	17	5	AAE20229	Aae20229 Colostrin	320	29	65.9	221	7	ADG90900	Adg90900 Human sec
248	29	65.9	17	8	ADN60296	Adn60296 Constitue	321	29	65.9	221	7	ADG99455	Adg99455 Human sec
249	29	65.9	17	8	ADS74386	Ads74386 Ovine col	322	29	65.9	221	7	ADG06548	Adg06548 Human PRO
250	29	65.9	17	9	ADW00452	Adw00452 Colostrin	323	29	65.9	221	7	ADG05499	Adg05499 Human PRO
251	29	65.9	18	4	AAB59341	Aab59341 Ewe colos	324	29	65.9	221	7	ADG82500	Adg82500 Human PRO
252	29	65.9	33	4	AAAI7706	Aai17706 Peptide #	325	29	65.9	221	8	ADG81753	Adg81753 Human sec
253	29	65.9	33	4	ABB36730	Abb36730 Peptide #	326	29	65.9	221	8	ADG81869	Adg81869 Human sec
254	29	65.9	33	4	AAB30220	Aab30220 Peptide #	327	29	65.9	221	8	ADG37727	Adg37727 Human sec
255	29	65.9	33	4	ABB31518	Abb31518 Peptide #	328	29	65.9	221	8	ADG37611	Adg37611 Human sec
256	29	65.9	33	4	ABB22061	Abb22061 Protein #	329	29	65.9	221	8	ADG95382	Adg95382 Human sec
257	29	65.9	33	4	AAAG69880	Aam69880 Human bon	330	29	65.9	221	8	ADG38082	Adg38082 Human PRO
258	29	65.9	33	4	AAAG57485	Aam57485 Human bra	331	29	65.9	221	8	ADG76171	Adg76171 Human PRO
259	29	65.9	33	4	ABG51579	Abg51579 Human liv	332	29	65.9	221	8	ADG39494	Adg39494 Human PRO
260	29	65.9	33	4	AAAG05368	Aam05368 Peptide #	333	29	65.9	221	8	ADG04298	Adg04298 Human PRO
261	29	65.9	33	5	ABG39510	Abg39510 Human pep	334	29	65.9	221	8	ADG39895	Adg39895 Human PRO
262	29	65.9	37	5	ABP27256	Abp27256 Streptoco	335	29	65.9	221	8	ADG19760	Adg19760 Human PRO
263	29	65.9	41	2	AAAY32240	Aay32240 Human bet	336	29	65.9	221	8	ADG77338	Adg77338 Human sec
264	29	65.9	45	3	AAAG1211	Aar91211 RPT1 zinc	337	29	65.9	221	8	ADG65446	Adg65446 Human PRO
265	29	65.9	45	3	AAAG60426	Aag60426 Arabidops	338	29	65.9	221	8	ADG76055	Adg76055 Human PRO
266	29	65.9	66	4	AAO05013	Aao05013 Human pol	339	29	65.9	221	8	ADG37966	Adg37966 Human PRO
267	29	65.9	81	3	AAAG34943	Aag34943 Arabidops	340	29	65.9	221	8	ADG64576	Adg64576 Human PRO
268	29	65.9	88	5	ADK36658	Adk36658 Novel hum	341	29	65.9	221	8	ADG38911	Adg38911 Human PRO
269	29	65.9	91	2	AAAB12053	Abb12053 Human gps	342	29	65.9	221	8	ADG51985	Adg51985 Human sec
270	29	65.9	93	4	AAAG66237	Aau66237 Propionib	343	29	65.9	221	8	ADG91016	Adg91016 Human sec
271	29	65.9	93	5	ABBA48290	Abb48290 Listeria	344	29	65.9	221	8	ADG38795	Adg38795 Human PRO
272	29	65.9	93	5	ABMG2756	Abmg2756 Propionib	345	29	65.9	221	8	ADG37495	Adg37495 Human sec
273	29	65.9	104	6	ADAJ5200	Ada5200 Acinetoba	346	29	65.9	221	8	ADG06311	Adg06311 Human PRO
274	29	65.9	112	2	AAAW75848	Aaw75848 Protein s	347	29	65.9	221	8	ADG90171	Adg90171 Human sec
275	29	65.9	112	2	AAAG68192	Aaw68192 Protein s	348	29	65.9	221	8	ADG38679	Adg38679 Human PRO
276	29	65.9	126	7	ADY31409	Adc31409 Human nov	349	29	65.9	221	8	ADG39610	Adg39610 Human PRO
277	29	65.9	126	8	ADY04994	Ady04994 Plant ful	350	29	65.9	221	8	ADG89215	Adg89215 Human PRO
278	29	65.9	136	3	AAAG34942	Aag34942 Arabidops	351	29	65.9	221	8	ADG88982	Adg88982 Human PRO
279	29	65.9	143	8	ADX66750	Adx66750 Plant ful	352	29	65.9	221	8	ADG19876	Adg19876 Human PRO
280	29	65.9	150	2	AAAW75849	Aaw75849 Protein s	353	29	65.9	221	8	ADG77454	Adg77454 Human sec
281	29	65.9	150	2	AAAG68193	Aaw68193 Protein s	354	29	65.9	221	8	ADG65330	Adg65330 Human PRO
282	29	65.9	158	8	ADK16034	Adk16034 Streptomy	355	29	65.9	221	8	ADG39378	Adg39378 Human PRO
283	29	65.9	165	4	ABG12127	Abg12127 Novel hum	356	29	65.9	221	8	ADG38563	Adg38563 Human sec
284	29	65.9	174	2	AAAW75850	Aaw75850 Protein s	357	29	65.9	221	8	ADG11116	Adg11116 Human sec
285	29	65.9	174	2	AAAG68194	Aaw68194 Protein s	358	29	65.9	221	8	ADG11000	Adg11000 Human sec
286	29	65.9	179	2	AAAW75843	Aaw75843 Vpr prote	359	29	65.9	221	8	ADH31528	Adh31528 Human PRO
287	29	65.9	179	2	AAAG68187	Aaw68187 Vpr bindi	360	29	65.9	221	8	ADH38776	Adh38776 Human sec
288	29	65.9	183	3	AAAY75341	Aay75341 Neisseria	361	29	65.9	221	8	ADH29411	Adh29411 Human sec
289	29	65.9	183	3	AAAY75342	Aay75342 Neisseria	362	29	65.9	221	8	ADH23714	Adh23714 Human sec
290	29	65.9	183	3	AAAY75340	Aay75340 Neisseria	363	29	65.9	221	8	ADH27044	Adh27044 Human sec
291	29	65.9	185	3	AAAG54838	Aag54838 Arabidops	364	29	65.9	221	8	ADH38312	Adh38312 Novel hum
292	29	65.9	190	5	ABG79648	Abg79648 Human nov	365	29	65.9	221	8	ADH26928	Adh26928 Human sec
293	29	65.9	221	4	AAAG93328	Aag93328 Human nov	366	29	65.9	221	8	ADH38196	Adh38196 Novel hum
294	29	65.9	221	4	AAAG81404	Aag81404 Human APP	367	29	65.9	221	8	ADH38892	Adh38892 Human sec
295	29	65.9	221	5	ABG79642	Abg79642 Human nov	368	29	65.9	221	8	ADH23830	Adh23830 Human sec
296	29	65.9	221	5	ABP64730	Abp64730 Human pro	369	29	65.9	221	8	ADH40205	Adh40205 Human PRO
297	29	65.9	221	6	ADA01370	Ada01370 Human PRO	370	29	65.9	221	8	ADH40090	Adh40090 Human PRO
298	29	65.9	221	6	ADA43799	Ada43799 Human sec	371	29	65.9	221	8	ADH31412	Adh31412 Human PRO
299	29	65.9	221	6	ADA43567	Ada43567 Human sec	372	29	65.9	221	8	ADH29290	Adh29290 Human sec
300	29	65.9	221	6	ADA01242	Ada01242 Human PRO	373	29	65.9	221	8	ADH49505	Adh49505 Novel hum
301	29	65.9	221	7	ADA01126	Ada01126 Human sec	374	29	65.9	221	8	ADH51969	Adh51969 Novel hum
302	29	65.9	221	7	ADA43683	Ada43683 Human sec	375	29	65.9	221	8	ADH49824	Adh49824 Novel hum
303	29	65.9	221	7	ADA06945	Ada06945 Human PRO	376	29	65.9	221	8	ADH52425	Adh52425 Novel hum
304	29	65.9	221	7	ADA08433	Ada08433 Novel hum	377	29	65.9	221	8	ADH52541	Adh52541 Novel hum
305	29	65.9	221	7	ADB99726	Adb99726 Human PRO	378	29	65.9	221	8	ADH58538	Adh58538 Novel hum
306	29	65.9	221	7	ADB87709	Adb87709 Human PRO	379	29	65.9	221	8	ADH51853	Adh51853 Novel hum
307	29	65.9	221	7	ADB66164	Adb66164 Human sec	380	29	65.9	221	8	ADH58414	Adh58414 Novel hum
308	29	65.9	221	7	ADB99842	Adb99842 Human PRO	381	29	65.9	221	8	ADH13611	Adh13611 Novel hum
309	29	65.9	221	7	ADB99497	Adb99497 Novel hum	382	29	65.9	221	8	ADK00867	Adk00867 Human PRO
310	29	65.9	221	7	ADB66048	Adb66048 Human sec	383	29	65.9	221	8	ADL08608	Adl08608 Human sec
311	29	65.9	221	7	ADC23446	Adc23446 Human tra	384	29	65.9	223	6	ABU40969	Abu40969 Protein e
312	29	65.9	221	7	ADC26139	Adc26139 Human PRO	385	29	65.9	227	7	ADF04270	Adf04270 Bacterial
313	29	65.9	221	7	ADE04966	Ade04966 Human PRO	386	29	65.9	247	7	ADG96016	Adg96016 Human uri
314	29	65.9	221	7	ADE11272	Ade11272 Human PRO	387	29	65.9	256	5	ABF63972	Abf63972 Human ORF
315	29	65.9	221	7	ADH8203	Adh8203 Human PRO	388	29	65.9	273	4	AAG71376	Aag71376 Human sec
316	29	65.9	221	7	ADD95498	Add95498 Human sec	389	29	65.9	275	7	ADC14241	Adc14241 Human enz

390	29	65.9	277	6	ABU12106	Abu12106 Human pro	463	29	65.9	433	8	ADX94671	Plant ful
391	29	65.9	292	4	AAB50860	Aab50860 Mevalonat	464	29	65.9	438	8	ADJ67902	A. aeolic
392	29	65.9	296	6	ABU97207	Abu97207 Enzyme po	465	29	65.9	438	8	ADJ68114	A. aeolic
393	29	65.9	296	6	ABM65275	Abm65275 Propionib	466	29	65.9	438	8	ADK01192	DNA polym
394	29	65.9	297	5	ABP28408	Abp28408 Streptoco	467	29	65.9	438	8	ADJ79411	A. aeolic
395	29	65.9	299	5	ABP66276	Abp66276 Bifidobac	468	29	65.9	438	8	ADJ784851	A. aeolic
396	29	65.9	300	4	ABM58826	Abm58826 Drosophil	469	29	65.9	438	8	ADM77639	DNA polym
397	29	65.9	317	6	ABU12119	Abu12119 Human pro	470	29	65.9	438	8	ADM66306	A. aeolic
398	29	65.9	321	3	AAG28325	Aag28325 Arabidops	471	29	65.9	438	8	ADO04359	A. aeolic
399	29	65.9	328	2	AAW91225	Aaw91225 Human pla	472	29	65.9	438	8	ADP82436	Aquifex a
400	29	65.9	328	2	AAW09433	Aaw09433 Human pla	473	29	65.9	438	8	ADP15643	A. aeolic
401	29	65.9	328	6	AAE04393	Aae04393 Human P2	474	29	65.9	438	9	ADY55134	A. aeolic
402	29	65.9	328	6	ABP81869	Abp81869 Human pur	475	29	65.9	438	9	ADZ76710	A. aeolic
403	29	65.9	328	7	ADC37341	Adc37341 Nuclear f	476	29	65.9	438	9	AEA24718	Aquifex a
404	29	65.9	328	7	ADD45306	Add45306 Human pro	477	29	65.9	438	9	AEA34141	Aquifex a
405	29	65.9	328	7	ADP38349	Adp38349 Human pro	478	29	65.9	438	9	ABE51545	Helicase
406	29	65.9	328	7	ADN39970	Adn39970 Cancer/an	479	29	65.9	441	8	ADY08712	Plant ful
407	29	65.9	328	8	ADO29600	Ado29600 Human GPC	480	29	65.9	448	5	ABP73518	Candida a
408	29	65.9	328	8	ADP49195	Adp49195 Human P2Y	481	29	65.9	451	8	ADX76883	Plant ful
409	29	65.9	328	8	ADR46666	Adr46666 Cancer-as	482	29	65.9	462	6	ABU18843	Protein e
410	29	65.9	328	9	ADV25075	Adv25075 Human P2Y	483	29	65.9	463	4	NAG71254	Human gen
411	29	65.9	330	6	ABP99787	Abp99787 Amino aci	484	29	65.9	463	5	ABG63465	Human alb
412	29	65.9	335	4	AAU40144	Aau40144 Propionib	485	29	65.9	463	8	ADL76730	Albumin f
413	29	65.9	335	6	ABM36663	Abm36663 Propionib	486	29	65.9	485	8	ADX88360	Plant ful
414	29	65.9	342	6	ABU17021	Abu17021 Protein e	487	29	65.9	489	4	AAG71293	Human gen
415	29	65.9	346	2	AAW21730	Aaw21730 Nuclear m	488	29	65.9	489	5	ABG63464	Human alb
416	29	65.9	350	3	AAG24054	Aag24054 Arabidops	489	29	65.9	489	8	ADL76729	Albumin f
417	29	65.9	356	4	ABB62811	Abb62811 Drosophil	490	29	65.9	496	8	ABM84531	Human dia
418	29	65.9	358	6	ADA33701	Ada33701 Acinetoba	491	29	65.9	497	4	ABB64609	Drosophil
419	29	65.9	360	7	ADC14211	Adc14211 Human enz	492	29	65.9	497	7	ADP66014	Human uri
420	29	65.9	363	2	AAW23658	Aaw23658 E6AP-bind	493	29	65.9	497	5	ABO82786	Pseudomon
421	29	65.9	363	2	AAW75699	Aaw75699 Vpr prote	494	29	65.9	502	5	ABP91715	Herbicida
422	29	65.9	363	2	AAW68185	Aaw68185 Vpr bindi	495	29	65.9	509	3	ABA41695	Human ORP
423	29	65.9	363	7	ADD45606	Add45606 Human Pro	496	29	65.9	511	7	ADD22428	HLA-B46 T
424	29	65.9	363	7	ADD45150	Add45150 Human Pro	497	29	65.9	511	7	ADI15924	Human PP
425	29	65.9	363	7	ADP59685	Adp59685 Human Pro	498	29	65.9	517	8	ABM84533	Human dia
426	29	65.9	363	7	ADP47527	Adp47527 Human Pro	499	29	65.9	527	7	ADC14245	Human enz
427	29	65.9	363	7	ADP59689	Adp59689 Human Pro	500	29	65.9	527	7	ABO67627	Klebeieil
428	29	65.9	363	8	ADP76421	Adp76421 Novel hum	501	29	65.9	538	8	ADP23393	Bacterial
429	29	65.9	363	8	ABM82047	Abm82047 Tumour-as	502	29	65.9	540	5	ABP93021	Herbicida
430	29	65.9	365	1	AAW91461	Aaw91461 Rpt-1 clo	503	29	65.9	540	6	ABU20640	Human hea
431	29	65.9	372	3	AAW16017	E. coli p	504	29	65.9	544	6	ABU20640	Protein e
432	29	65.9	372	4	AAG98319	Aag98319 Escherich	505	29	65.9	550	8	ADH09581	Human hos
433	29	65.9	374	2	AAW37994	Aaw37994 Mutant As	506	29	65.9	562	5	ABP66146	Bifidobac
434	29	65.9	374	2	AAW39875	Aaw39875 A. oryzae	507	29	65.9	565	3	AAW70011	Human Pro
435	29	65.9	374	5	ABH05613	Abh05613 Mutant As	508	29	65.9	565	3	AAW32435	Human ubi
436	29	65.9	374	8	ADT62067	Adt62067 Aspergill	509	29	65.9	565	4	AAW78944	Human pro
437	29	65.9	375	6	ABU11879	Abu11879 Human ABC	510	29	65.9	570	8	ADH09575	Human hos
438	29	65.9	379	8	ADH09576	Adh09576 Human hos	511	29	65.9	570	8	ABM84532	Human dia
439	29	65.9	381	8	ADH09577	Adh09577 Human hos	512	29	65.9	576	8	ADN20550	Bacterial
440	29	65.9	382	2	AAW97651	Aaw97651 Corn sugi	513	29	65.9	582	4	AAW79928	Human pro
441	29	65.9	382	2	AAW97651	Aaw97651 Corn sugi	514	29	65.9	590	8	ABM84535	Human dia
442	29	65.9	384	3	AAW26424	Aaw26424 Drosophil	515	29	65.9	598	8	ADP73557	Glycopept
443	29	65.9	384	4	ABP69417	Abp69417 Drosophil	516	29	65.9	618	7	ADC14242	Human enz
444	29	65.9	394	4	ABP68759	Abp68759 Drosophil	517	29	65.9	626	8	ABM84534	Human dia
445	29	65.9	395	4	AAW92970	Aaw92970 Human pro	518	29	65.9	646	7	ADD47487	Rat Prote
446	29	65.9	405	3	AAG24053	Aag24053 Arabidops	519	29	65.9	648	7	ABO68873	Pseudomon
447	29	65.9	406	3	ABE203919	AbE203919 Drosophil	520	29	65.9	651	6	ABO68873	Pseudomon
448	29	65.9	414	7	ABO63911	AbO63911 Klebeieil	521	29	65.9	651	6	ABU20351	Protein e
449	29	65.9	415	9	ABW92995	Abw92995 M. xanthu	522	29	65.9	652	4	ABB64472	Drosophil
450	29	65.9	418	2	AAW97650	Aaw97650 Soybean S	523	29	65.9	655	5	ABO06988	Human MD2
451	29	65.9	419	3	AAG24052	Aag24052 Arabidops	524	29	65.9	655	7	ADJ68514	Human hea
452	29	65.9	419	8	ADN73095	Adn73095 Thale cre	525	29	65.9	655	7	ADJ68728	Human hea
453	29	65.9	420	6	ADB16936	Adb16936 Corilla D	526	29	65.9	655	8	ABM81815	Tumour-as
454	29	65.9	420	6	ADB16934	Adb16934 Chimpanze	527	29	65.9	655	9	ADX07183	Cyclin-de
455	29	65.9	420	6	ADB16923	Adb16923 Wild type	528	29	65.9	691	3	AAW32253	Drosophil
456	29	65.9	420	6	ADB16938	Adb16938 Orangutan	529	29	65.9	691	4	ABB64167	Drosophil
457	29	65.9	420	6	ADB16963	Adb16963 Human DX	530	29	65.9	691	9	ABE53791	Drosophil
458	29	65.9	420	6	ADB16940	Adb16940 Pygmy chi	531	29	65.9	693	6	ABE30108	Drosophil
459	29	65.9	422	8	AAW97652	Aaw97652 Corn sugi	532	29	65.9	731	5	ABD92517	Herbicida
460	29	65.9	424	8	ADY11716	Ady11716 Plant ful	533	29	65.9	776	7	ADD71157	Plant ful
461	29	65.9	424	8	ADY23045	Ady23045 Plant ful	534	29	65.9	776	8	ABM82451	Tumour-as
462	29	65.9	432	8	ADS27613	AdS27613 Bacterial	535	29	65.9	776	9	ADY16233	PRO polyP



536	29	65.9	781	3	AAB07290	Aab07290 Human bet	609	28	63.6	69	4	AA013572	Aa013572 Human pol
537	29	65.9	781	3	AAY70740	Aay70740 Human bet	610	28	63.6	78	4	ABB37806	Abb37806 Peptide #
538	29	65.9	781	4	AAE06039	Aae06039 Mouse bet	611	28	63.6	78	4	AAm31203	Aam31203 Peptide #
539	29	65.9	781	4	AAE06038	Aae06038 Human bet	612	28	63.6	78	4	ABB23081	Abb23081 Protein #
540	29	65.9	781	4	AAU28118	Aau28118 Novel hum	613	28	63.6	78	4	AAm70911	Aam70911 Human bon
541	29	65.9	781	5	ABB57330	Abb57330 Mouse isc	614	28	63.6	78	4	AAm58422	Aam58422 Human bra
542	29	65.9	781	6	ABU05110	Abu05110 Human exp	615	28	63.6	78	4	ABG52628	Abg52628 Human liv
543	29	65.9	781	6	ABU05109	Abu05109 Human exp	616	28	63.6	78	5	ABG40707	Abg40707 Human pep
544	29	65.9	781	6	ABU05112	Abu05112 Human exp	617	28	63.6	85	9	ADY53759	Ady53759 Human ig
545	29	65.9	781	6	ABU05111	Abu05111 Human exp	618	28	63.6	99	3	AA844197	Aa844197 Human can
546	29	65.9	781	6	ABU05116	Abu05116 Human exp	619	28	63.6	106	4	AAm83784	Aam83784 Human imm
547	29	65.9	781	6	ABU05117	Abu05117 Human exp	620	28	63.6	108	4	ABBI7708	Abbi7708 Human ner
548	29	65.9	781	6	ABU05118	Abu05118 Human exp	621	28	63.6	111	7	ADf05771	Adf05771 Bacterial
549	29	65.9	781	6	ABU05113	Abu05113 Human exp	622	28	63.6	119	7	ABM87036	Abm87036 Rice abio
550	29	65.9	781	7	ADP65278	Adp65278 Human cat	623	28	63.6	126	3	AAg01514	Aag01514 Human sec
551	29	65.9	781	7	ADG87137	Adg87137 Human bet	624	28	63.6	130	4	AAb79555	Aab79555 Corynebac
552	29	65.9	781	8	ADJ62850	Adj62850 Human bet	625	28	63.6	130	4	AAg89870	Aag89870 C glutami
553	29	65.9	781	8	ADJ62851	Adj62851 Mouse bet	626	28	63.6	134	3	AAg36522	Aag36522 Arabidops
554	29	65.9	781	8	ADP74617	Adp74617 Amino aci	627	28	63.6	142	7	ADB65187	Adb65187 Human pro
555	29	65.9	781	8	ADO49109	Ado49109 Human ded	628	28	63.6	142	7	ADB64176	Adb64176 Human pro
556	29	65.9	781	8	ADS31844	Ads31844 Mouse bet	629	28	63.6	143	5	ABU05938	Abu05938 M. tuberc
557	29	65.9	781	8	ADY70397	Ady70397 Human bet	630	28	63.6	143	7	ADf58669	Adf58669 Human pol
558	29	65.9	781	9	ADY70272	Ady70272 Human bet	631	28	63.6	148	4	AAU23167	Aau23167 Novel hum
559	29	65.9	781	9	ADY70659	Ady70659 Human nic	632	28	63.6	151	3	AAg36521	Aag36521 Arabidops
560	29	65.9	781	9	ADZ03913	Adz03913 Human bet	633	28	63.6	151	8	ADL04822	Adl04822 M. catarr
561	29	65.9	781	9	ADZ85048	Adz85048 Full-leng	634	28	63.6	173	5	ABU05430	Abu05430 M. tuberc
562	29	65.9	781	9	AEA55036	Aea55036 Mouse bet	635	28	63.6	176	3	AAg20314	Aag20314 Arabidops
563	29	65.9	781	9	AE828123	Ae828123 Human bet	636	28	63.6	176	3	AAg38740	Aag38740 Arabidops
564	29	65.9	781	9	AE828123	Ae828123 Human bet	637	28	63.6	181	3	AAg38739	Aag38739 Arabidops
565	29	65.9	781	9	AE828123	Ae828123 Human bet	638	28	63.6	181	3	AAg20313	Aag20313 Arabidops
566	29	65.9	781	9	ADP98960	Adp98960 C. albica	639	28	63.6	184	7	ADf60497	Adf60497 Human con
567	29	65.9	782	9	AEA20901	Aea20901 Novel hum	640	28	63.6	190	6	ADU27626	Adu27626 Protein e
568	29	65.9	800	4	AAU28306	Aau28306 Novel hum	641	28	63.6	195	8	ADT59363	Adt59363 Plant pol
569	29	65.9	800	6	ABU05114	Abu05114 Human exp	642	28	63.6	202	7	ABO68368	Ab068368 Pseudomon
570	29	65.9	822	6	ABR52596	Abr52596 Protein s	643	28	63.6	209	8	ADN19637	Adn19637 Bacterial
571	29	65.9	822	7	ADK62982	Adk62982 Disease t	644	28	63.6	211	3	AA854371	Aa854371 Human pan
572	29	65.9	883	4	AAm51651	Aam51651 Synechoco	645	28	63.6	211	8	ADJ48391	Adj48391 Maize oil
573	29	65.9	890	3	AAU77290	Aau77290 Streptomy	646	28	63.6	214	7	ADH86943	Adh86943 Enterococ
574	29	65.9	890	3	AAU77290	Aau77290 Ksq-Atq l	647	28	63.6	215	4	AAU17439	Aau17439 Novel sig
575	29	65.9	968	7	ADJ69678	Adj69678 Human hea	648	28	63.6	215	7	ADB94147	Adb94147 Human nov
576	29	65.9	1005	2	AAJ75354	Aaj75354 Transposo	649	28	63.6	216	8	ADX73590	Adx73590 Plant ful
577	29	65.9	1005	2	AAW60181	Aaw60181 B. thurin	650	28	63.6	228	4	AA887649	Aa887649 Bovine ma
578	29	65.9	1090	5	ABU05722	Abu05722 Human tes	651	28	63.6	235	8	ADY75893	Ady75893 Plant ful
579	29	65.9	1090	5	AAU75360	Aau75360 Human hun	652	28	63.6	241	8	ADY12813	Ady12813 Plant ful
580	29	65.9	1090	7	ADB080345	Adb080345 Human MDD	653	28	63.6	247	8	ADY06264	Ady06264 Plant ful
581	29	65.9	1090	9	ADX98555	Adx98555 Human unc	654	28	63.6	250	8	ADN17546	Adn17546 Bacterial
582	29	65.9	1091	6	ABU54614	Abu54614 Human NOV	655	28	63.6	251	6	ABU39830	Abu39830 Protein e
583	29	65.9	1515	3	ABR97566	Abr97566 Novel hum	656	28	63.6	262	8	ADY09112	Ady09112 Plant ful
584	29	65.9	1763	8	ADL91599	Adl91599 Caenorhab	657	28	63.6	266	4	AA880279	Aa880279 Human pro
585	29	65.9	1869	4	ABBS8661	Abbs8661 Drosophil	658	28	63.6	266	4	AA864379	Aa864379 Amino aci
586	29	65.9	1996	2	AAW22607	Aaw22607 Platenoli	659	28	63.6	266	4	AAm39738	Aam39738 Human pol
587	29	65.9	1996	2	AAW23717	Aaw23717 Platenoli	660	28	63.6	267	8	ADY09260	Ady09260 Plant ful
588	29	65.9	3056	8	ADR43499	Adr43499 CSA-bind	661	28	63.6	268	6	ABU35585	Abu35585 Protein e
589	29	65.9	3076	8	ADQ26433	Adq26433 Mycobacte	662	28	63.6	270	5	AAE21324	Aae21324 Mouse Mrg
590	29	65.9	3076	8	ADR88328	Adr88328 Mycobacte	663	28	63.6	270	8	ADH08591	Adh08591 MrgB11. 3
591	29	65.9	4064	8	ADL98334	Adl98334 TRR-1, SE	664	28	63.6	271	4	AA898360	Aa898360 Cat SCF p
592	29	65.9	4545	2	AAW22611	Aaw22611 Hybrid sr	665	28	63.6	271	4	AAU02486	Aau02486 Cat SCF (
593	29	65.9	4550	2	AAW22606	Aaw22606 Platenoli	666	28	63.6	271	4	AA873573	Aa873573 Cat SCF (
594	29	65.9	4550	2	AAW23716	Aaw23716 Platenoli	667	28	63.6	271	4	AAU02772	Aau02772 Cat SCF (
595	28.5	64.8	101	4	AAU58380	Aau58380 Propionib	668	28	63.6	271	7	AAU05259	Aau05259 Cat stem
596	28.5	64.8	101	6	ABM54899	Abm54899 Propionib	669	28	63.6	271	7	ADf52480	Adf52480 Cat stem
597	28	63.6	14	2	AAU13429	Aau13429 N-termina	670	28	63.6	271	7	ABM85531	Abm85531 Human pro
598	28	63.6	14	2	AAU13428	Aau13428 N-termina	671	28	63.6	271	8	ADP99322	Adp99322 Cat stem
599	28	63.6	31	3	AA828317	Aa828317 Human sec	672	28	63.6	271	8	ADU50652	Adu50652 Cat stem
600	28	63.6	40	8	ABU18367	Abu18367 Breast ep	673	28	63.6	271	9	ADW93097	Adw93097 Cat stem
601	28	63.6	50	8	ADT39314	Adt39314 hSARS vir	674	28	63.6	271	9	ADZ47549	Adz47549 Cat stem
602	28	63.6	50	8	ADT78734	Adt78734 SARS viru	675	28	63.6	277	4	AA880305	Aa880305 Human pro
603	28	63.6	50	8	ADT36844	Adt36844 hSARS vir	676	28	63.6	277	4	AA880347	Aa880347 Human pro
604	28	63.6	61	4	AA89365	Aa89365 Human imm	677	28	63.6	282	7	ABM85530	Abm85530 Mouse pro
605	28	63.6	62	3	AA858819	Aa858819 Breast an	678	28	63.6	288	4	AA880343	Aa880343 Human pro
606	28	63.6	68	3	AA857116	Aa857116 Arabidops	679	28	63.6	289	4	AAm41524	Aam41524 Human pol
607	28	63.6	68	4	ABG03313	Abg03313 Novel hum	680	28	63.6	290	4	AA874471	Aa874471 Hevea bra
608	28	63.6	68	7	ADf60179	Adf60179 Human con	681	28	63.6	290	4	AA874470	Aa874470 Hevea bra

682	28	63.6	290	8	ADO54866	Ado54866 Para rubb	755	28	63.6	370	3	AAy70733	Aay70733 Human Wnt
683	28	63.6	290	8	ADO54867	Ado54867 Para rubb	756	28	63.6	370	6	ABU55882	Abu55882 Human WNT
684	28	63.6	290	9	ADV14249	Adv14249 Hevea bra	757	28	63.6	370	6	AAE34038	Aae34038 WNT-1 pro
685	28	63.6	292	6	ABU35185	Abu35185 Protein e	758	28	63.6	370	8	ADO08151	Ado08151 Human Wnt
686	28	63.6	296	8	ADs42674	Ads42674 Bacterial	759	28	63.6	370	8	ADO22214	Ado22214 Human WNT
687	28	63.6	299	9	ABM95717	Abm95717 M. xanthu	760	28	63.6	370	8	ADO49095	Ado49095 Human ded
688	28	63.6	301	6	ABU411204	Abu411204 Protein e	761	28	63.6	370	8	ADS31846	Ads31846 Mouse win
689	28	63.6	304	3	AAE57037	Aae57037 Human pro	762	28	63.6	370	8	ADU86428	Adu86428 Human win
690	28	63.6	304	8	ADL04486	Adl04486 M. catarr	763	28	63.6	370	9	ADV26372	Adv26372 Human Wnt
691	28	63.6	309	4	AAE67830	Aae67830 Amino aci	764	28	63.6	370	9	ADZ12508	Adz12508 Human can
692	28	63.6	309	7	ADD55762	Add55762 Thalecres	765	28	63.6	370	9	ADZ12505	Adz12505 Murine ca
693	28	63.6	309	7	ADD31067	Add31067 Plant tra	766	28	63.6	370	9	ADZ80631	Adz80631 Amino aci
694	28	63.6	309	8	ADI43805	Adi43805 Plant tra	767	28	63.6	370	9	ADZ80629	Adz80629 Amino aci
695	28	63.6	309	8	AD001745	Ad001745 Thalecres	768	28	63.6	370	9	ADZ71187	Adz71187 Mouse Wnt
696	28	63.6	309	9	AEA26639	Aea26639 Strees to	769	28	63.6	370	9	ADZ71185	Adz71185 Human Wnt
697	28	63.6	310	3	AAE20312	Aae20312 Arabidops	770	28	63.6	374	3	AAy77980	Aay77980 A. thalia
698	28	63.6	310	3	AAE38738	Aae38738 Arabidops	771	28	63.6	374	5	AAU75623	Aau75623 Chicken p
699	28	63.6	312	2	AAE97843	Aae97843 Kaposi's	772	28	63.6	374	6	ABG73575	Abg73575 Chicken p
700	28	63.6	312	2	AAE93605	Aae93605 Kaposi's	773	28	63.6	374	8	ADP29925	Adp29925 Human sec
701	28	63.6	312	4	ABR11044	Abri11044 Human APO	774	28	63.6	374	8	ADU92274	Adu92274 Thale cre
702	28	63.6	319	6	ADR07550	Adr07550 Alloiococ	775	28	63.6	375	2	AAW69888	Aaw69888 Chicken g
703	28	63.6	320	6	ABP60428	Abp60428 Potato pr	776	28	63.6	375	2	AAy33841	Aay33841 Amino aci
704	28	63.6	321	5	ABP51575	Abp51575 Human G p	777	28	63.6	375	2	AAy33937	Aay33937 Amino aci
705	28	63.6	321	7	ADl04275	Adl04275 Human G-p	778	28	63.6	375	2	AAy31192	Aay31192 Chicken G
706	28	63.6	323	6	ABO00535	Ab000535 Novel hum	779	28	63.6	375	4	AAE20133	Aae20133 Chicken g
707	28	63.6	324	5	ABP26378	Abp26378 Streptoco	780	28	63.6	375	5	AAE18662	Aae18662 Chicken p
708	28	63.6	324	8	ADV88921	Adv88921 Streptoco	781	28	63.6	375	6	ABG73561	Abg73561 Chicken p
709	28	63.6	324	8	ADV80174	Adv80174 Streptoco	782	28	63.6	375	6	ADA28702	Ada28702 Chicken m
710	28	63.6	324	8	ADV82302	Adv82302 Streptoco	783	28	63.6	375	8	ADM16475	Adm16475 Chicken p
711	28	63.6	325	5	ABE08771	Ab08771 Mouse G-p	784	28	63.6	375	8	ADM16498	Adm16498 Chicken p
712	28	63.6	327	6	ADY12330	Ady12330 Plant ful	785	28	63.6	376	2	AAW97118	Aaw97118 Human 26S
713	28	63.6	328	6	ABP57490	Abp57490 Mycobacte	786	28	63.6	376	3	AAy73429	Aay73429 Human sec
714	28	63.6	328	6	ADB07552	Adb07552 Alloiococ	787	28	63.6	376	6	ADA15587	Ada15587 A. thalia
715	28	63.6	331	7	ADF04464	Adf04464 Bacterial	788	28	63.6	376	7	ADE59046	Ade59046 Human Pro
716	28	63.6	331	8	ADx66533	Adx66533 Plant ful	789	28	63.6	376	7	ADE59044	Ade59044 Rat Prote
717	28	63.6	335	8	ADU66815	Adu66815 Mus muscu	790	28	63.6	376	8	ADO58710	Ado58710 Human reg
718	28	63.6	335	8	ADU66809	Adu66809 Human reg	791	28	63.6	376	8	ADO58710	Ado58710 Thalecres
719	28	63.6	336	8	ADU66808	Adu66808 Human reg	792	28	63.6	376	8	ABM81207	Abm81207 Tumour-as
720	28	63.6	337	5	ABG76775	Abg76775 Human G-p	793	28	63.6	376	8	ADs88344	Ads88344 Human pro
721	28	63.6	347	4	ABE69067	Ab69067 Drosophil	794	28	63.6	376	9	ADY70416	Ady70416 Human bet
722	28	63.6	347	4	ABE69067	Ab69067 Drosophil	795	28	63.6	376	9	AEA26745	Aea26745 Strees to
723	28	63.6	347	4	ABE69067	Ab69067 Drosophil	796	28	63.6	378	9	ADM04092	Adm04092 Human pro
724	28	63.6	348	7	ABU31804	Abu31804 Protein e	797	28	63.6	379	7	ABO78178	Ab078178 Pseudomon
725	28	63.6	352	6	ABO61072	Ab061072 Klebsiell	798	28	63.6	385	6	ABU65246	Abu65246 Novel hum
726	28	63.6	353	6	ABM69035	Abm69035 Phototrab	799	28	63.6	385	8	ADY07890	Ady07890 Plant ful
727	28	63.6	355	2	AAE48690	Aae48690 G-protein	800	28	63.6	386	2	AAE98521	Aae98521 Xenopus o
728	28	63.6	355	2	AAW02662	Aaw02662 G-protein	801	28	63.6	387	2	ADD71698	Add71698 Human uri
729	28	63.6	358	1	AAE90553	Aae90553 Muscarini	802	28	63.6	388	7	ADB84526	Adb84526 MSRV-1 po
730	28	63.6	358	7	ADC96406	Adc96406 E. faeciu	803	28	63.6	395	5	ABP73973	Abp73973 Candida a
731	28	63.6	358	8	ABM83349	Abm83349 Human dia	804	28	63.6	401	5	ABU20439	Abu20439 Protein e
732	28	63.6	358	8	ABM83350	Abm83350 Human dia	805	28	63.6	401	5	AAU77544	Aau77544 Murine re
733	28	63.6	359	4	ABE69924	Ab69924 Drosophil	806	28	63.6	403	5	AAE23220	Aae23220 Mouse rec
734	28	63.6	360	2	AAW19703	Aaw19703 Melanocor	807	28	63.6	403	7	AAE39511	Aae39511 Murine RA
735	28	63.6	360	2	AAW33723	Aaw33723 Human mel	808	28	63.6	406	6	ABU26682	Abu26682 Protein e
736	28	63.6	360	2	AAW79686	Aaw79686 Melanocor	809	28	63.6	412	9	ABM90514	Abm90514 M. xanthu
737	28	63.6	360	2	AAW92441	Aaw92441 Human MC3	810	28	63.6	418	9	ABM94824	Abm94824 M. xanthu
738	28	63.6	360	3	AAE18768	Aae18768 A human m	811	28	63.6	423	4	ABE68535	Ab68535 Drosophil
739	28	63.6	360	3	AAE18768	Aae18768 A human m	812	28	63.6	424	8	ADY22323	Ady22323 Plant ful
740	28	63.6	360	3	AAU05402	Aau05402 Melanocor	813	28	63.6	425	7	ADC96947	Adc96947 E. faeciu
741	28	63.6	360	4	AAE60969	Aae60969 Human MC3	814	28	63.6	425	7	ADC96947	Adc96947 E. faeciu
742	28	63.6	360	5	AAU95520	Aau95520 Human mel	815	28	63.6	428	8	ADN21346	Adn21346 Bacterial
743	28	63.6	360	6	ABP81836	Abp81836 Human mel	816	28	63.6	435	8	ADN21346	Adn21346 Bacterial
744	28	63.6	360	7	ADP64029	Adp64029 Human pro	817	28	63.6	445	6	ABU17231	Abu17231 Protein e
745	28	63.6	360	7	ADF72226	Adf72226 Human mel	818	28	63.6	445	6	ABU17231	Abu17231 Protein e
746	28	63.6	360	8	ADO29540	Ado29540 Human GPC	819	28	63.6	446	6	ADA36177	Ada36177 Acinetoba
747	28	63.6	360	8	ADQ39207	Adq39207 Human myo	820	28	63.6	449	8	ADs98822	Ads98822 Novel hum
748	28	63.6	360	9	ABE13432	Ab13432 Human MC3	821	28	63.6	449	8	ADs98075	Ads98075 Protein f
749	28	63.6	364	5	ABR08180	Ab08180 mRNA Guan	822	28	63.6	449	8	ADY23497	Ady23497 Plant ful
750	28	63.6	364	8	ADX71651	Adx71651 Plant ful	823	28	63.6	454	6	ADB09266	Adb09266 Alloiococ
751	28	63.6	369	8	ABM83418	Abm83418 Human dia	824	28	63.6	455	6	ADB09266	Adb09266 Alloiococ
752	28	63.6	370	2	AAy56108	Aay56108 Human int	825	28	63.6	456	4	AAW41537	Aaw41537 Human pol
753	28	63.6	370	3	AAE19786	Aae19786 Human Wnt	826	28	63.6	456	7	ADL21693	Adl21693 Human hum
754	28	63.6	370	3	AAy57594	Aay57594 Human Wnt	827	28	63.6	456	8	ADS98663	Ads98663 Protein f

828	28	63.6	458	8	ADP47887	Adp47887 Human CAT	901	28	63.6	749	4	AAB955181	Aab955181 Human pro
829	28	63.6	460	8	ADN22515	Adn22515 Bacterial	902	28	63.6	754	4	AAB95512	Aab95512 Human pro
830	28	63.6	466	3	AAy83044	Aay83044 F-box pro	903	28	63.6	758	4	AAU28071	Aau28071 Novel hum
831	28	63.6	466	6	AAU57684	Aau57684 Propionib	904	28	63.6	764	8	ADJ19401	Adj19401 Human NAL
832	28	63.6	466	6	ABM54203	Abm54203 Propionib	905	28	63.6	776	8	ADT49828	Adt49828 Murine IN
833	28	63.6	468	4	AAB96526	Aab96526 Putative	906	28	63.6	787	7	ADM05088	Adm05088 Human pro
834	28	63.6	469	9	ADV97864	Adv97864 Murine pr	907	28	63.6	793	5	AAE14781	Aae14781 Human imm
835	28	63.6	470	7	ADJ71007	Adj71007 Human hea	908	28	63.6	794	7	AEA90304	Aea90304 Human NOV
836	28	63.6	471	4	ABB65957	Abb65957 Drosophil	909	28	63.6	795	4	ADJ28114	Adj28114 Human NTR
837	28	63.6	472	5	AAC22449	Aac22449 Human F-b	910	28	63.6	814	7	AEA90306	Aea90306 Human NOV
838	28	63.6	472	9	ADY62365	Ady62365 Human F-b	911	28	63.6	814	9	ADY53753	Ady53753 Human imm
839	28	63.6	484	4	AAm39751	Aam39751 Human pol	912	28	63.6	817	4	ABM66979	Abm66979 Drosophil
840	28	63.6	484	7	ADM04681	Adm04681 Human pro	913	28	63.6	838	4	AAB95216	Aab95216 Human pro
841	28	63.6	486	8	ADY09545	Ady09545 Plant ful	914	28	63.6	840	6	ABU12317	Abu12317 Human PAT
842	28	63.6	489	4	ABG03185	Abg03185 Novel hum	915	28	63.6	846	5	ABP66206	Abp66206 Bifidobac
843	28	63.6	494	7	ABM90463	Abm90463 Rice abio	916	28	63.6	849	8	ADG21682	Adg21682 Bacterial
844	28	63.6	494	8	ADM48226	Adm48226 Polypepti	917	28	63.6	858	6	ABU22856	Abu22856 Protein e
845	28	63.6	496	6	ABU40961	Abu40961 Protein e	918	28	63.6	873	6	ABU12305	Abu12305 Human PAT
846	28	63.6	498	6	ABU50353	Abu50353 Protein e	919	28	63.6	886	9	AEA20278	Aea20278 Novel hum
847	28	63.6	512	3	AAB20573	Aab20573 Torenia h	920	28	63.6	890	8	ADJ57061	Adj57061 Human kar
848	28	63.6	514	4	ABM64398	Abm64398 Drosophil	921	28	63.6	890	8	ADP24044	Adp24044 PRO polyp
849	28	63.6	517	8	ADH61298	Adh61298 INTSIG pr	922	28	63.6	890	9	ADY18452	Ady18452 PRO polyp
850	28	63.6	520	8	ADS25003	Ads25003 Bacterial	923	28	63.6	890	9	ADY20315	Ady20315 PRO polyp
851	28	63.6	521	4	AAE04933	Aae04933 Human tra	924	28	63.6	893	7	ADD45197	Add45197 Human pro
852	28	63.6	529	2	AAy37027	Aay37027 Chlamydia	925	28	63.6	896	3	AAy92943	Aay92943 Rat MAGUI
853	28	63.6	529	4	ABM12368	Abm12368 Human bon	926	28	63.6	897	9	ADD45195	Add45195 Rat Prote
854	28	63.6	539	7	ADD43754	Add43754 Chlamydia	927	28	63.6	897	9	AEA20277	Aea20277 Novel hum
855	28	63.6	539	9	AEA19046	Aea19046 Chlamydia	928	28	63.6	898	4	ABG12152	Abg12152 Novel hum
856	28	63.6	540	6	ABU27721	Abu27721 Protein e	929	28	63.6	898	7	ADD42094	Add42094 Human MAG
857	28	63.6	542	7	ADP06579	Adp06579 Bacterial	930	28	63.6	911	6	ABU12308	Abu12308 Human PAT
858	28	63.6	552	6	ABP81972	Abp81972 Human KIA	931	28	63.6	927	4	ABG15257	Abg15257 Novel hum
859	28	63.6	552	7	ADC37441	Adc37441 Nuclear f	932	28	63.6	945	7	ABG15257	Abg15257 Novel hum
860	28	63.6	561	4	ABM66868	Abm66868 Drosophil	933	28	63.6	954	8	AAO13894	Aao13894 Human hea
861	28	63.6	561	4	ABM65492	Abm65492 Drosophil	934	28	63.6	954	8	ADM87806	Adm87806 Human EST
862	28	63.6	580	9	ABM97478	Abm97478 M. xanthu	935	28	63.6	954	9	AEA21090	Aea21090 Novel hum
863	28	63.6	587	4	AAm39752	Aam39752 Human pol	936	28	63.6	954	9	AEA21091	Aea21091 Novel hum
864	28	63.6	589	8	ADO29254	Ado29254 Mouse GPC	937	28	63.6	969	6	ABU12301	Abu12301 Human PAT
865	28	63.6	590	1	AAp96204	Aap96204 Human mus	938	28	63.6	979	4	ABM63728	Abm63728 Drosophil
866	28	63.6	590	4	AAm93244	Aam93244 Human pol	939	28	63.6	1009	6	ABU12312	Abu12312 Human PAT
867	28	63.6	590	4	AAE01972	Aae01972 Human cho	940	28	63.6	1016	6	ABU12311	Abu12311 Human PAT
868	28	63.6	590	4	AAE01970	Aae01970 Human cho	941	28	63.6	1025	6	ABR53367	Abr53367 Protein s
869	28	63.6	590	4	AAE01971	Aae01971 Human cho	942	28	63.6	1025	7	ADK63360	Adk63360 Disease t
870	28	63.6	590	4	AAE01973	Aae01973 Human cho	943	28	63.6	1026	5	ABB07497	Abb07497 Human lip
871	28	63.6	590	4	AAE01974	Aae01974 Human cho	944	28	63.6	1032	3	AAy92942	Aay92942 Rat MAGUI
872	28	63.6	590	4	AAE01976	Aae01976 Human cho	945	28	63.6	1032	6	ADD42093	Add42093 Human MAG
873	28	63.6	590	4	AAE01977	Aae01977 Human cho	946	28	63.6	1042	7	ABU30090	Abu30090 Protein e
874	28	63.6	590	4	AAE01975	Aae01975 Human cho	947	28	63.6	1044	7	ADC95602	Adc95602 E. faeciu
875	28	63.6	590	4	ABM56362	Abm56362 Non-endog	948	28	63.6	1048	7	ADC10174	Adc10174 Human NOV
876	28	63.6	590	6	ABM99724	Abm99724 Amino aci	949	28	63.6	1048	7	ABO60699	AbO60699 Klebsiell
877	28	63.6	590	7	ADK52582	Adk52582 Hematolog	950	28	63.6	1095	2	AAW80359	Aaw80359 An F-acti
878	28	63.6	590	8	ADL30644	Adl30644 Human pro	951	28	63.6	1096	6	ADP55479	Adp55479 Human str
879	28	63.6	590	8	ADO29253	Ado29253 Human GPC	952	28	63.6	1096	8	ADP55479	Adp55479 Human PRO
880	28	63.6	590	8	ABG03923	Abg03923 Novel hum	953	28	63.6	1098	6	ABO07120	AbO07120 Novel hum
881	28	63.6	594	4	ABG03923	Abg03923 Novel hum	954	28	63.6	1142	7	ADJ68817	Adj68817 Human hea
882	28	63.6	600	7	ADK14951	Adk14951 Urinary s	955	28	63.6	1142	8	ADT04110	Adt04110 Novel hum
883	28	63.6	604	8	ADP04455	Adp04455 Sea squir	956	28	63.6	1177	4	ABG15256	Abg15256 Novel hum
884	28	63.6	612	4	ABM65727	Abm65727 Drosophil	957	28	63.6	1204	8	ABM80800	Abm80800 Tumour-as
885	28	63.6	612	8	ADS96420	Ads96420 Drosophil	958	28	63.6	1204	9	ADY18010	Ady18010 PRO polyp
886	28	63.6	626	5	ABG31501	Abg31501 Hydrophob	959	28	63.6	1204	9	ADY18008	Ady18008 PRO polyp
887	28	63.6	627	8	ADS44707	Ads44707 Bacterial	960	28	63.6	1221	7	ADC94332	Adc94332 E. faeciu
888	28	63.6	630	4	AAb94610	Aab94610 Human pro	961	28	63.6	1227	7	ABB64208	Abb64208 Drosophil
889	28	63.6	637	7	ADM04513	Adm04513 Human pro	962	28	63.6	1274	6	ABO14653	AbO14653 Novel hum
890	28	63.6	645	4	ABM95795	Abm95795 Human pro	963	28	63.6	1397	4	AAy72670	Aay72670 Human NB-
891	28	63.6	646	9	ADY53755	Ady53755 Partial h	964	28	63.6	1408	8	ADK43753	Adk43753 Bacterial
892	28	63.6	655	6	ABU25241	Abu25241 Protein e	965	28	63.6	1424	4	AAy72674	Aay72674 Human NAC
893	28	63.6	668	4	AAU94215	Aau94215 Human pro	966	28	63.6	1428	4	ABG25753	Abg25753 Novel hum
894	28	63.6	671	5	ABM92516	Abm92516 Herbicida	967	28	63.6	1429	4	ABG62571	Abg62571 Human cas
895	28	63.6	677	9	ADY53756	Ady53756 Human neu	968	28	63.6	1429	5	ABG78455	Abg78455 Human CAR
896	28	63.6	681	7	ABO76944	AbO76944 Pseudomon	969	28	63.6	1429	5	ABG78472	Abg78472 Leucine-r
897	28	63.6	688	8	ADS11000	Ads11000 Human the	970	28	63.6	1429	5	ABB77916	Abb77916 Human leu
898	28	63.6	693	5	ABM90351	Abm90351 Human pol	971	28	63.6	1429	5	ABG97969	Abg97969 Human leu
899	28	63.6	717	8	ADU82857	Adu82857 Ligand up	972	28	63.6	1429	5	AAO17855	Aao17855 Pyrin dom
900	28	63.6	740	7	ABO66484	AbO66484 Klebsiell	973	28	63.6	1429	6	ABG71631	Abg71631 Human cas

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974 28 63.6 1429 6 ABP96889 Human cas
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976 28 63.6 1429 6 ABG71633 Human cas
977 28 63.6 1429 8 ADP12612 Protein e
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979 28 63.6 1429 8 ADP19826 Human PRO
980 28 63.6 1436 4 ABB68323 Drosophi
981 28 63.6 1442 4 AAY72671 Human NB-
982 28 63.6 1454 4 AAY72673 Human NAC
983 28 63.6 1473 4 AA06758 Human G-p
984 28 63.6 1473 4 AAY72669 Human NB-
985 28 63.6 1473 4 AAY72711 Human NAC
986 28 63.6 1473 8 AD019755 Human PRO
987 28 63.6 1473 8 ADP54962 Human PRO
988 28 63.6 1473 8 ADP24374 PRO poly
989 28 63.6 1473 9 ADV04710 Mutant NA
990 28 63.6 1473 9 ADV04711 Mutant NA
991 28 63.6 1473 9 ADV04709 Mutant NA
992 28 63.6 1473 9 ADV04679 NALP1, SE
993 28 63.6 1648 3 AAB43174 Human ORF
994 28 63.6 1654 4 ABB12450 Human bon
995 28 63.6 1867 4 AAB95564 Human pro
996 28 63.6 2214 9 ABM96789 M. xanthu
997 28 63.6 2626 8 ADK67822 Human BRC
998 28 63.6 3338 4 ABG09919 Novel hum
999 28 63.6 4829 4 AAB97833 Human apo
1000 28 63.6 9893 9 AEB00347 SARS coro
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## ALIGNMENTS

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RESULT 1
ID ABB08361 standard; protein; 9 AA.
XX ABB08361;
XX
XX 07-MAY-2002 (first entry)
XX
XX Synthetic epitope 1 of human cancer antigen eIF3.
XX Human; melanoma antigen eukaryotic initiation factor 3; eIF3;
XX ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;
XX anti-cancer; vaccine.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
FH Domain 1 /note= "HLA-2 binding residue"
FT Domain 2 /note= "HLA-2 binding residue"
FT Domain 3. .8 /note= "HLA-2 binding residue"
FT Domain 9 /note= "T-cell receptor (TCR) binding domain"
FT Domain /note= "HLA-2 binding residue"
XX
XX WO200192307-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US017456.
XX
XX 31-MAY-2000; 2000US-0209391P.
XX 17-AUG-2000; 2000US-0226258P.
XX 20-DEC-2000; 2000US-0257008P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Nicolette CA;
XX
XX WPI; 2002-139606/18.
XX
XX
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XX New therapeutic compounds useful against human ovarian cancer, for
PT modulating immune response in a subject, and for generating antibodies
PT that specifically recognize and bind to these molecules.
XX
XX Claim 29; Page 59; 68pp; English.
XX
XX The invention relates to novel therapeutic compounds, that are designed
CC to enhance binding to MHC molecules and to enhance immunoregulatory
CC properties relative to their natural counterparts. The activity of the
CC compounds of the invention may be described as cytostatic and
CC immunomodulatory. The compounds are useful against human ovarian cancer,
CC for modulating immune response in a subject, and for generating
CC antibodies that specifically recognize and bind to these molecules.
CC Compositions comprising the compounds are useful as components of anti-
CC cancer vaccines and to expand immune effector cells that are specific for
CC cells characterised by expression of antigen eIF3 (melanoma antigen
CC eukaryotic initiation factor). The peptides or polypeptides conjugated to
CC a detectable agent may be used in diagnostic procedures, such as in the
CC detection and purification of antibodies, and as immunogens for
CC production of antibodies. The polynucleotides can be used as primers for
CC detecting genes or gene transcripts expressed in APC to confirm
CC transduction of the polynucleotides into host cells. The current sequence
XX represents synthetic epitope 1 of human cancer antigen eIF3
XX
XX Sequence 9 AA;
SQ
XX
XX Query Match 100.0%; Score 44; DB 5; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FLQLLMEPV 9
XX DB 1 FLQLLMEPV 9
XX
XX RESULT 2
XX ABR82213
XX ID ABR82213 standard; peptide; 9 AA.
XX
XX AC ABR82213;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human antigen eIF3 derived compound 1.
XX
XX Eukaryotic translation initiation factor 3; eIF3; neoplasia; cancer;
XX cytostatic; gene therapy; human; antigen.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003050543-A1.
XX
XX 19-JUN-2003.
XX
XX 05-DEC-2001; 2001WO-US047997.
XX
XX 05-DEC-2001; 2001WO-US047997.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Nicolette CA;
XX
XX WPI; 2003-532936/50.
XX N-PSDB; ACC85030.
XX
XX Aiding in the diagnosis of a neoplastic condition, useful for treating
PT cancer and related malignancies comprises determining the amount of
PT expression of an eIF3 protein in a test sample isolated from the cell or
PT tissue.
XX
XX Claim 12; Page 30; 77pp; English.
XX
XX
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XX The invention relates to aiding in the diagnosis of a neoplastic  
 CC condition or susceptibility to a neoplastic condition of an animal cell  
 CC or tissue. The method involves determining the amount of expression of an  
 CC eukaryotic translation initiation factor 3 (eIF3) protein in a test  
 CC sample isolated from the cell or tissue, and diagnosing a neoplastic  
 CC condition or susceptibility to a neoplastic condition based on the amount  
 CC of expression of the eIF3 protein. The methods, compounds and kits are  
 CC useful in therapeutics, diagnostics and screening methods for human cancer  
 CC and related malignancies, e.g. ovarian, breast, lung, colon, prostate,  
 CC pancreatic or gastrointestinal cancer, or melanoma. Sequences ABR82213-16  
 CC represent compounds derived from the human antigen eIF3

SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9  
 |||||  
 Db 1 FLQLLMEPV 9

RESULT 3  
 ABB08366  
 ID ABB08366 standard; protein; 352 AA.

AC ABB08366;

XX 07-MAY-2002 (first entry)

XX Human cancer antigen eIF3 variant 1 amino acid sequence.

XX Human; melanoma antigen eukaryotic initiation factor 3; eIF3;  
 KW ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;  
 KW anti-cancer; vaccine.

XX Homo sapiens.

Key Location/Qualifiers  
 FT Misc-difference 242 /note= "wild-type Asn is replaced by Phe"  
 FT Domain 242 /note= "HLA-2 binding residue"  
 FT Domain 243 /note= "HLA-2 binding residue"  
 FT Domain 244..249 /note= "T-cell receptor (TCR) binding domain"  
 FT Misc-difference 248 /note= "wild-type Asp is replaced by Glu"  
 FT Misc-difference 249 /note= "wild-type Arg is replaced by Pro"  
 FT Domain 250 /note= "HLA-2 binding residue"

XX WO200192307-A2.

XX 06-DEC-2001.

XX 30-MAY-2001; 2001WO-US017456.

XX 31-MAY-2000; 2000US-0209391P.

XX 17-AUG-2000; 2000US-0226258P.

XX 20-DEC-2000; 2000US-0257008P.

XX (GENZ ) GENZYME CORP.

XX Nicolette Ca;

XX WPI; 2002-139606/18.

XX New therapeutic compounds useful against human ovarian cancer, for

PT modulating immune response in a subject, and for generating antibodies  
 PT that specifically recognize and bind to these molecules.

PS Claim 6; Page; 68pp; English.

XX The invention relates to novel therapeutic compounds, that are designed  
 CC to enhance binding to MHC molecules and to enhance immunoregulatory  
 CC properties relative to their natural counterparts. The activity of the  
 CC compounds of the invention may be described as cytostatic and  
 CC immunomodulatory. The compounds are useful against human ovarian cancer,  
 CC for modulating immune response in a subject, and for generating  
 CC antibodies that specifically recognize and bind to these molecules.  
 CC Compositions comprising the compounds are useful as components of anti-  
 CC cancer vaccines and to expand immune effector cells that are specific for  
 CC cells characterized by expression of antigen eIF3 (melanoma antigen  
 CC eukaryotic initiation factor). The peptides or polypeptides conjugated to  
 CC a detectable agent may be used in diagnostic procedures, such as in the  
 CC detection and purification of antibodies, and as immunogens for  
 CC production of antibodies. The polynucleotides can be used as primers for  
 CC detecting genes or gene transcripts expressed in APC to confirm  
 CC transduction of the polynucleotides into host cells. The current sequence  
 CC represents the human cancer antigen eIF3 variant 1 amino acid sequence.  
 CC Note: This sequence is not present in the specification, but may be  
 CC created from the sequence of the wild-type human cancer antigen eIF3  
 CC sequence given in ABB08366

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 44; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9  
 |||||  
 Db 242 FLQLLMEPV 250

RESULT 4

AAU22301

ID AAU22301 standard; protein; 67 AA.

XX AAU22301;

XX 18-DEC-2001 (first entry)

XX Human cardiovascular system antigen polypeptide SEQ ID No 1075.

KW Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;  
 KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;  
 KW antirheumatic; antiproliferative; cytostatic; cardiac; neuroprotective;  
 KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;  
 KW ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;  
 KW hyperproliferative disorder; breast; liver; cardiovascular disorder;  
 KW cerebrovascular disorder; nervous system disorder; bacterial infection;  
 KW fungal infection; viral infection; ocular disorder; endocrine disorder;  
 KW gastrointestinal disorder; renal disorder; respiratory disorder;  
 KW wound healing; skin aging; organ transplantation; tissue regeneration;  
 KW anti-infertility.

XX Homo sapiens.

XX WO200155321-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001340.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184564P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
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PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
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PR 12-SEP-2000; 2000US-0231968P.  
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PR 13-OCT-2000; 2000US-0239937P.

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PR 08-NOV-2000; 2000US-0246525P.  
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PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-451930/48.

N-PSDB; AAS35575.

XX New cardiovascular system related polynucleotides and polypeptides,  
PT useful for diagnosing, treating and/or preventing disorders of the  
XX cardiovascular system.

PS Claim 11; SEQ ID NO 1075; 674pp; English.

XX Sequences AAU21852-AAU22466 represent the cardiovascular system antigen  
CC polypeptides of the invention. Cardiovascular system antigens and their

CC associated polynucleotides are useful in the diagnosis, treatment and  
CC prevention of various types of disorders in e.g. humans, mice, rabbits,  
CC goats, horses, cats, dogs, chickens or sheep. A pathological condition  
CC can be determined by detecting the presence or absence of a mutation in a  
CC cardiovascular system antigen polynucleotide. The treatable disorders  
CC include autoimmune diseases such as rheumatoid arthritis,  
CC hyperproliferative disorders such as neoplasms of the breast or liver,  
CC cardiovascular disorders such as cardiac arrest, cerebrovascular  
CC disorders such as cerebral ischaemia, nervous system disorders such as  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,  
CC ocular disorders such as corneal infection, endocrine disorders such as  
CC premature labour and infertility, gastrointestinal disorders such as  
CC Crohn's disease, renal disorders such as glomerulonephritis and  
CC respiratory disorders such as asthma and pleurisy. The polypeptides can  
CC also be used to aid wound healing, to prevent skin aging due to sunburn,  
CC to maintain organs before transplantation, to regenerate tissues and in  
CC chemotaxis. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Query Match 79.5%; Score 35; DB 4; Length 67;  
Best Local Similarity 77.8%; Pred. No. 18;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9  
|||: ||  
Db 7 FLQLLTPV 15

RESULT 5  
AD546269  
ID ADE46269 standard; protein; 67 AA.

AC ADE46269;

XX 29-JAN-2004 (first entry)

XX Human cardiovascular system related polypeptide #450.

XX Human; cardiovascular system related polypeptide; cancer;  
KW proliferative disorder; foetal abnormality; developmental abnormality;  
KW haematopoietic disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
KW gastrointestinal disorder; pregnancy-related disorder;  
KW endocrine disorder.

XX Homo sapiens.

XX US2003059908-A1.

XX 27-MAR-2003.

XX 07-MAR-2002; 2002US-00091504.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 11-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.  
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PR 14-AUG-2000; 2000US-0224518P.  
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PR 14-AUG-2000; 2000US-0225447P.  
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PR 01-SEP-2000; 2000US-0229343P.  
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PR 05-SEP-2000; 2000US-0229509P.  
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PR 06-SEP-2000; 2000US-0230437P.  
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PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
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PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0232081P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
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PR 21-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
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PR 27-SEP-2000; 2000US-0235834P.  
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PR 29-SEP-2000; 2000US-0236327P.  
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PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
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PR 13-OCT-2000; 2000US-023937P.  
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PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.  
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PR 08-NOV-2000; 2000US-0246476P.  
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PR 08-NOV-2000; 2000US-0246610P.  
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PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
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PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
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PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
PR 17-JAN-2001; 2001US-00764869.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX PI Rosen CA, Ruben SM, Barash SC;  
XX  
XX WPI: 2003-743766/70.  
XX N-PSDB; ADE45654.  
XX  
XX New cardiovascular system related polynucleotides and polypeptides,  
PT useful for preventing, treating, or ameliorating a medical condition,  
PT such as cancer of cardiovascular tissues and cancer metastases.  
XX  
XX Claim 11; SEQ ID NO 1075; 262pp; English.  
XX  
XX The invention relates to human cardiovascular system related polypeptides  
CC and the polynucleotides encoding them. The polypeptides, polynucleotides  
CC and antibodies to the polypeptides are useful for diagnosing a  
CC pathological condition or a susceptibility to a pathological condition,  
CC for preventing, treating, or ameliorating a medical condition, such as  
CC cancer of cardiovascular system tissues, proliferative disorders, foetal  
CC and developmental abnormalities, haematopoietic disorders, diseases of  
CC the immune system, AIDS, autoimmune diseases (e.g., rheumatoid  
CC arthritis), inflammation, allergies, neurological disorders (e.g.,  
CC Alzheimer's disease, Parkinson's disease), cognitive disorders,

CC schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis,  
CC diabetes, atherosclerosis, cardiovascular disorders, angiogenic  
CC disorders, kidney disorders, gastrointestinal disorders, pregnancy-  
CC related disorders, endocrine disorders and infections. The nucleic acids  
CC are also useful for chromosome identification, radiation hybrid mapping  
CC or long-range restriction mapping. The polypeptides and polynucleotides  
CC may also be used as food additives or preservatives to increase or  
CC decrease storage capabilities, fat content or other nutritional  
CC components. This sequence represents a human cardiovascular system  
CC related polypeptide of the invention.

XX Sequence 67 AA;

Query Match 79.5%; Score 35; DB 7; Length 67;  
Best Local Similarity 77.8%; Pred. No. 18;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
|||:|  
DB 7 FLQLLLTPV 15

RESULT 6

ADJ07687

ID ADJ07687 standard; protein; 67 AA.

XX AC ADJ07687;

XX DT 04-NOV-2004 (first entry)

XX DE Human cardiovascular system associated polypeptide SeqID1075.

XX KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;  
KW breast neoplasms; liver neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; cerebral ischaemia;  
KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;  
KW ocular disorder; corneal infection; wound healing;  
KW epithelial cell proliferation; skin aging; sunburn;  
KW organ transplantation; cell culture; tissue regeneration; chemotaxis;  
KW food additive; preservative; cardiovascular system associated antigen;  
KW nuclear factor kappaB; NfkappaB; promoter element; human.

XX OS Homo sapiens.

XX XX US2004005575-A1.

XX XX 08-JAN-2004.

XX XX 26-AUG-2002; 2002US-00227577.

XX XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

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PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

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PR 14-AUG-2000; 2000US-0225267P.  
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PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
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PR 23-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231124P.  
PR 08-SEP-2000; 2000US-02311243P.  
PR 08-SEP-2000; 2000US-02311244P.  
PR 08-SEP-2000; 2000US-0231141P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
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PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
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PR 08-NOV-2000; 2000US-0246526P.  
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PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
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PR 17-NOV-2000; 2000US-0249209P.  
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PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
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PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
PR 17-JAN-2001; 2001US-0076486P.  
PR 07-MAR-2002; 2002US-00091504.  
XX  
(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Ruben SM, Barash SC;  
WPI; 2004-081713/08.  
N-PSDB; ADJ07072.  
New cardiovascular system-related nucleic acid molecule, useful for  
diagnosing, preventing or treating diseases of the cardiovascular system,  
and in chromosome mapping, drug screening or in pharmacogenomics.  
Claim 11; SEQ ID NO 1075; 262pp; English.  
The invention relates to an isolated nucleic acid molecule encoding a  
human cardiovascular system associated polypeptide (or antigens), or its  
fragment. Also included recombinant vectors, recombinant host cells, an  
isolated human cardiovascular system associated polypeptide (including  
its fragment, allelic variant, species homologue or epitope), an isolated  
antibody that binds specifically to a human cardiovascular system  
associated polypeptide, diagnosing a pathological condition or  
susceptibility to a pathological condition (comprising determining the  
presence or absence of a mutation in human cardiovascular system  
associated nucleic acid and diagnosing a condition based on the presence  
or absence of the mutation), identifying a binding partner to human  
cardiovascular system associated polypeptides, the gene corresponding to  
the human cardiovascular system associated cDNA sequence and identifying  
an activity in a biological assay comprising expressing the human  
cardiovascular system associated cDNA in a cell, isolating the  
supernatant, detecting an activity in a biological assay and identifying  
the protein in the supernatant having the activity. The human

CC cardiovascular system associated nucleic acids and polypeptides are used  
CC to prevent, treat or ameliorate a medical condition (for example in  
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep), for  
CC example autoimmune diseases such as rheumatoid arthritis,  
CC hyperproliferative disorders, for example neoplasms of the breast or

Query Match 79.5%; Score 35; DB 8; Length 67;  
Best Local Similarity 77.8%; Pred. No. 18;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMPEV 9  
Db 7 FLQLLTPV 15

RESULT 7  
ABB99785  
ID ABB99785 standard; protein; 329 AA.

XX AC ABB99785;

XX DT 24-MAR-2003 (first entry)

XX DE Amino acid sequence of canine PXR ligand binding domain.

XX KW Pregnane X nuclear receptor; PXR; P450 3A4 monooxygenase;  
XX drug metabolism.

XX OS Canis sp.

XX PN WO200294865-A1.

XX PD 28-NOV-2002.

XX PF 24-MAY-2002; 2002WO-US016445.

XX PR 24-MAY-2001; 2001US-0293380P.

XX PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX PI Klier SA, Maglich JM, Moore JT, Moore LB, Willson TM;

XX DR WPI; 2003-148458/14.

XX DR N-PSDB; AB223279.

XX PT New pregnane X nuclear receptor polypeptide that modulate P450 3A4 levels  
or activity, useful in comparative pharmacology and for selecting  
PT appropriate pre-clinical animal models predictive of human PXR activity.

XX PS Claim 1; Page 47-48; 56pp; English.

XX CC The present sequence is a pregnane X nuclear receptor (PXR) ligand  
binding domain. PXR polypeptides modulate P450 3A4 monooxygenase levels  
or activity. P450 3A4 catalyses the metabolism of more than 60% of all  
CC drugs that are in use, including steroids, immunosuppressive agents,  
CC imidazole antimycotics, and macrolide antibiotics. The polypeptide is  
CC useful in comparative pharmacology and for selecting appropriate pre-  
CC clinical animal models predictive of human PXR activity

XX SQ Sequence 329 AA;

Query Match 79.5%; Score 35; DB 6; Length 329;  
Best Local Similarity 77.8%; Pred. No. 94;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMPEV 9  
Db 210 FQQLLEFPV 218

RESULT 8  
ABP53033

ID ABP53033 standard; protein; 307 AA.

XX ABP53033;  
AC 06-NOV-2002 (first entry)  
DT C. elegans RNase H homologous protein sequence SEQ ID NO:3.  
DE RNase H; antisense technology; inhibition.

XX KW Caenorhabditis elegans.

XX OS WO200264841-A1.

XX PN 22-AUG-2002.

XX PD 12-FEB-2002; 2002WO-US004243.

XX PF 12-FEB-2001; 2001US-00781712.

XX PR (ISIS-) ISIS PHARM INC.

XX PA Crooke ST, Lima WF, Wu H;

XX PI WPI; 2002-657606/70.

XX DR Use of a mammalian, particularly human, RNase H, for treating an animal  
with a disease or condition associated with a human RNase H, for  
inhibiting the expression of a protein, or for reducing cellular RNA via  
antisense technology.

XX PS Example 1; Fig 1; 70pp; English.

XX CC The present invention describes a method for promoting the inhibition of  
the expression of a protein comprising employing a mammalian RNase H  
polypeptide so that cleavage of an RNA strand of an oligonucleotide-RNA  
complex duplex occurs. Also described is a compound 8 to 50 nucleobases  
in length targeted to the nucleic acid encoding the human RNase HII  
polypeptide, where the compound specifically hybridises with and inhibits  
the expression of a human RNase HII polypeptide. The compound, which is  
an antisense oligonucleotide, is useful for inhibiting the expression of  
a human RNase HII polypeptide in cells or tissues, as well as for  
treating an animal with a disease or condition associated with a human  
RNase HII polypeptide. The method is useful for inhibiting the expression  
of a protein, particularly for reducing cellular RNA via antisense  
technology. The present sequence represents a protein sequence given in  
comparison with the human RNase HII protein sequence, given in the  
exemplification of the present invention

XX SQ Sequence 307 AA;

Query Match 77.3%; Score 34; DB 5; Length 307;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMPEV 9

Db 227 FLQLSVEPV 235

RESULT 9

ADV69954

ID ADV69954 standard; protein; 307 AA.

XX AC ADV69954;

XX DT 24-FEB-2005 (first entry)

XX DE Nematode RNase H2 protein.

XX KW Mammalian RNase H; RNase H1; RNase H2; gene expression;  
antisense technology; enzyme.

XX OS Caenorhabditis elegans.



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PR 16-AUG-1996; 96US-0024022P.
PA (SMK ) SMITHKLINE BEECHAM CORP.
XX Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;
PI Stodola RK;
XX WPI: 1998-159452/14.
DR N-PSDB; AA296294.
XX Streptococcus pneumoniae proteins and related DNA - useful for screening
  compounds for antibacterial activity.
XX Claim 5; Page 430-431; 640pp; English.
XX This invention describes novel isolated Streptococcus pneumoniae
  polynucleotides (see AA296173-296494) and their encoded proteins (see
  AA295792-296182). The DNA, vectors and host cells described in the method
  of the invention are useful for the recombinant expression of the
  CC polypeptides. The polypeptides are useful for treatment or prevention of
  CC disease, or diagnosis of disease related to expression or activity of
  CC such a polypeptide. They can also be used to screen for compounds which
  CC interact with and inhibit or activate such a polypeptide. The
  CC polypeptides (or DNA encoding them, via gene therapy) are also useful for
  CC inducing an immunological response in a mammal. The antagonists are
  CC useful to inhibit such bacterial polypeptides. The polypeptides are
  CC particularly useful to identify antimicrobial compounds and antibiotics.
  CC They are also useful to determine their role in pathogenesis of
  CC infection, dysfunction and disease
XX Sequence 318 AA;

Query Match 77.3%; Score 34; DB 2; Length 318;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLMEP 8
Db 152 FLQVLMDP 159

RESULT 12
ABG61495
ID ABG61495 standard; protein; 318 AA.
XX
XX ABG61495;
XX 07-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Iron uptake ABC transporter polypeptide #2.
XX
XX Iron uptake ABC transporter; Streptococcal iron transporter; Sit;
KW antimicrobial; antibacterial; veterinary treatment; passive immunisation.
XX
XX Salmonella sp.
OS
XX WO200234773-A2.
PN
XX 02-MAY-2002.
PD
XX
XX 26-OCT-2001; 2001WO-GB004749.
PF
XX
XX 26-OCT-2000; 2000GB-00026231.
PR
XX 21-NOV-2000; 2000GB-00028345.
PR
XX 02-FEB-2001; 2001GB-00002656.
PR
XX 02-MAY-2001; 2001US-0288118P.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA
XX Holden DW, Brown JS;
PI
XX WPI: 2002-463352/49.
XX

DR N-PSDB; ABK83158.
XX Novel Streptococcus pneumoniae iron uptake ABC transporter peptide,
PT useful in screening assay for identifying antimicrobial drug and in
PT diagnostic assay for detecting streptococcal microorganism.
XX
XX PS Disclosure; Page 51-52; 159pp; English.
XX The invention relates to a Streptococcus pneumoniae iron uptake ABC
  transporter peptide called Streptococcal iron transporter (Sit) and the
  CC polynucleotide encoding it. The sequences are useful for therapeutic or
  CC diagnostic purposes, in screening assays for the identification of an
  CC antimicrobial drug, and in diagnostic assays for the detection of a
  CC streptococcal microorganism. The sequences are used for the manufacture
  CC of a medicament for the treatment or prevention of a condition associated
  CC with infection by S. pneumoniae or other gram positive bacteria,
  CC preferably for veterinary treatment, and in the production of monoclonal
  CC and polyclonal antibodies for use in passive immunisation. This sequence
  CC represents an S. pneumoniae iron uptake ABC transporter. (Updated on 07-
  CC AUG-2003 to correct OS field.)
XX
XX Sequence 318 AA;
Query Match 77.3%; Score 34; DB 5; Length 318;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLMEP 8
Db 152 FLQVLMDP 159

RESULT 13
ABU02362
ID ABU02362 standard; protein; 318 AA.
XX
XX AC ABU02362;
XX
XX 23-OCT-2003 (revised)
DT 11-FEB-2003 (first entry)
XX
XX S. pneumoniae type 4 strain protein from coding region #1940.
XX
XX Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
XX gene therapy; vaccine.
XX
XX Streptococcus pneumoniae; type 4 strain.
OS
XX WO200277021-A2.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 27-MAR-2002; 2002WO-IB002163.
PF
XX
XX 27-MAR-2001; 2001GB-00007658.
PR
XX
XX (CHIR-) CHIRON SPA.
PA
XX (GENO-) INST GENOMIC RES.
XX
XX Massignani V, Tettelin H, Fraser C;
PI
XX
XX WPI: 2003-040579/03.
DR
XX N-PSDB; ABX07652.
DR
XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
PT ear infection.
XX
XX Claim 1; SEQ ID NO 3880; 56pp; English.
PS
XX The invention relates to a protein comprising or having at least 50%
  CC

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CC identity to any of the 2469 amino acid sequences, identified in the  
 CC specification (available on a computer readable format), or its fragment,  
 CC expressed from 2469 of 2489 identified DNA coding regions from the  
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as  
 CC ABS56454. Also included are an antibody which binds one of the proteins,  
 CC treating a patient by administering the protein, DNA or antibody (in a  
 CC composition), a kit comprising first and second primers, which are the  
 CC nucleic acid cited above or fragments between nucleotides 8-100 of a  
 CC sequence not defined in the specification, for amplifying a target  
 CC sequence contained within a Streptococcus nucleic acid sequence, where  
 CC the first primer is substantially complementary to the target sequence  
 CC and the second primer is substantially complementary to the complement of  
 CC the target sequence, and where the parts of the primers having  
 CC substantial complementarity define the termini of the target sequence to  
 CC be amplified, assay comprising contacting a test compound with the  
 CC protein, and determining whether the test compound binds to the protein  
 CC and a Streptococcus pneumoniae bacterium, where one or more genes  
 CC encoding the proteins has been rendered inactive. The proteins, nucleic  
 CC acid molecules, antibody and compositions are useful as medicaments for  
 CC treating or preventing a disease or infection due to streptococcus  
 CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis  
 CC media or ear infection. They are also useful in developing vaccines,  
 CC diagnostics and antibiotics. The methods are useful for identifying  
 CC immunodominant proteins. The present sequence is one of the 2469 proteins  
 CC expressed by the identified coding regions from the genomic sequence.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 23-OCT-2003 to  
 CC standardise OS field)

XX SQ Sequence 318 AA;

Query Match 77.3%; Score 34; DB 6; Length 318;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLMPEP 8  
 |||:|:|  
 Db 152 FLQVLMDDP 159

RESULT 14

ADK46461  
 ID ADK46461 standard; protein; 318 AA.

XX AC ADK46461;

XX DT 20-MAY-2004 (first entry)

XX XX Streptococcus pneumoniae protein, Seq ID No 2976.

XX DE Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.

XX KW Streptococcus pneumoniae.

XX OS US6699703-B1.

XX PN 02-MAR-2004.

XX PD 26-MAY-2000; 2000US-00583110.

XX PF 02-JUL-1997; 97US-0051553P.

XX PR 12-MAY-1998; 98US-0085131P.

XX PR 30-JUN-1998; 98US-00107433.

XX XX (GENO-) GENOME THERAPEUTICS CORP.

XX PA Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Houseweart CE;

XX PI WPI; 2004-212399/20.

XX DR N-PSDB; ADK43800.

XX XX New nucleic acid molecules and polypeptides useful for diagnosing,

PT preventing and treating pathological conditions resulting from bacterial  
 PT infection, e.g. Streptococcus pneumoniae infection, and in drug  
 PT screening.

XX PS Disclosure; SEQ ID NO 2976; 301pp; English.

XX XX The invention relates to isolated Streptococcus pneumoniae nucleic acids  
 CC and polypeptides. The nucleic acids and proteins are useful for  
 CC diagnosing, preventing and treating pathological conditions resulting  
 CC from bacterial infection, such as S. pneumoniae infection. These may also  
 CC be used for drug screening procedures. The present sequence represents a  
 CC Streptococcus pneumoniae polypeptide of the invention. Note: The sequence  
 CC data for this patent did not appear in the printed specification but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

XX SQ Sequence 318 AA;

Query Match 77.3%; Score 34; DB 8; Length 318;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLMPEP 8  
 |||:|:|  
 Db 152 FLQVLMDDP 159

RESULT 15

ADR96441  
 ID ADR96441 standard; protein; 336 AA.

XX AC ADR96441;

XX XX 16-DEC-2004 (first entry)

XX DE Novel S. pneumoniae protein sequence, SEQ ID 5076.

XX XX Meningitis; bacteraemia; pneumonia; otitis media; vaccine;

XX KW bacterial infection.

XX OS Streptococcus pneumoniae.

XX PN US6800744-B1.

XX XX 05-OCT-2004.

XX XX 30-JUN-1998; 98US-00107433.

XX PR 02-JUL-1997; 97US-0051553P.

XX PR 12-MAY-1998; 98US-0085131P.

XX XX (GENO-) GENOME THERAPEUTICS CORP.

XX PI Doucette-Stamm LA, Bush D;

XX XX WPI; 2004-697205/68.

XX DR N-PSDB; ADR93838.

XX XX New isolated nucleic acid encoding a Streptococcus pneumoniae  
 PT polypeptide, useful for diagnosing, preventing and/or treating  
 PT pathological conditions resulting from the bacterial infection.

XX PS Disclosure; SEQ ID NO 5076; 151pp; English.

XX XX The invention relates to an isolated nucleic acid comprising a sequence  
 CC encoding a Streptococcus pneumoniae ADR91366polypeptide, or its  
 CC fragments, with any of 9 fully defined sequences (appearing as ADR94308,  
 CC ADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682,  
 CC ADR96079) or any of the fully defined sequences appearing as ADR91705,  
 CC ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or  
 CC ADR93476 or at least 20 or 30 consecutive nucleotides of the nucleotide  
 CC sequences, or at least 40, 60 or 300 consecutive nucleotides, which is  
 CC hybridisable under high stringency conditions to the nucleotide sequence.

CC The nucleic acids and proteins are chosen from 5206 disclosed sequences.  
 CC Also included are a recombinant expression vector comprising the isolated  
 CC nucleic acid cited above operably linked to a transcription regulatory  
 CC element, a cell comprising the recombinant expression vector and a probe  
 CC comprising at least 20 consecutive nucleotides of the nucleotide  
 CC sequences as cited above. The methods and compositions of the present  
 CC invention are useful for the diagnosis, prevention and/or treatment of  
 CC pathological conditions resulting from bacterial infection by  
 CC *Streptococcus pneumoniae* e.g. pneumonia, bacteraemia, meningitis and  
 CC otitis media. The present sequence is one of the 2603 disclosed S.  
 CC *pneumoniae* protein sequences. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=6800744B1.

XX SQ Sequence 336 AA;  
 Query Match 77.3%; Score 34; DB 8; Length 336;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLOLMPEP 8  
 Db 170 FLOVLMMDP 177  
 |||:|:|

RESULT 16  
 AEA60311  
 ID AEA60311 standard; protein; 336 AA.  
 AC AEA60311;  
 DT 25-AUG-2005 (first entry)  
 DE *Streptococcus pneumoniae* ORF amino acid sequence SEQ ID NO:5076.  
 KW bacterial infection; *Streptococcus pneumoniae* infection; antibacterial;  
 KW vaccine.  
 OS *Streptococcus pneumoniae*.  
 XX US2005136404-A1.  
 PN 23-JUN-2005.  
 PD 10-JUL-2003; 2003US-00617320.  
 PF 02-JUL-1997; 97US-0051553P.  
 PR 12-MAY-1998; 98US-0085131P.  
 PR 30-JUN-1998; 98US-00107433.  
 XX (DOUC/) DOUCETTE-STAMM L A.  
 PA (BUSH/) BUSH D.  
 XX Doucette-Stamm LA, Bush D;  
 PI WPI; 2005-477576/48.  
 DR N-PSDB; AEA57708.  
 XX New isolated nucleic acid molecules and encoded polypeptides useful for  
 PT diagnosing, preventing or treating bacterial infections, particularly  
 PT *Streptococcus pneumoniae* infection.

XX Claim 5; SEQ ID NO 5076; 144pp; English.  
 PS The invention relates to an isolated nucleic acid molecule for detecting,  
 CC preventing or treating pathological conditions resulting from bacterial  
 CC infection. The isolated nucleic acid comprises: (a) any of the 2603  
 CC nucleotide sequences of AEA55236 to AEA57839; (b) a nucleotide sequence  
 CC encoding a *Streptococcus pneumoniae* polypeptide comprising any of the  
 CC 2603 amino acid sequences of AEA57839 to AEA60441; or (c) a nucleotide  
 CC sequence of at least 8 nucleotides in length, where the sequence is  
 CC hybridizable to a nucleic acid having any of the nucleotide sequences in

CC (a). Also described: (1) a recombinant expression vector comprising the  
 CC above nucleic acid operably linked to a transcription regulatory element;  
 CC (2) a cell comprising the recombinant expression vector; (3) producing an  
 CC *S. pneumoniae* polypeptide; (4) a probe comprising a nucleotide sequence  
 CC consisting of at least 8 nucleotides of any of AEA55236 to AEA57839; (5)  
 CC treating a subject for *S. pneumoniae* infection; (6) a recombinant or  
 CC substantially pure preparation of an *S. pneumoniae* polypeptide or its  
 CC fragment, where the polypeptide is selected from AEA57839 to AEA60441;  
 CC (7) a vaccine composition for preventing or treating an *S. pneumoniae*  
 CC infection, comprising an amount of the above nucleic acid or polypeptide;  
 CC (8) detecting the presence of a *Streptococcus* nucleic acid in a sample;  
 CC (9) a computer readable medium having recorded the nucleotide sequences  
 CC of AEA55236 to AEA57839; (10) a computer based system for identifying  
 CC fragments of the *Streptococcus* genome of commercial importance. The  
 CC composition and methods are useful for diagnosing, preventing or treating  
 CC bacterial infections, particularly *S. pneumoniae* infection. The present  
 CC sequence represents a *S. pneumoniae* ORF amino acid sequence from the  
 CC present invention. Note - The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from the USPTO web site.

XX SQ Sequence 336 AA;  
 Query Match 77.3%; Score 34; DB 9; Length 336;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLMPEP 8  
 Db 170 FLOVLMMDP 177  
 |||:|:|  
 RESULT 17  
 ADX76583  
 ID ADX76583 standard; protein; 504 AA.  
 AC ADX76583;  
 DT 21-APR-2005 (first entry)  
 DE Plant full length insert polypeptide seqid 45949.  
 XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 XX protein content.  
 OS Unidentified.  
 XX US2004034888-A1.  
 PN 19-FEB-2004.  
 PD 28-APR-2003; 2003US-00425114.  
 PF 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX (LIUJ/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABAJ/) TABASKA J E.  
 XX (CAOY/) CAO Y.  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 DR WPI; 2004-180133/17.  
 XX

PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.

XX Claim 1; SEQ ID NO 45949; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This is the amino acid sequence of a plant full length insert  
CC polypeptide that can be used in the recombinant DNA construct of the  
CC invention.

XX SQ Sequence 504 AA;

Query Match 77.3%; Score 34; DB 8; Length 504;  
Best Local Similarity 77.8%; Pred. No. 2.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
| | | | |  
DB 67 FCQLLMHPV 75

RESULT 18

ABM87623  
ID ABM87623 standard; protein; 759 AA.

XX AC ABM87623;

XX XX 02-JUN-2005 (first entry)

XX DE Rice abiotic stress responsive polypeptide SEQ ID NO:5869.

XX KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.

XX OS Oryza sativa.

XX XX WO2003008540-A2.

XX XX 30-JAN-2003.

XX XX 21-JUN-2002; 2002WO-US013668.

XX XX 22-JUN-2001; 2001US-0300112P.

XX PR 24-AUG-2001; 2001US-0314662P.

XX PR 26-SEP-2001; 2001US-0325277P.

XX PR 21-NOV-2001; 2001US-0332132P.

XX XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;

XX PI Moughamer T, Provart N, Ricke D, Zhu T;

XX XX WPI; 2003-248011/24.

XX XX New stress-responsive nucleic acid, useful for altering the  
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
PT stress, salt stress or osmotic stress.

XX XX

PS Claim 1; SEQ ID NO 5869; 89pp; English.

XX The invention relates to novel abiotic stress responsive polynucleotides  
CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
CC cells, and plants containing such polynucleotides. Also disclosed are  
CC methods for using the polynucleotides and polypeptides to alter the  
CC responsiveness of a plant to abiotic stress. The invention is useful in  
CC agriculture. The nucleic acid is useful for determining whether a test  
CC plant has been exposed to an abiotic stress condition. It is also useful  
CC for selecting an agent that alters abiotic stress regulated  
CC polynucleotide expression in a plant cell, and to identify a homolog or  
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
CC molecule and the polypeptide encoded by it are useful in altering the  
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
CC stress, osmotic stress or any of their combinations. The present sequence  
CC is used in the exemplification of the invention

XX SQ Sequence 759 AA;

Query Match 77.3%; Score 34; DB 7; Length 759;  
Best Local Similarity 77.8%; Pred. No. 3.6e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
| | | | |  
DB 206 FCQLLMHPV 214

RESULT 19

AAV57148

ID AAV57148 standard; protein; 2785 AA.

XX AC AAV57148;

XX XX 28-FEB-2000 (first entry)

XX DE Human down-regulated in metastasis (DRIM) amino acid sequence.

XX KW Down-regulated in metastasis; DRIM; human; antimetastatic activity;  
XX KW antibody; tumour; treatment; therapy.

XX OS Homo sapiens.

XX XX WO9960116-A1.

XX XX 25-NOV-1999.

XX XX 17-MAY-1999; 99WO-EP003396.

XX XX 18-MAY-1998; 98EP-00303895.

XX XX (HOFF ) ROCHE DIAGNOSTICS GMBH.

XX XX (ISIS-) ISIS INNOVATION LTD.

XX PI Weidle U, Tarin D;

XX XX WPI; 2000-053296/04.

XX XX N-PSDB; AA245136.

XX PT New polypeptide with antimetastatic activity, useful for therapeutic  
XX compositions for tumor therapy.

XX PS Claim 2; Page 42-49; 54pp; English.

XX This is the amino acid sequence of the human down-regulated in metastasis  
CC (DRIM) protein. The protein has antimetastatic activity. The DRIM protein  
CC is active in both its glycosylated and unglycosylated form, and can be  
CC produced by recombinant technology in prokaryotic cells. DRIM mRNA is  
CC strongly expressed in heart, skeletal muscle, pancreas, testis and ovary  
CC tissues. The nucleotide and protein sequences can be used to create anti-  
CC DRIM antibodies. The nucleic acids are useful in therapeutic  
CC compositions, especially for treating tumours. They are also useful for  
CC activating polynucleotides from the 5' untranslated region in gene





PR	04-MAY-1999;	99US-0132484P.	PR	22-JUL-1999;	99US-0145085P.
PR	05-MAY-1999;	99US-0132485P.	PR	22-JUL-1999;	99US-0145087P.
PR	06-MAY-1999;	99US-0132486P.	PR	22-JUL-1999;	99US-0145089P.
PR	06-MAY-1999;	99US-0132487P.	PR	23-JUL-1999;	99US-0145192P.
PR	07-MAY-1999;	99US-0132863P.	PR	23-JUL-1999;	99US-0145145P.
PR	11-MAY-1999;	99US-0134256P.	PR	23-JUL-1999;	99US-0145218P.
PR	14-MAY-1999;	99US-01344218P.	PR	23-JUL-1999;	99US-0145224P.
PR	14-MAY-1999;	99US-01344219P.	PR	26-JUL-1999;	99US-0145276P.
PR	14-MAY-1999;	99US-01344221P.	PR	27-JUL-1999;	99US-0145913P.
PR	14-MAY-1999;	99US-0134370P.	PR	27-JUL-1999;	99US-0145918P.
PR	18-MAY-1999;	99US-0134768P.	PR	27-JUL-1999;	99US-0145919P.
PR	18-MAY-1999;	99US-0134941P.	PR	28-JUL-1999;	99US-0145951P.
PR	20-MAY-1999;	99US-0135124P.	PR	02-AUG-1999;	99US-0146386P.
PR	21-MAY-1999;	99US-0135353P.	PR	02-AUG-1999;	99US-0146388P.
PR	24-MAY-1999;	99US-0135629P.	PR	02-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0147038P.
PR	27-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
PR	28-MAY-1999;	99US-0136782P.	PR	04-AUG-1999;	99US-0147302P.
PR	01-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0147192P.
PR	03-JUN-1999;	99US-0137528P.	PR	06-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	99US-0139119P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	99US-0139459P.	PR	20-AUG-1999;	99US-0149929P.
PR	18-JUN-1999;	99US-0139460P.	PR	23-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149930P.
PR	18-JUN-1999;	99US-0139462P.	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151066P.
PR	21-JUN-1999;	99US-0139817P.	PR	27-AUG-1999;	99US-0151080P.
PR	22-JUN-1999;	99US-0139899P.	PR	30-AUG-1999;	99US-0151303P.
PR	23-JUN-1999;	99US-0140353P.	PR	31-AUG-1999;	99US-0151438P.
PR	23-JUN-1999;	99US-0140354P.	PR	01-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-0152363P.
PR	28-JUN-1999;	99US-0140823P.	PR	10-SEP-1999;	99US-0153070P.
PR	29-JUN-1999;	99US-0140991P.	PR	13-SEP-1999;	99US-0153758P.
PR	30-JUN-1999;	99US-0141287P.	PR	15-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0141842P.	PR	16-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-0155139P.
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142320P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144321P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144684P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.

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PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 22-OCT-1999; 99US-0161404P.
PR 22-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 25-OCT-1999; 99US-0161408P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 75.0%; Score 33; DB 3; Length 296;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEP 8
Db 217 FLQLMEP 224
|||||

RESULT 22
AAG82085
ID AAG82085 standard; protein; 305 AA.
AC AAG82085;
XX
XX 03-SEP-2001 (first entry)
XX
XX S. epidermidis open reading frame protein sequence SEQ ID NO:1264.
XX
XX Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination;
XX endocarditis.
XX
XX Staphylococcus epidermidis.
XX
XX WO200134809-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US030782.
XX
XX 09-NOV-1999; 99US-0164258P.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Kimmerly WJ;
XX
XX WPI; 2001-316495/33.
XX
XX N-PSDB; AAH52935.
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis.
XX
XX Claim 18; Page 361; 2189pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AG81454 to AAG83120, from Staphylococcus epidermidis. (I
XX and (II) can have antibacterial activity and therefore can be used in
XX vaccination. The nucleic acids (I) may be used to produce the S.
XX epidermidis polypeptides (II) via the production of vectors containing
XX them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to

CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to AAH55098
CC represent oligonucleotide sequences and primers which are used in the
CC exemplification of the present invention. N.B. The present invention
CC specifically claims all the polynucleotide sequences given in the
CC sequence listing of the present specification, however the sequence
CC listing only goes up to SEQ ID NO:4454 so even though sequences are given
CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
CC for SEQ ID NO:4455 to 4464
XX
XX Sequence 305 AA;
SQ
Query Match 75.0%; Score 33; DB 4; Length 305;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEP 8
Db 138 FLQLMEP 145
|||||

RESULT 23
ABM72286
ID ABM72286 standard; protein; 318 AA.
XX
XX AC ABM72286;
XX
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus protein #1526.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.
XX
XX Staphylococcus aureus.
XX
XX WO200294868-A2.
XX
XX 28-NOV-2002.
XX
XX 27-MAR-2002; 2002WO-IB002637.
XX
XX 27-MAR-2001; 2001GB-00007661.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Masignani V, Mora M, Scarselli M;
XX
XX WPI; 2003-120786/11.
XX
XX N-PSDB; ACF73846.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
XX preventing Staphylococcal infection, specifically an infection caused by
XX S. aureus, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 3052; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
XX Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to Staphylococcus bacteria, specifically an
XX infection caused by S. aureus. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel S. aureus proteins of the invention
XX
XX Sequence 318 AA;
SQ
Query Match 75.0%; Score 33; DB 6; Length 318;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 FLQLMPEP 8  
 Db 151 FLQLMPEP 158

RESULT 24  
 ABP40680  
 ID ABP40680 standard; protein; 324 AA.  
 XX AC ABP40680;  
 XX DT 24-JUL-2002 (first entry)  
 XX DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5525.  
 XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
 XX KW antibacterial; gene therapy.  
 XX OS Staphylococcus epidermidis.  
 XX PN US6380370-B1.  
 XX PD 30-APR-2002.  
 XX PF 13-AUG-1998; 98US-00134001.  
 XX PR 14-AUG-1997; 97US-0055779P.  
 XX PR 08-NOV-1997; 97US-0064964P.  
 XX PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX PI Doucette-Stamm LA, Bush D;  
 XX DR WPI; 2002-381255/41.  
 XX DR N-PSDB; ABN93225.  
 XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermis  
 PT polypeptide, useful for diagnosing and treating bacterial infections.  
 XX PS Disclosure; SEQ ID NO 5525; 267pp; English.  
 XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have  
 CC antibacterial activity and can be used in gene therapy. The sequences can  
 CC also be used in the diagnosis and treatment of bacterial infections,  
 CC particularly S. epidermidis infections. The sequences can be used to  
 CC screen for compounds able to interfere with the S. epidermidis life cycle  
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from the USPTO web site  
 XX SQ Sequence 324 AA;  
 Query Match 75.0%; Score 33; DB 5; Length 324;  
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMPEP 8  
 Db 157 FLQLMNP 164

RESULT 25  
 ADS07952  
 ID ADS07952 standard; protein; 324 AA.  
 XX AC ADS07952;  
 XX DT 04-NOV-2004 (first entry)  
 XX DE Staphylococcus epidermis polypeptide seqid 7247.

XX KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;  
 KW recombinant expression vector; infection; computer readable medium;  
 KW computer based system.  
 XX OS Staphylococcus epidermidis.  
 XX PN US2004147734-A1.  
 XX PD 29-JUL-2004.  
 XX PF 01-DEC-2003; 2003US-00724972.  
 XX PR 08-NOV-1997; 97US-0064964P.  
 XX PR 13-AUG-1998; 98US-00134001.  
 XX PR 29-NOV-1999; 99US-00450969.  
 XX (DOUC/) DOUCETTE-STAMM L.  
 XX PA (BUSH/) BUSH D.  
 XX PI Doucette-Stamm L, Bush D;  
 XX DR WPI; 2004-580138/56.  
 XX DR N-PSDB; ADS04180.  
 XX PT New isolated polypeptide and encoding nucleic acid derived from  
 PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or  
 PT treating an S. epidermidis bacterial infection.  
 XX PS Claim 17; SEQ ID NO 7247; 741pp; English.  
 XX CC The invention describes an isolated nucleic acid comprising a nucleotide  
 CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
 CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
 CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
 CC given in the specification. Also described are: a recombinant expression  
 CC vector; a cell comprising a recombinant expression vector of (1);  
 CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
 CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
 CC vaccine composition for prevention or treatment of an S. epidermidis  
 CC infection, comprising a nucleic acid cited above and a carrier; treating  
 CC a subject for S. epidermidis infection; a recombinant or substantially  
 CC pure preparation of an S. epidermidis polypeptide or its fragment; a  
 CC vaccine composition for prevention or treatment of an S. epidermidis  
 CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
 CC sample; a computer readable medium having recorded in it the nucleotide  
 CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
 CC system for identifying fragments of the Staphylococcus genome of  
 CC commercial importance; a computer based system for identifying fragments  
 CC of the Staphylococcus plasmids of commercial importance; identifying  
 CC commercially important nucleic acid fragments of the Staphylococcus  
 CC genome and/or plasmids; and identifying an expression modulating fragment  
 CC of the Staphylococcus genome and/or plasmids. The methods and  
 CC compositions of the present invention are useful for the diagnosis,  
 CC prevention and/or treatment of an Staphylococcus epidermidis bacterial  
 CC infection. This is the amino acid sequence of a S. epidermis protein of  
 CC the invention.  
 XX SQ Sequence 324 AA;  
 Query Match 75.0%; Score 33; DB 8; Length 324;  
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMPEP 8  
 Db 157 FLQLMNP 164

RESULT 26  
 AAG44342  
 ID AAG44342 standard; protein; 345 AA.  
 XX



PR 26-AUG-1999; 99US-0150884P.  
 PR 27-AUG-1999; 99US-0151065P.  
 PR 27-AUG-1999; 99US-0151066P.  
 PR 27-AUG-1999; 99US-0151080P.  
 PR 30-AUG-1999; 99US-0151303P.  
 PR 31-AUG-1999; 99US-015138P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153758P.  
 PR 15-SEP-1999; 99US-0154018P.  
 PR 16-SEP-1999; 99US-0154039P.  
 PR 20-SEP-1999; 99US-0154779P.  
 PR 22-SEP-1999; 99US-0155139P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0155659P.  
 PR 28-SEP-1999; 99US-0156458P.  
 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157117P.  
 PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158232P.  
 PR 12-OCT-1999; 99US-0158369P.  
 PR 13-OCT-1999; 99US-0159293P.  
 PR 13-OCT-1999; 99US-0159294P.  
 PR 13-OCT-1999; 99US-0159295P.  
 PR 14-OCT-1999; 99US-0159329P.  
 PR 14-OCT-1999; 99US-0159330P.  
 PR 14-OCT-1999; 99US-0159331P.  
 PR 14-OCT-1999; 99US-0159637P.  
 PR 14-OCT-1999; 99US-0159638P.  
 PR 18-OCT-1999; 99US-0159584P.  
 PR 21-OCT-1999; 99US-0160741P.  
 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160980P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161404P.  
 PR 25-OCT-1999; 99US-0161405P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161922P.  
 PR 28-OCT-1999; 99US-0161993P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 75.0%; Score 33; DB 3; Length 345;  
 Best Local Similarity 87.5%; Pred. No. 2.6e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLLMEP 8  
 Db 266 FLQLLMEP 273

RESULT 27

AA71459  
 ID AAY71459 standard; protein; 368 AA.

XX AC AAY71459;

XX 04-OCT-2000 (first entry)

XX Maize Rad23 protein #2.

XX Rad23; maize; ATCC No: PTA-531; recombinant expression cassette; wheat;

KW transgenic plant; soybean; sunflower; sorghum; canola; modulator.  
 XX Zea mays.  
 XX WO200031268-A1.  
 XX 02-JUN-2000.  
 XX 12-OCT-1999; 99WO-US024129.  
 XX 23-NOV-1998; 98US-0109728P.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 XX Mahajan PB, Tagliani L;  
 XX WPI; 2000-400078/34.  
 XX N-PSDB; AAD01231.  
 XX Isolated nucleic acid encoding maize RAD23 protein is used to modulate the levels of polypeptides in plant or in assays for identifying compounds that bind to and/or increase/decrease enzymatic activity of catalytically active polypeptides.  
 XX Claim 11b; Page 78-79; 82pp; English.  
 XX The present sequence is the maize Rad23 protein #2. It is isolated from a Zea mays cell line, B73 callus tissue regenerated five days after transfer of the callus from medium containing auxin to a medium devoid of exogenous auxin. The cDNA is deposited under the ATCC No: PTA-531. Maize Rad23 DNA sequence operably linked to a promoter, can be used to construct a recombinant expression cassette. This expression cassette can be used to generate a dicot or monocot transgenic plant e.g., maize, soybean, sunflower, sorghum, canola, wheat, etc. It can also be used to modulate the levels of Rad23 polypeptide expression in a plant or in assays to identify compounds, that bind to and/or modulate the enzymatic activity of catalytically active polypeptides  
 XX Sequence 368 AA;  
 SQ

Query Match 75.0%; Score 33; DB 3; Length 368;  
 Best Local Similarity 87.5%; Pred. No. 2.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLLMEP 8  
 Db 291 FLQLLMEP 298

RESULT 28

AAG44341  
 ID AAG44341 standard; protein; 368 AA.

XX AC AAG44341;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 55531.

XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.



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PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 23-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 75.0%; Score 33; DB 3; Length 368;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEP 8
DB 289 FLQLNEP 296

RESULT 29
AAW75700
ID AAW75700 standard; peptide; 409 AA.
XX
AC AAW75700;
XX
DT 29-OCT-1998 (first entry)
XX
DE Vpr protein binding HHR23B amino acid sequence.
XX
KW Lentiviral infection; Vpr protein; HIV infection; cell stasis;
cell death; HHR23A; Rad23 protein.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Domain 184..232
FT /note= "highly conserved internal repeat domain"
FT Domain 360..385
FT /note= "highly conserved internal repeat domain"
FT Domain 386..409
FT /note= "highly conserved internal repeat domain"
XX
PN WO9835234-A1.
XX
PD 13-AUG-1998.
XX
PF 11-FEB-1998; 98WO-US003008.
XX
PR 11-FEB-1997; 97US-00797907.
XX
XX

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PA (REGC ) UNIV CALIFORNIA.
XX
PI Chen ISY, Jowett JBM, Withers-Ward E;
XX
DR WPI; 1998-447375/38.
XX
FT Identification of compounds binding the HIV-1 Vpr protein - that block
PT Vpr-mediated cell stasis, useful for treating HIV-1 or other lentiviral
FT infections.
XX
PS Disclosure; Fig 2; 63pp; English.
XX
CC This represents the amino acid sequence of the HHR23A protein (a human
CC homologue of the S. cerevisiae Rad23 protein). This protein can bind to
CC the Vpr protein encoded by the HIV genome. The invention provides a
CC method of identifying an agent for use in treating lentiviral infections.
CC The method comprises contacting a cellular target of the Vpr protein with
CC the agent to be tested, and assessing the ability of the agent to block
CC interaction of the Vpr protein with the cellular target, where an agent
CC which blocks this interaction is an anti-lentiviral agent. Alternatively,
CC the agent contacts a cell expressing the Vpr protein under conditions
CC where the Vpr protein induces cell stasis in the absence of the agent.
CC Identification of the agent is then observed by blockage of Vpr-induced
CC cell stasis. The method allows the identification of compounds that block
CC Vpr-mediated cell stasis and ultimately cell death. The compounds can
CC thus be used in the treatment of HIV and other lentiviral infections
XX
SQ Sequence 409 AA;

Query Match 75.0%; Score 33; DB 2; Length 409;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9
DB 324 FLQLNEPV 332

RESULT 30
AAW68186
ID AAW68186 standard; protein; 409 AA.
XX
AC AAW68186;
XX
DT 25-MAR-2003 (revised)
DT 29-OCT-1998 (first entry)
XX
DE Vpr binding protein HHR23B amino acid sequence.
XX
KW Lentivirus; Vpr protein; HIV infection; cell stasis; cell death; cancer;
HHR23B; Rad23 protein.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Domain 184..232
FT /note= "highly conserved internal repeat domain"
FT Domain 360..385
FT /note= "highly conserved internal repeat domain"
FT Domain 386..409
FT /note= "highly conserved internal repeat domain"
XX
PN WO9835032-A2.
XX
PD 13-AUG-1998.
XX
PF 11-FEB-1998; 98WO-US003390.
XX
PR 11-FEB-1997; 97US-00798597.
PR 24-OCT-1997; 97US-00959279.
XX
PA (REGC ) UNIV CALIFORNIA.
XX

```

PI Chen ISY, Jowett JBM, Withers-Ward E, Stewart SA, Poon B;  
 PI Feigon J, Dieckmann T;  
 XX WPI; 1998-447229/38.  
 XX  
 PT Arresting cell growth using lentivirus Vpr virion protein - used for  
 PT treatment of cancer and screening for agents that reduce Vpr binding,  
 PT e.g. anti-HIV agents.  
 XX  
 XX Disclosure; Fig 1; 71pp; English.  
 PS  
 CC This represents the amino acid sequence of the HHR23B protein (a human  
 CC homologue of the S. cerevisiae Rad23 protein). This protein can bind to  
 CC the Vpr protein encoded by the HIV genome. This is used as a cellular  
 CC target in the method of the invention of identifying antitumour  
 CC therapeutic candidates. The invention provides a method for arresting the  
 CC growth of a cell by treatment with a Vpr lentivirus protein or its  
 CC analogue. Agents that reduce binding of Vpr to a cellular target are  
 CC useful for treating HIV (human immune deficiency virus) infection or more  
 CC generally for restoring growth. The antitumour agent identified is useful  
 CC for treating any type of cancer, since it induces cell stasis (blocks  
 CC development at the G2 stage) and death. The agents can also be used for  
 CC treating autoimmune diseases. (Updated on 25-MAR-2003 to correct PI  
 CC field.)  
 XX  
 SQ Sequence 409 AA;  
 Query Match 75.0%; Score 33; DB 2; Length 409;  
 Best Local Similarity 66.7%; Pred. NO. 3.1e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLOQLMEPV 9  
 |:|:| |||  
 Db 324 FIQLMEPV 332  
 RESULT 31  
 ABU07460  
 ID ABU07460 standard; protein; 409 AA.  
 AC ABU07460;  
 XX  
 DT 28-JAN-2003 (first entry)  
 XX  
 DE Protein differentially regulated in prostate cancer #63.  
 XX  
 KW Prostate cancer; gene expression; differential regulation;  
 KW molecular marker; drug target; cancer detection; cancer diagnosis;  
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200281638-A2.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 08-APR-2002; 2002WO-US010824.  
 XX  
 PR 06-APR-2001; 2001US-0281731P.  
 PR 06-APR-2001; 2001US-0281732P.  
 XX  
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
 XX  
 PI Sun Z, Jay G;  
 XX  
 DR WPI; 2003-058520/05.  
 DR N-PSDB; ABX10362.  
 XX  
 XX Novel genes which are differentially regulated in prostate cancer, useful  
 PT for diagnosing prostate cancer in prostate tissue sample and assessing  
 PT therapeutic or preventive intervention in prostate cancer patients.  
 XX  
 PS Claim 1; Page 331-332; 416pp; English.

XX The invention describes genes (I) which are differentially regulated in  
 CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a  
 CC sample comprising prostate tissue, which involves determining the number  
 CC of target genes which are differentially-regulated in the sample, where  
 CC the number is indicative of the probability that the sample comprises  
 CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive  
 CC intervention in a subject having a prostate cancer, which involves  
 CC determining the expression levels in a sample comprising prostate tissue  
 CC of target genes which are differentially-regulated in prostate cancer.  
 CC Preferably, the expression levels of at least 10 genes are determined.  
 CC (I) is also useful for identifying agents that modulate a biological  
 CC activity of a polypeptide differentially-regulated in prostate cancer  
 CC cells, which involves contacting a polypeptide differentially-regulated  
 CC in prostate cancer cells with a test agent under conditions effective for  
 CC the test agent to modulate a biological activity of the polypeptide, and  
 CC determining whether the test agent modulates the biological activity. (I)  
 CC is useful as molecular markers, as drug targets, and for detecting,  
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,  
 CC preventing or treating, determining predisposition to diseases and  
 CC conditions especially relating to prostate cancer. (I) and its expression  
 CC products are used in the diagnostic test to assay for presence of cancer  
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in  
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type  
 CC of cancer, its stage of development, the nature of genetic defect, etc.  
 CC The polypeptide encoded by (I) can be used as target for therapy or drug  
 CC discovery. (I) can also be used for expressing the polypeptide and thus  
 CC for searching specific binding partners of the polypeptide. (I) is useful  
 CC in therapeutic applications to treat prostate cancer. The identification  
 CC of specific genes, and groups of genes, expressed in pathways  
 CC physiologically relevant to prostate cancer permits the definition of  
 CC functional and disease pathways and the delineation of targets in these  
 CC pathways which are useful in diagnostic, therapeutic, and clinical  
 CC applications. This is the amino acid sequence of a protein differentially  
 CC regulated in prostate cancer  
 XX  
 SQ Sequence 409 AA;

Query Match 75.0%; Score 33; DB 6; Length 409;  
 Best Local Similarity 66.7%; Pred. NO. 3.1e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOQLMEPV 9  
 |:|:| |||  
 Db 324 FIQLMEPV 332

RESULT 32  
 ADN03716  
 ID ADN03716 standard; protein; 409 AA.  
 XX  
 AC ADN03716;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Antipsoriatic protein sequence #55.  
 XX  
 KW antipsoriatic; gene therapy; psoriasis; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004028479-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003WO-US030907.  
 XX  
 PR 25-SEP-2002; 2002US-0414006P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
 PI Wu TD;



XX WPI; 2004-305105/28.  
 DR N-PSDB; ADN03715.  
 XX  
 PT New PRO nucleic acid or polypeptide, useful for preparing a  
 PT pharmaceutical composition for diagnosing or treating psoriasis in a  
 PT mammal.  
 XX  
 PS Claim 9; SEQ ID NO 110; 3069pp; English.  
 XX  
 CC The invention relates to novel polynucleotide and polypeptides for  
 CC treating psoriasis or a sequence having at least 80% identity to the  
 CC above sequences. The nucleic acid is useful for preparing a composition  
 CC for diagnosing or treating psoriasis in a mammal. This sequence  
 CC corresponds to one of the polypeptides of the invention.  
 XX  
 SQ Sequence 409 AA;  
 XX  
 Query Match 75.0%; Score 33; DB 8; Length 409;  
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1 FLQLLMEPV 9  
 Db 324 FIQMLNEPV 332  
 XX  
 RESULT 33  
 ADQ65876  
 ID ADQ65876 standard; protein; 409 AA.  
 XX  
 AC ADQ65876;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Novel human protein sequence #849.  
 XX  
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;  
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;  
 KW cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1440981-A2.  
 XX  
 PD 28-JUL-2004.  
 XX  
 PF 21-JAN-2004; 2004EP-00001196.  
 XX  
 PR 21-JAN-2003; 2003JP-00102206.  
 PR 09-MAY-2003; 2003JP-00131392.  
 XX  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Nagai K, Irie R;  
 XX  
 DR WPI; 2004-535376/52.  
 DR N-PSDB; ADQ63688.  
 XX  
 XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,  
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
 PS Claim 1; SEQ ID NO 3037; 2449pp; English.  
 XX  
 CC The invention relates to 2495 novel polynucleotides (I) and their encoded  
 CC polypeptides, sequences hybridizing to these nucleotides, sequences  
 CC encoding partial polypeptides and sequences having 70% or 90% identity to  
 CC the nucleotide and protein sequences. The nucleotides and polypeptides  
 CC are useful as diagnostic markers or therapeutic target for the diseases  
 CC or morbid states. They are also useful for treating osteoporosis,  
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,

CC dementia and various cancers. This sequence corresponds to a protein  
 CC sequence of the invention.  
 XX  
 SQ Sequence 409 AA;  
 XX  
 Query Match 75.0%; Score 33; DB 8; Length 409;  
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1 FLQLLMEPV 9  
 Db 324 FIQMLNEPV 332  
 XX  
 RESULT 34  
 ADW08718  
 ID ADW08718 standard; protein; 409 AA.  
 XX  
 AC ADW08718;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Human protein which is down-regulated in HCV-infected tissue - SEQ ID 55.  
 XX  
 KW gene targeting; hepatitis C virus infection; protein deactivation;  
 KW protein activation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1493750-A2.  
 XX  
 PD 05-JAN-2005.  
 XX  
 PF 28-JUN-2004; 2004EP-00015098.  
 XX  
 PR 30-JUN-2003; 2003GB-00015248.  
 XX  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Berndt P, Kilby PM, Rugman P;  
 XX  
 DR WPI; 2005-050476/06.  
 XX  
 PT New targets for an antiviral compound having at least one down- and up-  
 PT regulated hepatitis C virus (HCV) polypeptide, useful in predicting  
 PT outcomes, treating or preventing HCV infections.  
 XX  
 PS Claim 1; SEQ ID NO 55; 346pp; English.  
 XX  
 CC The invention comprises the amino acid sequences of protein targets for  
 CC anti-hepatitis C virus (anti-HCV) drugs. The human protein targets of the  
 CC invention are either up-regulated or down-regulated in HCV-infected  
 CC tissue. The proteins of the invention are useful in the preparation of a  
 CC medicament for the treatment or prevention of HCV infection. The present  
 CC amino acid sequence represents a human protein of the invention which is  
 CC down-regulated in HCV-infected tissue.  
 XX  
 SQ Sequence 409 AA;  
 XX  
 Query Match 75.0%; Score 33; DB 9; Length 409;  
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1 FLQLLMEPV 9  
 Db 324 FIQMLNEPV 332  
 XX  
 RESULT 35  
 ADY14438  
 ID ADY14438 standard; protein; 409 AA.  
 XX  
 AC ADY14438;

```
XX 05-MAY-2005 (first entry)
XX PRO polypeptide SEQ ID NO 244.
XX
XX Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
XX Antiallergic; ds; gene; diagnosis.
XX Homo sapiens.
XX WO2005016962-A2.
XX
XX 24-FEB-2005.
XX
XX 11-AUG-2004; 2004WO-US026249.
XX
XX 11-AUG-2003; 2003US-0493546P.
XX (GETH ) GENENTECH INC.
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX WPI; 2005-182330/19.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
XX Claim 8; SEQ ID NO 244; 159pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX composition, and method are useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis. The present sequence represents a DNA encoding a PRO
XX polypeptide.
XX
XX Sequence 409 AA;
XX
XX Query Match 75.0%; Score 33; DB 9; Length 409;
XX Best Local Similarity 66.7%; Pred. No. 3.1e+02;
XX Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 FLQLLMEPV 9
XX |.:|:|
XX 324 FIQLNLEPV 332
XX
XX Db
XX
XX RESULT 36
XX ABB57171
XX ID ABB57171 standard; protein; 416 AA.
XX
XX AC ABB57171;
XX
XX DT 07-MAR-2002 (first entry)
XX
XX DE Mouse ischaemic condition related protein sequence SEQ ID NO:415.
XX
XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
XX OS Mus musculus.
XX
XX PN WO20018188-A2.
XX
XX PD 22-NOV-2001.
XX
XX PF 18-MAY-2001; 2001WO-JP004192.
XX
XX PR 18-MAY-2000; 2000JP-00145977.
XX
XX
XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
XX WPI; 2002-034733/04.
XX N-PSDB; ABI99464.
XX
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX expression levels of particular genes defined in the specification or by
XX determining the expression profile of a gene group comprising these
XX genes.
XX
XX Claim 2; Page 1132-1134; 2690pp; English.
XX
XX The present invention describes a method for examining ischaemic
XX conditions, comprising measuring the expression levels of particular
XX genes (I) in a test sample or determining the expression profile of a
XX gene group in the sample comprising genes selected from (I). The method
XX is useful for examining the ischaemic condition (e.g. compressive
XX ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX expression levels of particular genes (ABI99202 to ABI99912, encoding the
XX protein sequences in ABB57020 to ABB57374) or by determining the
XX expression profile of a gene group comprising these genes. The expression
XX levels or expression profiles produced by these genes are used as an
XX indicator when screening for ischaemic condition-improving drugs or
XX therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
XX primers for a mouse ischaemic condition related sequence, which are used
XX in the exemplification of the present invention
XX
XX Sequence 416 AA;
XX
XX Query Match 75.0%; Score 33; DB 5; Length 416;
XX Best Local Similarity 66.7%; Pred. No. 3.1e+02;
XX Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 FLQLLMEPV 9
XX |.:|:|
XX 324 FIQLNLEPV 332
XX
XX Db
XX
XX RESULT 37
XX ABB66967
XX ID ABB66967 standard; protein; 2764 AA.
XX
XX AC ABB66967;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster polypeptide SEQ ID NO 27693.
XX
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX OS Drosophila melanogaster.
XX
XX PN WO200171042-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX
XX PR 23-MAR-2000; 2000US-0191637P.
XX
XX PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX N-PSDB; ABL11070.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX
```

PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 27693; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 2764 AA;  
 Query Match 75.0%; Score 33; DB 4; Length 2764;  
 Best Local Similarity 55.6%; Pred. No. 2.2e+03;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLMEPV 9  
 Db 1340 YLQMLEPL 1348  
 RESULT 38  
 AAE05485  
 ID AAE05485 standard; protein; 2802 AA.  
 AC  
 XX AAE05485;  
 XX  
 DT 24-SEP-2001 (first entry)  
 XX  
 DE Drosophila neurofibromatosis type 1 (NF1) protein.  
 XX  
 KW Neurofibromatosis type 1; NF1; cyclic AMP; therapy; benign tumour;  
 KM malignant tumour; short stature; hyperpigmentation; white matter lesion;  
 KW learning disability.  
 XX  
 OS Drosophila sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1219..1580  
 FT /note= "Catalytic GAP-related domain (GRD)"  
 XX  
 PN US6261761-B1.  
 XX  
 PD 17-JUL-2001.  
 XX  
 PF 04-APR-2000; 2000US-00542331.  
 XX  
 PR 24-MAR-1997; 97US-0041469P.  
 PR 24-MAR-1998; 98US-00046745.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Zhong Y, Guo H;  
 XX  
 DR WPI; 2001-450484/48.  
 XX  
 PT Identifying compounds that induce production of cyclic AMP, by incubating  
 PT compound with separate cellular preparations that differ by  
 PT neurofibromatosis type I protein content and determining amount of cAMP  
 PT produced.  
 XX  
 PS Example 1; Col 11-26; 23pp; English.  
 XX  
 CC The present invention relates to a method for identifying a compound that  
 CC stimulate cyclic AMP formation comprising incubating compound with  
 CC separate cellular preparations that differ by neurofibromatosis type I  
 CC (NF1) protein content and determining amount of cyclic AMP produced. The

CC compounds identified are used for the prevention of diseases associated  
 CC with a defect in the NF1 protein. The diseases include neurofibromatosis  
 CC type 1, benign tumours, malignant tumours, short stature,  
 CC hyperpigmentation, white matter lesions in the brain and learning  
 CC disabilities. The present sequence is Drosophila sp. neurofibromatosis  
 CC type 1 (NF1) protein  
 XX  
 SQ Sequence 2802 AA;  
 Query Match 75.0%; Score 33; DB 4; Length 2802;  
 Best Local Similarity 55.6%; Pred. No. 2.2e+03;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLMEPV 9  
 Db 1340 YLQMLEPL 1348  
 RESULT 39  
 ABB63789  
 ID ABB63789 standard; protein; 2802 AA.  
 XX  
 AC ABB63789;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 18159.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US009231.  
 PF  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL07892.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 18159; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 2802 AA;  
 Query Match 75.0%; Score 33; DB 4; Length 2802;  
 Best Local Similarity 55.6%; Pred. No. 2.2e+03;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLMEPV 9

```

Db      1340 YLQMLLEPL 1348
      :||:|:|:|:
RESULT 40
ABB08077
ID ABB08077 standard; protein; 2802 AA.
XX
AC ABB08077;
XX
DT 10-SEP-2002 (first entry)
XX
DE Drosophila neurofibromatosis 1 (NFI) protein.
XX
KW NFI; pharmaceutical; memory; learning defect; neurofibromatosis 1;
KW neotropic.
XX
OS Drosophila sp.
XX
PN US6365126-B1.
XX
PD 02-APR-2002.
XX
PF 23-FEB-2000; 2000US-00510791.
XX
PR 24-MAR-1997; 97US-0041469P.
PR 24-MAR-1998; 98US-00046745.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Zhong Y, Guo H, Tong J;
XX
DR WPI; 2002-487726/52.
XX
PT Screening an agent for ability to treat learning and short term memory
PT defects associated with defect in Neurofibromatosis 1 protein, by
PT administering agent to animal and assessing memory formation or learning
PT ability.
XX
PS Example 1; Fig 2A-D; 40pp; English.
XX
CC The invention relates to screening a pharmaceutical agent (PA) for its
CC ability to treat short term memory and learning defects in an animal,
CC associated with a defect in Neurofibromatosis 1 (NFI) protein. The method
CC involves administering PA to the animal, training the animal, assessing
CC memory formation or learning ability in the trained animal and comparing
CC it with that produced by training protocol in a control animal not
CC treated with PA. The identified agent is useful for treating learning or
CC short term memory defect associated with NFI protein in an animal. The
CC present sequence represents the Drosophila NFI protein sequence
XX
SQ Sequence 2802 AA;
      Query Match      75.0%; Score 33; DB 5; Length 2802;
      Best Local Similarity 55.6%; Pred. No. 2.2e+03;
      Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLLMPEV 9
      :||:|:|:
Db      1340 YLQMLLEPL 1348

RESULT 41
ADA34524
ID ADA34524 standard; protein; 107 AA.
XX
AC ADA34524;
XX
DT 20-NOV-2003 (first entry)
XX
DE Acinetobacter baumannii protein #1685.
XX
KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;

KW      plant biocontrol agent.
XX
OS Acinetobacter baumannii.
XX
PN US6562958-B1.
XX
PD 13-MAY-2003.
XX
PF 04-JUN-1999; 99US-00328352.
XX
PR 09-JUN-1998; 98US-0088701P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton G, Bush D;
XX
DR WPI; 2003-576092/54.
DR N-PSDB; ADA30398.
XX
PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX
PS Example; SEQ ID NO 5811; 328pp; English.
XX
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for an A.
CC baumannii protein.
XX
SQ Sequence 107 AA;
      Query Match      72.7%; Score 32; DB 6; Length 107;
      Best Local Similarity 66.7%; Pred. No. 1.3e+02;
      Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLLMPEV 9
      :|:|:|:|:
Db      2 YLEKLMPEV 10

RESULT 42
ADH86453
ID ADH86453 standard; protein; 195 AA.
XX
AC ADH86453;
XX
DT 22-APR-2004 (first entry)
XX
DE Enterococcus faecalis polypeptide #933.
XX
KW Enterococcus faecalis infection; transcription regulatory element;
KW antibacterial.
XX
OS Enterococcus faecalis.
XX
PN US6617156-B1.
XX
PD 09-SEP-2003.
XX
PF 13-AUG-1998; 98US-00134000.
XX
PR 15-AUG-1997; 97US-0055778P.
XX
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
XX

```

PI Doucette-Stamm LA, Bush D;  
 XX  
 DR WPI; 2003-895394/82.  
 DR N-PSDB; ADH83048.  
 XX  
 PT New nucleic acid comprising a sequence encoding an *Enterococcus faecalis*  
 PT polypeptide, useful for preparing a composition for diagnosing or  
 PT treating *E. faecalis* infection.  
 XX  
 PS Disclosure; SEQ ID NO 4338; 193pp; English.  
 XX  
 CC The invention relates to *Enterococcus faecalis* polynucleotides and  
 CC polypeptides. The invention also relates to a recombinant expression  
 CC vector comprising a polynucleotide operably linked to a transcription  
 CC regulatory element, a cell comprising a recombinant vector, a method for  
 CC producing an *E. faecalis* polypeptide, an isolated nucleic acid comprising  
 CC a sequence not given in the specification, a recombinant vector  
 CC comprising the nucleic acid and a cell comprising the recombinant vector.  
 CC The polynucleotides can be used to detect the presence of *E. faecalis* in  
 CC a sample. The sequences are useful for preparing a composition for  
 CC diagnosing or treating *Enterococcus faecalis* infection. This sequence  
 CC represents an *E. faecalis* polypeptide of the invention.  
 XX  
 SQ Sequence 195 AA;  
 Query Match 72.7%; Score 32; DB 7; Length 195;  
 Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLMEP 8  
 DB 27 FLQVIMDP 34  
 RESULT 43  
 ADX90400  
 ID ADX90400 standard; protein; 272 AA.  
 XX  
 AC ADX90400;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Plant full length insert polypeptide seqid 53064.  
 XX  
 KW plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content.  
 XX  
 OS Unidentified.  
 XX  
 US2004034888-A1.  
 PN  
 XX  
 PD 19-FEB-2004.  
 XX  
 XX 28-APR-2003; 2003US-00425114.  
 PF  
 XX 06-MAY-1999; 99US-00304517.  
 PR  
 XX 05-NOV-2001; 2001US-00985678.  
 XX  
 PA (LIU/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX  
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 PI N-PSDB; ADR21274.  
 DR GENBANK; EAA01603.

DR WPI; 2004-180133/17.  
 XX  
 PT New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 PS Claim 1; SEQ ID NO 53064; 15pp; English.  
 XX  
 CC The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.seqdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX  
 SQ Sequence 272 AA;  
 Query Match 72.7%; Score 32; DB 8; Length 272;  
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLQLMEPV 9  
 DB 113 FYQLLVEPL 121  
 RESULT 44  
 ADR21275  
 ID ADR21275 standard; protein; 290 AA.  
 XX  
 AC ADR21275;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Mosquito FGE orthologue protein SEQ ID NO:54.  
 XX  
 KW formylglycine generating enzyme; FGE;  
 KW Calpha-formylglycine generating activity; immunogenic;  
 KW Multiple Sulphatase Deficiency; MSD; gene therapy; sulphatase deficiency;  
 KW Mucopolysaccharidosis; Metachromatic Leukodystrophy; X-linked Ichthyosis;  
 KW FGE orthologue.  
 XX  
 OS Anopheles gambiae.  
 XX  
 PN WO2004072275-A2.  
 XX  
 PD 26-AUG-2004.  
 XX  
 XX 10-FEB-2004; 2004WO-US003632.  
 PF  
 XX 11-FEB-2003; 2003US-0447747P.  
 PR  
 XX (TRAN-) TRANSKARYOTIC THERAPIES INC.  
 PA  
 XX Von Figura K, Schmidt B, Dierks T, Heartlein MW, Ballabio A;  
 PI Cosma MP;  
 XX  
 DR WPI; 2004-625871/60.  
 DR N-PSDB; ADR21274.  
 DR GENBANK; EAA01603.

XX New nucleic acid molecule encoding Formylglycine Generating Enzyme,  
PT useful for diagnosing and treating Multiple Sulfatase Deficiency and  
PT other sulfatase deficiencies, e.g. Mucopolysaccharidosis or Metachromatic  
XX Leukodystrophy.  
XX  
PS Claim 19; SEQ ID NO 54; 224pp; English.  
XX  
CC The present invention describes an isolated formylglycine generating  
CC enzyme (FGE) nucleic acid molecule (1). Also described: (1) an expression  
CC vector comprising (1) operably linked to a promoter; (2) a host cell  
CC transformed or transfected with the expression vector of (1); (3) an  
CC isolated polypeptide encoded by (1), where the polypeptide, or its  
CC fragment, has Calpha-formylglycine generating activity and is immunogenic  
CC ; (4) an isolated binding polypeptide which binds selectively a  
CC polypeptide of (3); (5) a family of isolated polypeptides having Calpha-  
CC formylglycine generating activity; (6) a method for determining the level  
CC of FGE expression in a subject; (7) a method for identifying an agent  
CC useful in modulating Calpha-formylglycine generating activity; (8) a  
CC method of diagnosing or determining Multiple Sulphatase Deficiency (MSD)  
CC in a subject; (9) a kit comprising a package containing an agent that  
CC selectively binds to (1) or its expression product, and a control for  
CC comparing to a measured value of binding of the agent to (1) or its  
CC expression product; (10) a method for treating MSD in a subject; (11) a  
CC method for increasing Calpha-formylglycine generating activity in a  
CC subject; (12) a method for increasing Calpha-formylglycine generating  
CC activity in a cell; (13) a pharmaceutical composition comprising an agent  
CC comprising (1), or a sulphatase that is produced by a cell, in a  
CC pharmaceutical amount to treat MSD, and a pharmaceutical carrier; (14) a  
CC method for identifying a candidate agent useful in the treatment of MSD;  
CC (15) a method for increasing sulphatase activity in a cell; (16) an  
CC isolated variant allele of a human FGE gene, which encodes a variant FGE  
CC polypeptide; (17) an isolated variant human FGE polypeptide; (18) an  
CC antibody having the variant human FGE polypeptide of (17) as an immunogen  
CC ; and (19) a sulphatase-producing cell comprising a sulphatase with an  
CC increased expression, and an FGE with an increased expression, where the  
CC ratio of active sulphatase to total sulphatase produced by the cell is  
CC increased by at least 5% over the ratio of active sulphatase to total  
CC sulphatase produced by the cell in the absence of the FGE. (1) can be  
CC used in gene therapy. The nucleic acid molecule (1), compositions, and  
CC methods of the present invention can be used for diagnosing and treating  
CC MSD and other sulphatase deficiencies, e.g. Mucopolysaccharidosis,  
CC Metachromatic Leukodystrophy, or X-linked Ichthyosis. The gene mutated in  
CC MSD is FGE, which maps to human chromosome 3p26. The present sequence  
CC represents an FGE orthologue, which is used in an example from the  
XX present invention.  
XX  
SQ Sequence 290 AA;  
Query Match 72.7%; Score 32; DB 8; Length 290;  
Best Local Similarity 77.8%; Pred. No. 3.5e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FQQLMEPV 9  
| | | | |  
Db 84 FQQLSEPV 92  
RESULT 45  
AAAY42689  
ID AAAY42689 standard; protein; 316 AA.  
XX  
AC AAAY42689;  
XX  
DT 17-JAN-2000 (first entry)  
XX  
DE His6-pregnane X receptor (PXR) sequence.  
XX  
KW Human; nuclear receptor; pregnane X receptor; PXR; CYP; CYP3A4;  
KW cytochrome P-450 mono-oxygenase; drug interaction; hPXR.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..11  
FT /label= His6  
FT Protein 12..316  
FT /label= hPXR  
XX  
PN WO200197856-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 21-JUN-2001; 2001WO-IB001629.  
XX  
PR 21-JUN-2000; 2000US-00598267.

XX WO9948915-A1.  
XX 30-SEP-1999.  
XX  
XX 26-MAR-1999; 99WO-US006737.  
XX  
XX 27-MAR-1998; 98US-0079593P.  
XX (GLAX ) GLAXO GROUP LTD.  
XX  
XX Klierer SA, Willson TM;  
XX  
XX WPI; 1999-601202/51.  
XX  
PT New human pregnane X receptor, used to identify specific modulators and  
PT agents that induce expression of cytochrome P-450 mono-oxygenase.  
XX  
PS Example 6; Page 37; 69pp; English.  
XX  
CC The invention provides an isolated human nuclear receptor (designated  
CC pregnane X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase  
CC (CYP) promoter. The hPXR is used to identify its specific modulators,  
CC and compounds that induce CYP3A4 expression (i.e. to identify drug  
CC interactions, since CYP3A4 is involved in many biotransformations of  
CC drugs). The modulators are potentially useful for: associating particular  
CC diseases and conditions with PXR and for treating such conditions.  
CC Antibodies raised against hPXR can be used for determination and  
CC purification of hPXR. The present sequence represents a histidine-6  
CC tagged partial PXR (His6-PXR) sequence  
XX  
SQ Sequence 316 AA;  
Query Match 72.7%; Score 32; DB 2; Length 316;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FQQLMEPV 9  
| | | | |  
Db 197 FQQLLEPM 205  
RESULT 46  
AAMS0626  
ID AAMS0626 standard; protein; 316 AA.  
XX  
AC AAMS0626;  
XX  
DT 04-APR-2002 (first entry)  
XX  
DE His6-tagged human pregnane X receptor.  
XX  
KW Pregnane X; receptor; hPXR; human; liver; CYP3A4;  
KW cytochrome P450 monoxygenase; cirrhosis; cholangitis; hepatitis;  
KW cholestasis; hepatotropic; antiinflammatory; therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..11  
FT /label= His6  
FT Protein 12..316  
FT /label= hPXR  
XX  
PN WO200197856-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 21-JUN-2001; 2001WO-IB001629.  
XX  
PR 21-JUN-2000; 2000US-00598267.

XX PA (GLAX ) GLAXO GROUP LTD.  
 XX PI Klierwer SA, Jones SA, Willson TM;  
 XX DR WPI; 2002-139767/18.  
 XX PT Compound that induces cytochrome P-450 monooxygenase 3A4 gene expression  
 PT for treating cholestatic liver disease comprising administering compound  
 PT identified by determining binding of test compound to human pregnane X  
 PT receptor.  
 XX PS Example 6; Page 40; 63pp; English.  
 XX CC The present sequence is that of a recombinant protein comprising an N-  
 CC terminal His6 tag followed by amino acids 130-434 of the novel human  
 CC pregnane X receptor (PXR, AM50626). A DNA sequence encoding His6-PXR was  
 CC constructed in vector PRSET1. Plasmid His6-PXR/PRSET1 was cotransformed  
 CC with a plasmid encoding retinoic acid receptor-alpha (RXR-alpha) into  
 CC Escherichia coli BL21(DE3), and an His6-PXR/RXR-alpha complex was  
 CC obtained. hPXR is a novel member of the nuclear receptor superfamily. It  
 CC binds to a DNA response element in the cytochrome P450 monooxygenase  
 CC CYP3A4 gene promoter as a heterodimer with RXR, and is activated by  
 CC compounds known to modulate CYP3A4 expression. The invention provides  
 CC nucleic acids encoding hPXR, expression vectors, host cells, methods of  
 CC making the receptor, and methods of using the receptor or receptor-  
 CC encoding sequences to screen for compounds capable of modulating CYP  
 CC (e.g. CYP3A4) gene expression. Such compounds are useful for treating  
 CC cholestatic liver disease (claimed), such as primary biliary cirrhosis,  
 CC primary sclerosing cholangitis, autoimmune hepatitis with cholestatic  
 CC features, autoimmune cholangitis, cholestasis of pregnancy, paediatric  
 CC cholestatic syndromes, and drug-induced cholestasis  
 XX SQ Sequence 316 AA;  
 Query Match 72.7%; Score 32; DB 5; Length 316;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 FLOLLMEPV 9  
 Db 197 FQQLLEPM 205  
 RESULT 47  
 ADW68625  
 ID ADW68625 standard; protein; 322 AA.  
 AC ADW68625;  
 XX 07-APR-2005 (first entry)  
 XX DE Human transcriptional regulation protein - SEQ ID 20.  
 XX KW transcription regulation; inflammatory disease; antiinflammatory;  
 KW liver tumor; stomach tumor; colon tumor; intestine tumor; leukemia;  
 KW cytostatic; lymphoma; diabetes; antidiabetic; obesity; anorectic;  
 KW rheumatoid arthritis; antiarthritic; antirheumatic.  
 XX OS Homo sapiens.  
 XX JP2005021093-A.  
 XX PD 27-JAN-2005.  
 XX PF 03-JUL-2003; 2003JP-00191215.  
 XX PR 03-JUL-2003; 2003JP-00191215.  
 XX PA (BIOT-) BIOTECHNOLOGY KAIHATSU GIJUTSU KENKYU KU.  
 XX (Z01J-) Z01JIN KK.  
 XX WPI; 2005-145738/16.  
 DR N-PSDB; ADM68615.  
 XX New protein with transcriptional regulation activity, useful as a target  
 PT in screening to identify modulators which are potentially useful for  
 PT treating inflammatory diseases.  
 XX Claim 1; SEQ ID NO 20; 167pp; Japanese.  
 XX The invention comprises the amino acid and coding sequences of human  
 CC proteins which possess transcriptional regulation activity. The DNA and  
 CC protein sequences of the invention are useful in the diagnosis of;  
 CC inflammatory diseases, liver cancer, stomach cancer, colon cancer, small  
 CC intestine cancer, leukemia, lymphoma, diabetes, obesity, and rheumatoid  
 CC arthritis. The present amino acid sequence represents a human  
 CC transcriptional regulation protein of the invention.  
 XX SQ Sequence 322 AA;  
 Query Match 72.7%; Score 32; DB 9; Length 322;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 FLOLLMEPV 9  
 Db 203 FQQLLEPM 211  
 RESULT 48  
 ADC95833  
 ID ADC95833 standard; protein; 323 AA.  
 AC ADC95833;  
 XX 01-JAN-2004 (first entry)  
 XX DE E. faecium protein sequence SEQ ID 5460.  
 XX KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;  
 KW abdominal-pelvic infection.  
 XX OS Enterococcus faecium.  
 XX US6583275-B1.  
 XX 24-JUN-2003.  
 XX PF 30-JUN-1998; 98US-00107532.  
 XX PR 02-JUL-1997; 97US-0051571P.  
 XX PR 14-MAY-1998; 98US-0085598P.  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 XX Doucette-Stamm LA, Bush D;  
 WPI; 2003-799836/75.  
 N-PSDB; ADC92179.  
 New isolated nucleic acid derived from Enterococcus faecium encoding an  
 Enterococcus faecium polypeptide useful for detection, prevention and  
 treatment of a pathological condition resulting from a bacterial  
 infection.  
 Example 1; SEQ ID NO 5460; 243pp; English.  
 The invention relates to an isolated nucleic acid derived from  
 Enterococcus faecium encoding an Enterococcus faecium polypeptide having  
 one of 10 fully defined sequences given in the for comprising 40  
 sequential nucleotides chosen from any of the nucleic acids, its  
 complement or sequences hybridising to it). Also included are a  
 recombinant vector comprising the nucleic acid operably linked to  
 transcription regulatory element, a cell comprising the vector and a  
 single-stranded probe comprising the nucleic acid. The nucleic acids are

CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acid is useful for diagnosing pathological conditions  
CC resulting from E. faecium bacterial infection (e.g. urinary tract  
CC infection, bacteraemia, endocarditis, wounds and abdominal-peivic  
CC infection) and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of Candida albicans -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium proteins.  
XX  
SQ

Sequence 323 AA;

Query Match 72.7%; Score 32; DB 7; Length 323;  
Best Local Similarity 62.5%; Pred. No. 3.9e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLMEP 8  
Db 155 FQVIMDP 162  
|||:|:

RESULT 49

AAU78295  
ID AAU78295 standard; protein; 329 AA.

AC AAU78295;

XX 18-JUN-2002 (first entry)

XX Human Pregnane X Receptor (PXR) ligand binding domain (LDB) protein.

XX Human; pregnane X; receptor; PXR; ligand binding domain; LDB; xenobiotic.

XX Homo sapiens.

XX WO200218420-A2.

XX 07-MAR-2002.

XX 17-AUG-2001; 2001WO-BF009488.

XX 28-AUG-2000; 2000EP-00118634.

XX (LION-) LION BIOSCIENCE AG.

XX Albers M, Ellwanger S, Koesgl M, Loeser E;

XX WPI; 2002-292195/33.

XX N-PSDB; ABK47576.

XX New nucleic acids and cofactors of the pregnane x nuclear receptor (PXR),  
PT which the nucleic acid encode, useful for screening agonists or  
PT antagonists of PXR, and for determining a subject's response to  
PT xenobiotic substances or drugs.

PS Claim 13; Fig 6; 102pp; English.

XX The present invention relates to a new nucleic acid molecule and its  
CC encoded polypeptide. The nucleic acid codes for a cofactor of the  
CC pregnane x nuclear receptor (PXR). The polypeptide encoded by the nucleic  
CC acid comprises 225 amino acids or 293 amino acids fully defined in the  
CC specification. The nucleic acid is useful for making vectors and  
CC transforming cells, both of which are ultimately useful for producing the  
CC cofactor proteins. The nucleic acids may also be used for determining a  
CC subject's response to xenobiotic substances or drugs. The proteins or  
CC complexes are useful for screening substances that bind the proteins or  
CC complexes, particularly agonists or antagonists of PXR. The present amino  
CC acid sequence represents the human PXR ligand binding domain (LBD) of the  
CC invention

Sequence 329 AA;

Query Match 72.7%; Score 32; DB 5; Length 329;  
Best Local Similarity 66.7%; Pred. No. 4e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLMEPV 9  
Db 210 FQQLLEPM 218  
|||:|:

RESULT 50

ADT59178  
ID ADT59178 standard; protein; 362 AA.

XX ADT59178;

XX 13-JAN-2005 (first entry)

XX Plant polypeptide, SEQ ID 9255.

XX Plant; transgenic; cold tolerance; growth rate; drought tolerance;  
KW disease resistance; galactomannan production; plant growth regulator;  
KW heat tolerance; herbicide tolerance; lignin production;  
KW extreme osmotic condition tolerance; pathogens resistance;  
KW pest resistance; yield improvement; seed oil yield; seed protein yield.

XX Viridiplantae.

XX US2004216190-A1.

XX 28-OCT-2004.

XX 18-DEC-2003; 2003US-00739930.

XX 28-APR-2003; 2003US-00424599.

XX 28-APR-2003; 2003US-00425115.

XX (KOVA/) KOVALIC D K.

XX Kovalic DK;

XX WPI; 2004-757369/74.

XX New recombinant DNA constructs useful in the field of biochemistry and  
PT genetics, and in particular for producing transgenic plants with improved  
PT biological characteristics.

PS Claim 2; SEQ ID NO 9255; 14pp; English.

XX The invention relates a recombinant DNA construct comprising a  
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:  
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences  
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,  
CC Arabidopsis, wheat and rape but the specification does not indicate which  
CC sequences is derived from which organism. Also included is a method of  
CC producing a plant having an improved property, comprising transforming a  
CC plant with a recombinant DNA construct comprising a promoter region  
CC functional in a plant cell operably joined to a polynucleotide encoding a  
CC polypeptide associated with the property, and growing the transformed  
CC plant. The property is selected from improving plant cold tolerance, for  
CC manipulating growth rate in plant cells by modification of the cell cycle  
CC pathway, for improving plant drought tolerance, for providing increased  
CC resistance to plant disease, for galactomannan production, for production  
CC of plant growth regulators, for improving plant heat tolerance, for  
CC improving plant tolerance to herbicides, for increasing the rate of  
CC homologous recombination in plants, for lignin production, for improving  
CC plant tolerance to extreme osmotic conditions, for improving plant  
CC tolerance to pathogens or pests, for yield improvement by modification of  
CC photosynthesis, for modifying seed oil yield and/or content, for  
CC modifying seed protein yield and/or content, for yield improvement by  
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake  
CC and for yield improvement by providing improved plant growth and  
CC development under at least one stress condition. The polynucleotide may  
CC also encode a plant transcription factor. The methods and compositions of



CC the present invention are useful in the field of biochemistry and  
CC genetics, in particular for producing transgenic plants with improved  
CC biological characteristics such as increased yield, improved nitrogen  
CC flow, increasing plant tolerance to cold or heat, improving plant  
CC tolerance to extreme osmotic and drought conditions, and improving plant  
CC tolerance to plant pests or pathogens. They can also be used in physical  
CC arrays of molecules, plant breeding markers, computer-based storage and  
CC analysis systems. The present sequence is one of the 5544 plant protein  
CC sequences of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=20040216190.

XX

SQ Sequence 362 AA;

Query Match 72.7%; Score 32; DB 8; Length 362;  
Best Local Similarity 87.5%; Pred. No. 4.4e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMEPV 9  
|||  
Db 132 LQLTEPV 139

Search completed: May 9, 2006, 02:16:01  
Job time : 131.4 secs

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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:17:29 ; Search time 16.4 Seconds  
(without alignments)  
52.802 Million cell updates/sec

Title: US-09-870-216C-3  
Perfect score: 44  
Sequence: 1 FLQLMEPV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	35	79.5	379	T14337	RAD23 protein, iso
2	34	77.3	318	E95218	iron-compound ABC
3	34	77.3	318	C98082	hypothetical prote
4	34	77.3	1254	T24897	hypothetical prote
5	33	75.0	113	H86296	F309.1 protein - A
6	33	75.0	318	G89845	hypothetical prote
7	33	75.0	409	S44346	RAD23 protein homo
8	33	75.0	908	S07649	gene col intron 1
9	33	75.0	2764	T13949	neurofibromin - fr
10	33	75.0	2802	T13945	neurofibromin - fr
11	33	75.0	2802	T13947	neurofibromin - fr
12	32	72.7	382	T14336	RAD23 protein, iso
13	32	72.7	480	A82042	xanthine/uracil pe
14	32	72.7	504	T04076	protoporphyrinogen
15	32	72.7	536	F86251	hypothetical prote
16	32	72.7	643	A41120	prostaglandin tran
17	32	72.7	687	B64126	transposase homolo
18	32	72.7	1101	S58108	hypothetical prote
19	32	72.7	1510	T16927	hypothetical prote
20	31	70.5	142	C36179	gonadotropin II be
21	31	70.5	142	I50143	gonadotropin II be
22	31	70.5	255	A69939	conserved hypothet
23	31	70.5	342	T29192	hypothetical prote
24	31	70.5	401	T01001	hypothetical prote
25	31	70.5	456	S69677	hypothetical prote
26	31	70.5	539	T10826	reticuline oxidase
27	31	70.5	639	A55019	muscarinic acetylch
28	31	70.5	730	T43317	pgl-1 protein - Ca
29	31	70.5	771	T29177	hypothetical prote

probable helicase  
Gem-interacting pr  
MHC class III hist  
protein P12K11.4 [  
hypothetical prote  
hypothetical prote  
probable membrane  
gonadotropin beta  
hypothetical prote  
dipeptide abc tran  
probable dipeptide  
hypothetical prote  
protein F20B17.8 [  
lipid-A-disacchari  
F22M8.11 protein -  
hypothetical prote  
hypothetical prote  
matrix metalloprot  
DNA topoisomerase  
plakoglobin - Afri  
band 3 anion trans  
translation elonga  
translation elonga  
band 3 anion trans  
chromosome 5 GAP-1  
band 3 protein - m  
hypothetical prote  
glutamate synthase  
hypothetical prote  
hypothetical prote  
E7 protein - Europ  
transcription init  
14.6K membrane pro  
hypothetical prote  
chemotaxis protein  
H+-transporting tw  
hypothetical prote  
recR protein - Dei  
hypothetical prote  
hypothetical prote  
hypothetical prote  
p2y6 receptor - hu  
ribonucleoside red  
probable transcrip  
transcription init  
hypothetical prote  
probable topoisome  
RAD23 protein homo  
RAD23 protein homo  
regulatory protein  
glycosyltransferas  
RAD 23B protein -  
two-component syst  
msAP1a - mouse  
NADH2 dehydrogenas  
replicative DNA he  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable membrane  
probable ribonucle  
probable nuclear d  
reticuline oxidase  
85K SH3 domain-con  
properin convert  
acyl-CoA dehydroge  
hypothetical prote  
beta-catenin - mou  
beta-catenin - Afr  
beta-catenin - hum

103	29	65.9	822	2	S56801	hypothetical prote	176	28	63.6	627	2	S46820	hypothetical prote
104	29	65.9	845	2	S32819	translation elonga	177	28	63.6	634	1	A55683	L-iduronidase (EC
105	29	65.9	849	2	G64342	hypothetical prote	178	28	63.6	671	2	T51789	hypothetical prote
106	29	65.9	893	2	G59431	phosphatidylinosit	179	28	63.6	672	2	A41075	inositol-1,4,5-tri
107	29	65.9	908	2	T48899	disease resistance	180	28	63.6	694	2	F90609	exodeoxyribonuclea
108	29	65.9	922	2	T18878	hypothetical prote	181	28	63.6	731	2	S18243	photosystem I prot
109	29	65.9	970	2	S29069	inositol polyphosp	182	28	63.6	733	2	S06902	photosystem I prot
110	29	65.9	974	2	T29007	translation elonga	183	28	63.6	734	1	S26072	photosystem I prot
111	29	65.9	987	2	H86197	hypothetical prote	184	28	63.6	734	2	S73206	photosystem I prot
112	29	65.9	1005	2	I40588	transposase (tn540	185	28	63.6	734	2	T07280	photosystem I P700
113	29	65.9	1133	2	T30561	scythe protein - A	186	28	63.6	735	2	S41481	P700 chlorophyll a
114	29	65.9	1210	2	T39055	hypothetical prote	187	28	63.6	736	2	B28341	photosystem I P700
115	29	65.9	1602	2	H70984	probable polyketid	188	28	63.6	737	2	T06839	probable photosyst
116	29	65.9	1763	2	T19183	hypothetical prote	189	28	63.6	741	1	S20923	photosystem I prot
117	29	65.9	1769	2	T19184	hypothetical prote	190	28	63.6	741	2	AC2450	photosystem I core
118	29	65.9	2073	1	BWASBE	bimE protein - Eme	191	28	63.6	742	2	I39616	photosystem I prot
119	29	65.9	3076	2	A87058	fatty acid synthas	192	28	63.6	742	2	AB2470	photosystem I P700
120	29	65.9	3944	2	T19997	hypothetical prote	193	28	63.6	755	2	T46411	hypothetical prote
121	28	63.6	111	2	D72707	hypothetical prote	194	28	63.6	770	2	T01527	hypothetical prote
122	28	63.6	143	2	B70596	hypothetical prote	195	28	63.6	771	2	AB2160	gene coxII intron
123	28	63.6	149	1	G70400	phosphonistidine p	196	28	63.6	827	2	S25949	translation elonga
124	28	63.6	155	2	T37559	ubiquitin-conjugat	197	28	63.6	830	2	A34347	major acidic nucle
125	28	63.6	170	2	F85093	hypothetical prote	198	28	63.6	1023	2	JC4013	probable membrane
126	28	63.6	173	2	H87009	probable membrane	199	28	63.6	1025	2	S50293	guanylate kinase-i
127	28	63.6	182	2	H75941	hypothetical prote	200	28	63.6	1032	2	T18293	neurabin - rat
128	28	63.6	189	2	F82969	hypothetical prote	201	28	63.6	1095	2	T43275	two-component sens
129	28	63.6	194	2	A75515	conserved hypothet	202	28	63.6	1131	2	AD2166	hypothetical prote
130	28	63.6	197	2	I50469	RAG-1 protein - sa	203	28	63.6	1192	2	T17255	hypothetical prote
131	28	63.6	202	2	D84305	hypothetical prote	204	28	63.6	1202	2	T37867	hypothetical prote
132	28	63.6	268	2	D64223	probable 1-acylgly	205	28	63.6	1408	2	S57049	hypothetical prote
133	28	63.6	271	2	B87266	conserved hypothet	206	28	63.6	3083	2	AH2493	hypothetical prote
134	28	63.6	275	2	T17127	hypothetical prote	207	28	63.6	3845	2	T31067	BIR repeat contain
135	28	63.6	308	2	AF0461	probable membrane	208	28	63.6	9376	2	T14593	syringomycin synth
136	28	63.6	310	2	T46035	ATMYB84 - Arabidop	209	27.5	62.5	478	2	AD0043	aspartate ammonia-
137	28	63.6	315	2	B83778	ferrichrome ABC tr	210	27	61.4	76	2	AH2310	hypothetical prote
138	28	63.6	328	2	D70574	hypothetical prote	211	27	61.4	81	2	S56702	E7 protein - deer
139	28	63.6	328	2	E72264	conserved hypothet	212	27	61.4	102	1	W7WLDP	platelet factor 4
140	28	63.6	360	2	B46647	melanocortin recep	213	27	61.4	104	1	PFHUA4	unknown protein en
141	28	63.6	366	2	D83350	hypothetical prote	214	27	61.4	104	2	C85716	hypothetical prote
142	28	63.6	370	1	TWMT1	transforming prote	215	27	61.4	117	2	T17733	hypothetical flag
143	28	63.6	370	1	TWMT1	transforming prote	216	27	61.4	128	2	AD1163	hypothetical flag
144	28	63.6	370	1	TWMT1	transforming prote	217	27	61.4	128	2	AD1522	hypothetical prote
145	28	63.6	372	2	T10202	hypothetical prote	218	27	61.4	130	2	B83992	hypothetical prote
146	28	63.6	374	2	T05891	myb-related protei	219	27	61.4	142	2	T18166	hypothetical prote
147	28	63.6	375	2	AG1993	hypothetical prote	220	27	61.4	155	2	I45913	interleukin-2 prec
148	28	63.6	376	2	T51673	myb-related trans	221	27	61.4	155	2	S38662	interleukin-2 - go
149	28	63.6	386	2	S41497	thyroid hormone re	222	27	61.4	155	2	S11488	hypothetical prote
150	28	63.6	387	2	S77268	carboxynorspermid	223	27	61.4	171	2	T18167	NAD(P)H-flavin oxi
151	28	63.6	402	2	T09062	probable advanced	224	27	61.4	200	2	AF2578	thermophilic NAD(P
152	28	63.6	404	2	T07121	protoporphyrinogen	225	27	61.4	200	2	E97360	hypothetical prote
153	28	63.6	406	2	E81300	probable glucose-6	226	27	61.4	215	2	A81410	hypothetical prote
154	28	63.6	411	2	D83973	hypothetical prote	227	27	61.4	217	2	B83604	hypothetical prote
155	28	63.6	421	2	T44511	hypothetical prote	228	27	61.4	230	2	H90043	hypothetical prote
156	28	63.6	426	2	T44522	hypothetical prote	229	27	61.4	232	2	B64442	hypothetical prote
157	28	63.6	428	2	S70670	3-deoxy-D-manno-2-	230	27	61.4	235	2	H70848	probable maturase
158	28	63.6	436	2	S42160	MS51 protein - ye	231	27	61.4	238	2	S24267	cooB protein - Bac
159	28	63.6	436	2	E59237	probable glutamate	232	27	61.4	248	2	C71624	variant-specific s
160	28	63.6	447	2	E84155	hypothetical prote	233	27	61.4	252	2	G75340	hypothetical prote
161	28	63.6	460	2	T21678	hypothetical prote	234	27	61.4	256	2	S27109	MADS box protein A
162	28	63.6	468	2	B75053	dinf related PAB14	235	27	61.4	257	2	T26312	hypothetical prote
163	28	63.6	472	2	C71172	hypothetical prote	236	27	61.4	261	2	S24418	dmpB protein - Pse
164	28	63.6	498	2	A10482	phosphate transpor	237	27	61.4	271	2	C96015	probable hydroxypp
165	28	63.6	529	2	F71547	probable oligopept	238	27	61.4	272	2	T25874	hypothetical prote
166	28	63.6	589	2	A29476	muscarinic acetyl	239	27	61.4	279	2	A40027	cyclin G1 homolog
167	28	63.6	589	2	B29514	muscarinic acetyl	240	27	61.4	286	2	T47064	hypothetical prote
168	28	63.6	590	2	S10128	muscarinic acetyl	241	27	61.4	286	2	A10230	probable binding-p
169	28	63.6	590	2	S01114	muscarinic acetyl	242	27	61.4	289	2	S72392	hypothetical prote
170	28	63.6	590	2	S47572	muscarinic acetyl	243	27	61.4	292	2	T44230	hypothetical prote
171	28	63.6	592	2	B82498	sulfate permease f	244	27	61.4	292	2	T44044	glycoprotein limpo
172	28	63.6	598	2	T32430	hypothetical prote	245	27	61.4	296	2	B82092	outer membrane pro
173	28	63.6	611	2	A72393	hypothetical prote	246	27	61.4	306	2	JC4347	uroporphyrin-III C
174	28	63.6	612	2	T13616	hypothetical prote	247	27	61.4	318	2	A65041	hypothetical prote
175	28	63.6	627	2	A69663	DNA mismatch repai	248	27	61.4	318	2	A12236	hypothetical prote

249	27	61.4	321	1	R5UBP0	acidic ribosomal p	322	27	61.4	552	2	D96808	protein P28KL9.6 [
250	27	61.4	330	2	D95963	probable phosphate	323	27	61.4	653	2	S27270	proprotein convert
251	27	61.4	338	2	F71690	hypothetical prote	324	27	61.4	686	1	E71106	probable DNA topoi
252	27	61.4	341	2	T50053	probable esterase	325	27	61.4	705	2	S45769	probable membrane
253	27	61.4	348	1	D8E003	dihydroorotase (EC	326	27	61.4	709	2	T00664	hypothetical prote
254	27	61.4	348	2	D85668	dihydro-orotase [i	327	27	61.4	713	2	H97827	organic solvent to
255	27	61.4	348	2	H90808	dihydro-orotase [i	328	27	61.4	731	2	S46813	lanosterol synthas
256	27	61.4	354	2	T27712	hypothetical prote	329	27	61.4	731	2	T28744	hypothetical prote
257	27	61.4	358	2	T05051	fructose-bisphosph	330	27	61.4	734	1	A2LVP7	photosystem I P700
258	27	61.4	358	2	T08635	hypothetical prote	331	27	61.4	734	1	A2NTP7	photosystem I P700
259	27	61.4	359	2	B82291	probable spermidin	332	27	61.4	734	1	A2R2P7	photosystem I P700
260	27	61.4	364	2	T25086	hypothetical prote	333	27	61.4	734	2	S60184	photosystem I prot
261	27	61.4	368	2	A75377	6-phosphogluconate	334	27	61.4	734	2	T07544	photosystem I prot
262	27	61.4	375	2	T40115	uv excision repair	335	27	61.4	734	2	S00445	photosystem I prot
263	27	61.4	375	2	T25089	hypothetical prote	336	27	61.4	734	2	S00704	photosystem I prot
264	27	61.4	391	2	H87422	L-lactate 2-monoox	337	27	61.4	735	2	S58551	photosystem I prot
265	27	61.4	396	1	A58938	surface protein rh	338	27	61.4	735	2	C95936	conserved hypotet
266	27	61.4	403	2	S45176	26S proteinase reg	339	27	61.4	747	2	T40728	hypothetical prote
267	27	61.4	405	2	T29639	hypothetical prote	340	27	61.4	768	2	D86404	unknown protein [i
268	27	61.4	407	2	D86706	hypothetical prote	341	27	61.4	773	2	A46627	carnitine palmitoy
269	27	61.4	409	2	T40969	hypothetical prote	342	27	61.4	780	2	T44218	DNA helicase/prima
270	27	61.4	409	2	C87319	hypothetical prote	343	27	61.4	780	2	T44033	origin binding pro
271	27	61.4	413	2	T06325	malate dehydrogena	344	27	61.4	782	2	G96698	hypothetical prote
272	27	61.4	413	2	D72388	hypothetical prote	345	27	61.4	791	2	T30896	hypothetical prote
273	27	61.4	414	2	T15086	hypothetical prote	346	27	61.4	795	2	F86529	60 kDa inner membr
274	27	61.4	419	2	T23949	hypothetical prote	347	27	61.4	795	2	E81575	inner membrane pro
275	27	61.4	421	1	A34003	gastric intrinsic	348	27	61.4	795	2	G72092	60 kDa inner membr
276	27	61.4	422	2	T18805	cytochrome P450 CY	349	27	61.4	817	2	S33793	hypothetical prote
277	27	61.4	423	2	G71315	probable DNA polym	350	27	61.4	827	2	C84546	hypothetical prote
278	27	61.4	428	2	AF1384	hypothetical prote	351	27	61.4	835	2	T34770	probable transport
279	27	61.4	435	2	D82955	probable MFS dicar	352	27	61.4	844	2	T41085	anion transporter
280	27	61.4	439	2	T25494	probable cytochrom	353	27	61.4	849	2	S64195	probable ubiquitin
281	27	61.4	439	2	AC0462	glycerol-3-phospha	354	27	61.4	859	2	B96625	HTF1 protein - yea
282	27	61.4	448	2	E96601	hypothetical prote	355	27	61.4	867	2	B96625	hypothetical prote
283	27	61.4	452	2	E72108	hypothetical prote	356	27	61.4	868	2	A82722	bifunctional diam
284	27	61.4	452	2	F86514	hypothetical prote	357	27	61.4	876	2	T51951	gamma-adaptin 1 [i
285	27	61.4	452	2	E81562	hypothetical prote	358	27	61.4	883	2	T23948	hypothetical prote
286	27	61.4	456	2	A90013	conserved hypotet	359	27	61.4	885	2	D86151	F22M8.8 protein -
287	27	61.4	463	2	T28748	hypothetical prote	360	27	61.4	906	2	T48898	disease resistance
288	27	61.4	464	2	G83957	probable heat-shoc	361	27	61.4	921	2	AE0332	conserved hypotet
289	27	61.4	467	2	T21236	hypothetical prote	362	27	61.4	922	2	A30816	band 3 anion trans
290	27	61.4	467	2	E69601	ATP-dependent Clp	363	27	61.4	982	1	A44831	phosphoenolpyruvat
291	27	61.4	467	2	A85363	probable calmoduli	364	27	61.4	982	2	AE2413	phosphoenolpyruvat
292	27	61.4	467	2	T40513	yeast erol homolog	365	27	61.4	1037	2	S37879	nuclear pore prote
293	27	61.4	478	2	H90445	hypothetical prote	366	27	61.4	1070	2	T06733	kinesin homolog F2
294	27	61.4	479	1	B64043	conserved hypotet	367	27	61.4	1076	2	B85295	probable DNA misa
295	27	61.4	489	2	A47200	EcoA system protei	368	27	61.4	1076	2	T05793	meh3 protein homol
296	27	61.4	490	2	T41293	EcoG type I restri	369	27	61.4	1081	2	T51613	DNA mismatch repai
297	27	61.4	492	2	F86384	probable protein f	370	27	61.4	1098	2	T41493	hypothetical prote
298	27	61.4	493	2	F86133	hypothetical prote	371	27	61.4	1146	1	I64112	transcription/rep
299	27	61.4	493	2	C91292	hypothetical prote	372	27	61.4	1158	2	T43519	condensin complex
300	27	61.4	495	2	T31203	hypothetical prote	373	27	61.4	1171	2	T05039	hypothetical prote
301	27	61.4	502	2	AD0691	conserved hypotet	374	27	61.4	1175	2	S26874	DNA-directed RNA p
302	27	61.4	505	2	T51403	hypothetical prote	375	27	61.4	1198	2	T49726	hypothetical prote
303	27	61.4	511	2	E90600	hypothetical prote	376	27	61.4	1225	2	T48251	ubiquitin-protein
304	27	61.4	512	2	G75367	potassium uptake p	377	27	61.4	1244	2	S76102	hypothetical prote
305	27	61.4	514	2	T28855	hypothetical prote	378	27	61.4	1246	2	C36806	hypothetical prote
306	27	61.4	515	2	S52321	penton base protei	379	27	61.4	1257	2	T09493	period protein hom
307	27	61.4	532	2	A34329	60K esterase (EC 3	380	27	61.4	1257	2	T13957	period protein PER
308	27	61.4	539	2	T39506	importin alpha sub	381	27	61.4	1276	2	S75801	probable phytochro
309	27	61.4	543	2	B97092	ABC-type transport	382	27	61.4	1305	2	T12897	DNA polymerase III
310	27	61.4	544	2	AD1979	permease protein o	383	27	61.4	1307	2	T25106	hypothetical prote
311	27	61.4	555	2	T24671	hypothetical prote	384	27	61.4	1418	2	T15232	hypothetical prote
312	27	61.4	560	2	S56142	calcium-binding pr	385	27	61.4	1684	2	T02632	hypothetical prote
313	27	61.4	561	2	AI11409	potassium-transport	386	27	61.4	1716	2	T14103	probable DNA-dir
314	27	61.4	561	2	AI1785	potassium-transport	387	27	61.4	1717	2	T13961	DNA-directed RNA p
315	27	61.4	571	2	AI2908	hypothetical prote	388	27	61.4	1783	2	T42386	unconventional myo
316	27	61.4	588	2	AI3543	60K inner membrane	389	27	61.4	1809	2	S57329	tubercous sclerosis
317	27	61.4	588	2	G97683	prsd protein (U991	390	27	61.4	1812	2	I49350	breast/ovarian can
318	27	61.4	600	2	AH2623	60 kd inner-membra	391	27	61.4	1822	2	T14106	probable GTPase-ac
319	27	61.4	600	2	G97405	60K inner-membrane	392	27	61.4	1829	2	T26135	hypothetical prote
320	27	61.4	614	2	T16268	hypothetical prote	393	27	61.4	1863	1	A58881	breast/ovarian can
321	27	61.4	630	2	S77148	hypothetical prote	394	27	61.4	1867	2	S22775	MOT1 protein - yea

395	27	61.4	2199	2	T40008	Cdc20p - fission y	468	26	59.1	247	2	T41383	hypothetical prote
396	27	61.4	2670	2	A46719	inositol 1,4,5-tri	469	26	59.1	251	2	H75586	probable urea/short
397	27	61.4	2671	2	A46719	inositol 1,4,5-tri	470	26	59.1	254	2	T18987	hypothetical prote
398	27	61.4	2693	2	A49743	IP3 receptor, XIP3	471	26	59.1	256	2	F84612	hypothetical prote
399	27	61.4	2695	2	S54974	type 1 inositol 1,	472	26	59.1	258	1	C69175	heat shock protein
400	27	61.4	2701	2	S17796	inositol-trisphosp	473	26	59.1	258	2	H96013	conserved hypotet
401	27	61.4	2713	2	A55713	inositol 1,4,5-tri	474	26	59.1	258	2	H82142	tRNA-(MS[2]IO[6]A)
402	27	61.4	2734	2	B35719	inositol 1,4,5-tri	475	26	59.1	259	2	AB3572	succinoglycan bios
403	27	61.4	2749	1	ACMSIT	inositol 1,4,5-tri	476	26	59.1	265	2	G81241	capsule polysaccha
404	27	61.4	2749	2	A36579	inositol 1,4,5-tri	477	26	59.1	265	2	G82013	capsule polysaccha
405	27	61.4	2761	2	T29285	hypothetical prote	478	26	59.1	265	2	S15222	ctrC protein - Nei
406	27	61.4	2783	2	T31431	inositol 1,4,5-tri	479	26	59.1	269	2	A64216	protein X homolog
407	27	61.4	2833	2	A43360	inositol 1,4,5-tri	480	26	59.1	271	2	T40982	hypothetical prote
408	27	61.4	3175	1	RRWEV	genome polyprotein	481	26	59.1	272	2	T05929	hypothetical prote
409	27	61.4	3511	2	A59295	unconventional myo	482	26	59.1	273	2	S38102	hypothetical prote
410	27	61.4	3530	2	A59266	hypothetical prote	483	26	59.1	275	1	B64077	bis(5'-nucleosyl)-
411	27	61.4	3738	2	T05501	TipC protein - sli	484	26	59.1	279	2	A95397	hypothetical prote
412	27	61.4	3848	2	T17414	Fl protein - avian	485	26	59.1	279	2	F95128	degV family protei
413	27	61.4	3951	1	VFIHB1	ryanodine receptor	486	26	59.1	279	2	C97999	conserved hypotet
414	27	61.4	4859	2	S74173	ryanodine receptor	487	26	59.1	282	2	AD0848	Iron transport pro
415	27	61.4	4868	2	B54161	ryanodine-binding	488	26	59.1	282	2	E64063	hypothetical prote
416	27	61.4	4869	2	S66572	ryanodine receptor	489	26	59.1	282	2	T50833	nematode resistanc
417	27	61.4	4872	2	S27272	ryanodine receptor	490	26	59.1	284	2	E70304	4-hydroxybenzoate
418	27	61.4	4967	2	S72269	ryanodine receptor	491	26	59.1	286	2	T16681	hypothetical prote
419	27	61.4	4969	2	A37113	ryanodine receptor	492	26	59.1	287	2	B82172	conserved hypotet
420	27	61.4	5032	1	A35041	ryanodine receptor	493	26	59.1	290	2	D71546	probable DNA pol I
421	27	61.4	5035	1	I46646	ryanodine receptor	494	26	59.1	290	2	F81700	DNA polymerase III
422	27	61.4	5037	1	A54161	ryanodine-binding	495	26	59.1	291	2	S22041	hypothetical prote
423	27	61.4	5037	2	B35041	ryanodine receptor	496	26	59.1	291	2	AB3083	conserved hypotet
424	26	60.2	740	2	F82614	conserved hypotet	497	26	59.1	291	2	F98203	hypothetical prote
425	26	59.1	17	2	S41207	F420-non-reducing-	498	26	59.1	292	2	C65070	hypothetical prote
426	26	59.1	75	2	S36119	preoptic area regu	499	26	59.1	294	2	AD0184	UTP-glucose-1-phos
427	26	59.1	83	2	H75625	hypothetical prote	500	26	59.1	296	2	AG0187	conserved hypotet
428	26	59.1	91	2	T03202	hypothetical prote	501	26	59.1	297	2	AF2980	hypothetical prote
429	26	59.1	92	2	T30414	conotoxin homolog	502	26	59.1	297	2	H98302	dehydrogenase/redu
430	26	59.1	100	2	G69268	hypothetical prote	503	26	59.1	299	2	H83749	transporter, dme f
431	26	59.1	109	2	C72494	hypothetical prote	504	26	59.1	299	2	AF3578	ribosomal protein
432	26	59.1	112	2	AF2627	hypothetical prote	505	26	59.1	300	1	S75015	hypothetical prote
433	26	59.1	115	2	B71141	hypothetical prote	506	26	59.1	300	2	F83621	UTP-glucose-1-phos
434	26	59.1	120	2	S78179	succinate dehydrog	507	26	59.1	302	1	JC2265	glucose-1-phosphat
435	26	59.1	126	2	A69177	hypothetical prote	508	26	59.1	302	2	AB0650	glucose-1-phosphat
436	26	59.1	137	2	D69337	hypothetical prote	509	26	59.1	302	2	B90846	glucose-1-phosphat
437	26	59.1	140	2	T26470	hypothetical prote	510	26	59.1	302	2	A85704	membrane glycoprot
438	26	59.1	142	2	H71022	hypothetical prote	511	26	59.1	303	2	A40807	hypothetical prote
439	26	59.1	144	2	F91130	hypothetical prote	512	26	59.1	309	2	D70464	hypothetical prote
440	26	59.1	144	2	F85975	hypothetical prote	513	26	59.1	312	2	G71146	hypothetical prote
441	26	59.1	149	2	T26679	hypothetical prote	514	26	59.1	320	2	D96750	unknown protein F2
442	26	59.1	154	2	AH1951	hypothetical prote	515	26	59.1	324	2	F69504	proliferating-cell
443	26	59.1	173	2	S76779	hypothetical prote	516	26	59.1	325	2	T07666	lipoxigenase (EC 1
444	26	59.1	177	2	T45393	hypothetical prote	517	26	59.1	332	2	B82607	conserved hypotet
445	26	59.1	187	2	T05570	pollen-specific pr	518	26	59.1	333	2	T28466	ribonucleoside-dip
446	26	59.1	188	2	S68256	phospholipase C (B	519	26	59.1	333	2	H36839	C8L protein - vari
447	26	59.1	188	2	D95303	hypothetical prote	520	26	59.1	336	2	S04739	site-specific DNA-
448	26	59.1	191	2	B86664	hypothetical prote	521	26	59.1	336	2	A88957	protein ZK697.10 [
449	26	59.1	192	2	H70672	probable resolvase	522	26	59.1	337	2	S74732	hypothetical prote
450	26	59.1	195	2	E70555	hypothetical prote	523	26	59.1	341	2	T23116	hypothetical prote
451	26	59.1	196	2	G65039	hypothetical prote	524	26	59.1	342	2	A40191	platelet-activatin
452	26	59.1	206	2	T23852	hypothetical prote	525	26	59.1	347	2	T21067	hypothetical prote
453	26	59.1	206	2	AH2070	iron(II) transport	526	26	59.1	347	2	T27315	hypothetical prote
454	26	59.1	213	2	H75254	probable 1-acylgly	527	26	59.1	348	1	DEEBOT	dihydroorotase (EC
455	26	59.1	215	2	T18842	hypothetical prote	528	26	59.1	348	2	AD0638	dihydroorotase (EC
456	26	59.1	216	2	AC1155	probable transaldo	529	26	59.1	348	2	D87097	conserved hypotet
457	26	59.1	216	2	AF1513	probable transaldo	530	26	59.1	348	2	T49166	hypothetical prote
458	26	59.1	220	2	T26991	hypothetical prote	531	26	59.1	348	2	AG1161	hypothetical prote
459	26	59.1	221	2	T45044	hypothetical prote	532	26	59.1	348	2	AD1520	hypothetical prote
460	26	59.1	222	2	T26500	peptidylprolyl iso	533	26	59.1	351	2	D84541	hypothetical prote
461	26	59.1	225	2	I67934	neurofibromatosis	534	26	59.1	354	2	C82038	nitrogen regulatio
462	26	59.1	234	2	S66732	probable membrane	535	26	59.1	355	2	S58401	synaptotagmin VIII
463	26	59.1	238	2	T29797	hypothetical prote	536	26	59.1	358	2	I38121	protein kinase - h
464	26	59.1	240	2	D97762	probable ABC trans	537	26	59.1	360	1	B32890	translation releas
465	26	59.1	241	2	D84138	hypothetical prote	538	26	59.1	360	1	FCBCR1	translation releas
466	26	59.1	242	2	F30315	methyl viologen-re	539	26	59.1	360	2	AB0720	peptide chain rele
467	26	59.1	246	2	I53855	neurofibromatosis	540	26	59.1	360	2	A85701	peptide chain rele

541	26	59.1	360	2	D90843	peptide chain rele	614	516	2	C64735	probable copper-bi
542	26	59.1	361	2	D72721	hypothetical prote	615	518	2	B71545	probable oligopept
543	26	59.1	362	2	T01198	endonuclease homol	616	518	2	T25507	hypothetical prote
544	26	59.1	371	2	C83991	hypothetical prote	617	519	2	AE0726	probable membrane
545	26	59.1	371	2	B86489	protein T32E20.25	618	520	2	B81699	peptide ABC transp
546	26	59.1	373	2	S17955	long-chain-fatty-a	619	520	2	T21462	hypothetical prote
547	26	59.1	373	2	S15161	long-chain-fatty-a	620	522	2	B86294	hypothetical prote
548	26	59.1	374	2	T09771	phosphatidate cyti	621	523	2	T28727	hypothetical prote
549	26	59.1	380	2	T04863	shaggy-like protei	622	524	2	T46310	hypothetical prote
550	26	59.1	383	2	A36117	corticosteroid-bin	623	525	2	B86463	hypothetical prote
551	26	59.1	383	2	T04150	RAD23 protein homo	624	526	2	A81135	phosphoribosylamin
552	26	59.1	393	2	A13546	hypothetical prote	625	528	2	T39856	probable chaperoni
553	26	59.1	394	2	G69621	iron-uptake system	626	530	2	H81885	purH bifunctional
554	26	59.1	395	2	A86583	aromatic AA aminot	627	530	2	A54965	probable vesicular
555	26	59.1	395	2	B72042	aromatic-amino-aci	628	532	2	C86515	oligopeptide bindi
556	26	59.1	395	2	S73531	CDP-diglyceride sy	629	532	2	A72107	peptide ABC transp
557	26	59.1	398	2	C91063	hypothetical prote	630	532	2	T39658	vesicular acetylch
558	26	59.1	399	2	I78852	neurofibromatosis	631	532	2	T52102	probable nuclear t
559	26	59.1	400	2	A46297	beta-1,6-N-acetyl/g	632	532	2	T52268	importin alpha [va
560	26	59.1	404	2	S03638	triose phosphate/3	633	532	2	H92680	hypothetical prote
561	26	59.1	407	2	S77922	shaggy-like protei	634	532	2	T35119	probable aminotran
562	26	59.1	407	2	A72691	probable spermidin	635	533	2	AC0414	probable exported
563	26	59.1	407	2	H86386	hypothetical prote	636	560	2	S38035	probable serine/th
564	26	59.1	409	2	G83871	multidrug-efflux t	637	564	2	B65011	Probable oxalyli-Co
565	26	59.1	411	2	G95241	MATE efflux family	638	564	2	E91035	Probable oxalyli-Co
566	26	59.1	412	2	S71266	shaggy-like protei	639	564	2	G85879	Probable oxalyli-Co
567	26	59.1	412	2	A84715	probable shaggy-li	640	579	2	AC2200	potassium-transpor
568	26	59.1	413	2	AC0834	probable membrane	641	584	2	G82079	single-stranded-DN
569	26	59.1	413	2	AE2502	hypothetical prote	642	594	2	T30908	hypothetical prote
570	26	59.1	414	2	S75832	penicillin-binding	643	598	2	D84242	hypothetical prote
571	26	59.1	417	2	T05207	hypothetical prote	644	599	2	JH0259	prostaglandin-endo
572	26	59.1	422	2	A49837	clathrin-associate	645	599	2	A29947	prostaglandin-endo
573	26	59.1	425	2	T23603	hypothetical prote	646	600	2	S00561	prostaglandin-endo
574	26	59.1	426	2	B98106	hypothetical prote	647	600	2	A28960	prostaglandin-endo
575	26	59.1	431	2	H75072	hypothetical prote	648	602	2	S39782	cyclooxygenase 1 -
576	26	59.1	434	2	AF2164	hypothetical prote	649	602	2	A35564	prostaglandin-endo
577	26	59.1	434	2	E82244	sensor histidine k	650	602	2	S69198	prostaglandin G/H
578	26	59.1	437	2	B49274	protein farnesyltr	651	609	2	S36569	E1 protein - human
579	26	59.1	437	2	C89274	protein farnesyltr	652	613	2	A82834	hypothetical prote
580	26	59.1	437	2	A40037	protein farnesyltr	653	626	2	A41284	translation initia
581	26	59.1	439	2	S49559	phage Hau3 resista	654	627	2	T37293	cholesterol O-acetyl
582	26	59.1	442	2	A57041	transcription regu	655	629	2	B83107	chemotactic trans
583	26	59.1	443	2	G59102	hypothetical prote	656	632	2	S64786	hypothetical prote
584	26	59.1	444	2	AD2031	hypothetical prote	657	632	2	AF1189	transcription anti
585	26	59.1	447	2	C83890	beta-glucosidase b	658	632	2	AG1547	transcription anti
586	26	59.1	453	2	T00724	presenilin homolog	659	633	2	T02673	heterogeneous nucl
587	26	59.1	454	2	A82394	hypothetical prote	660	638	2	S36546	E1 protein - human
588	26	59.1	454	2	T41020	probable Uridine k	661	638	2	T13691	hypothetical prote
589	26	59.1	457	2	S60597	1-phosphatidylinos	662	642	2	S36511	E1 protein - human
590	26	59.1	459	2	A82675	heat shock protein	663	642	2	C89124	protein K07C11.9 [
591	26	59.1	460	2	T10995	NADH2 dehydrogenas	664	643	1	W1WL42	E1 protein - human
592	26	59.1	461	2	T07646	hypothetical prote	665	650	2	AB1738	probable Na+/H+ an
593	26	59.1	466	2	A11894	two-component sens	666	650	2	A11368	probable Na+/H+ an
594	26	59.1	468	2	E87400	oxidoreductase, FA	667	654	2	F71298	probable methyl-ac
595	26	59.1	469	2	S09189	49K protein - Stre	668	654	2	A96235	hydroxamate-depend
596	26	59.1	471	2	T02186	hypothetical prote	669	654	2	AC3051	hypothetical prote
597	26	59.1	472	2	A69018	probable coenzyme	670	658	2	A33598	endoglucanase 3 (E
598	26	59.1	472	2	T35936	probable dehydroge	671	662	2	T17211	hypothetical prote
599	26	59.1	472	2	S62494	probable GTPase-ac	672	675	2	T40680	hypothetical prote
600	26	59.1	476	2	T42692	hypothetical prote	673	680	2	S26764	major coat protein
601	26	59.1	486	2	AE0392	X-His dipeptidase	674	682	2	F70421	conserved hypotet
602	26	59.1	488	2	A83367	probable phosphoma	675	687	2	T27683	hypothetical prote
603	26	59.1	488	2	T21701	hypothetical prote	676	690	2	A87580	sensory box histid
604	26	59.1	497	2	S52097	cytochrome P450I1I	677	693	2	B97903	elongation factor
605	26	59.1	498	2	AH2468	hypothetical prote	678	693	2	B95032	translation elonga
606	26	59.1	499	2	S48907	probable purine nu	679	693	2	T33251	hypothetical prote
607	26	59.1	502	2	JX0334	cytochrome P450 3A	680	709	2	B69607	elongation factor
608	26	59.1	504	2	A60564	cytochrome P450 3A	681	711	2	A90023	DNA topoisomerase
609	26	59.1	504	2	A22631	cytochrome P450 3A	682	716	2	B71673	hypothetical prote
610	26	59.1	507	1	C53308	probable hydro-lya	683	716	2	AC2449	ABC transporter AT
611	26	59.1	515	2	A43289	CDC4L protein - hu	684	722	2	AF1956	ABC transporter AT
612	26	59.1	516	2	G90644	hypothetical prote	685	737	2	T31349	hypothetical prote
613	26	59.1	516	2	G85495	hypothetical prote	686	743	2	D84545	probable salt-indu

687	26	59.1	752	2	E82146	Rec2-related prote	760	26	59.1	4588	2	T28667	dynein beta heavy
688	26	59.1	780	2	H64830	probable membrane	761	25	56.8	32	2	S59800	50K protein - rat
689	26	59.1	780	2	D90753	hypothetical prote	762	25	56.8	68	2	A95993	hypothetical prote
690	26	59.1	780	2	B85617	hypothetical prote	763	25	56.8	75	2	H84631	hypothetical prote
691	26	59.1	785	2	T19741	hypothetical prote	764	25	56.8	78	2	T21426	transcription regu
692	26	59.1	790	2	E48327	COI intron A prote	765	25	56.8	78	2	AE2890	hypothetical prote
693	26	59.1	790	2	T30081	hypothetical prote	766	25	56.8	87	2	G70663	hypothetical prote
694	26	59.1	809	2	T16448	hypothetical prote	767	25	56.8	91	2	G69887	hypothetical prote
695	26	59.1	813	2	S76607	hypothetical prote	768	25	56.8	96	2	A97666	hypothetical prote
696	26	59.1	848	1	JC1351	transforming growt	769	25	56.8	99	2	G83618	malonate decarboxy
697	26	59.1	875	2	AB1125	E. col YbgG protei	770	25	56.8	99	2	C29826	hypothetical l1k p
698	26	59.1	875	2	A11485	E. col YbgG protei	771	25	56.8	100	2	S67141	hypothetical prote
699	26	59.1	877	2	A32949	DNA-directed DNA p	772	25	56.8	102	2	S76816	hypothetical prote
700	26	59.1	877	2	E95003	DNA polymerase I {	773	25	56.8	105	1	CUAI	plastocyanin - Ana
701	26	59.1	877	2	H97875	DNA-directed DNA p	774	25	56.8	105	2	AH1992	hypothetical prote
702	26	59.1	882	2	A42855	N-heparan sulfate	775	25	56.8	112	2	D97804	hypothetical prote
703	26	59.1	882	2	A57169	[heparan sulfate]-	776	25	56.8	112	2	S12196	vascular endotheli
704	26	59.1	883	2	A49733	[heparan sulfate]-	777	25	56.8	118	2	A75343	conserved hypothet
705	26	59.1	906	2	G96621	probable disease r	778	25	56.8	121	2	A84906	probable auxin-reg
706	26	59.1	913	2	T46339	hypothetical prote	779	25	56.8	125	2	A75601	transcription repr
707	26	59.1	980	2	T30089	probable zinc prot	780	25	56.8	129	2	JT0666	hypothetical 14.7K
708	26	59.1	988	2	S55945	zinc proteinase (B	781	25	56.8	130	2	T29284	hypothetical prote
709	26	59.1	1003	2	F81731	glycyl-tRNA synthe	782	25	56.8	134	2	I50729	gene Wnt-1 protein
710	26	59.1	1003	2	B71469	glycine-tRNA ligas	783	25	56.8	136	2	T47982	hypothetical prote
711	26	59.1	1010	2	C81524	glycyl-tRNA synthe	784	25	56.8	138	2	A37075	hypothetical prote
712	26	59.1	1014	2	H86608	glycyl tRNA synthe	785	25	56.8	139	2	AB1839	plastocyanin precu
713	26	59.1	1014	2	A72016	glycine-tRNA ligas	786	25	56.8	139	2	S06999	plastocyanin precu
714	26	59.1	1017	2	PC4035	cell-cycle-depende	787	25	56.8	139	2	I39614	plastocyanin precu
715	26	59.1	1038	2	T30304	protein RanBP7 - A	788	25	56.8	141	2	T39245	ef-hand protein -
716	26	59.1	1047	2	A12002	hypothetical prote	789	25	56.8	142	2	I51232	gonadotropin II be
717	26	59.1	1092	2	T20117	hypothetical prote	790	25	56.8	144	2	AC1934	hypothetical prote
718	26	59.1	1094	2	C59434	KIAA1688 protein {	791	25	56.8	144	2	D90125	hypothetical prote
719	26	59.1	1113	2	T00271	hypothetical prote	792	25	56.8	145	2	C84447	hypothetical prote
720	26	59.1	1133	2	T12529	hypothetical prote	793	25	56.8	145	2	T38623	very hypothetical
721	26	59.1	1148	2	D82091	exodeoxyribonuclea	794	25	56.8	147	2	H75319	hypothetical prote
722	26	59.1	1148	2	A28614	nonstructural poly	795	25	56.8	148	1	D64705	conserved hypothet
723	26	59.1	1159	1	A44280	inner layer protei	796	25	56.8	149	1	MCAS	calmodulin - Emeri
724	26	59.1	1165	2	A46180	adenyl cyclase t	797	25	56.8	149	2	JC4216	calmodulin - Asper
725	26	59.1	1166	2	A92201	adenylate cyclase	798	25	56.8	149	2	S58709	calmodulin - Neuro
726	26	59.1	1168	2	S76195	hypothetical prote	799	25	56.8	149	2	C83056	hypothetical prote
727	26	59.1	1173	1	A53430	1-phosphatidylinos	800	25	56.8	150	2	S55882	CGH finger protei
728	26	59.1	1174	2	T49868	related to suppres	801	25	56.8	152	1	B24427	interleukin-3 prec
729	26	59.1	1182	2	D71638	DNA polymerase III	802	25	56.8	152	1	A24427	interleukin-3 prec
730	26	59.1	1215	2	AE1178	pyruvate-flavodoxi	803	25	56.8	152	1	S42720	interleukin-3 prec
731	26	59.1	1216	2	A28822	1-phosphatidylinos	804	25	56.8	152	2	H83900	hypothetical prote
732	26	59.1	1216	2	A28821	1-phosphatidylinos	805	25	56.8	152	2	T72634	probable translati
733	26	59.1	1218	2	E84537	hypothetical prote	806	25	56.8	153	2	H97327	transcription regu
734	26	59.1	1227	2	AG2504	hypothetical prote	807	25	56.8	154	2	T15439	hypothetical prote
735	26	59.1	1282	2	T30804	p-glycoprotein 6 -	808	25	56.8	157	2	S14021	hypothetical prote
736	26	59.1	1441	1	GNVULC	M polyprotein prec	809	25	56.8	163	2	B82708	hypothetical prote
737	26	59.1	1441	1	GNVUSV	M polyprotein prec	810	25	56.8	163	2	D86230	hypothetical prote
738	26	59.1	1447	2	S63669	UDFglucose-glycopr	811	25	56.8	165	2	G84617	hypothetical prote
739	26	59.1	1507	2	S26765	genome polyprotein	812	25	56.8	166	2	A85077	hypothetical prote
740	26	59.1	1507	2	T18544	alpha-2-macroglobu	813	25	56.8	167	2	S52970	NADH2 dehydrogenas
741	26	59.1	1541	2	T30227	pipecolate-incorpo	814	25	56.8	167	2	S57644	feline interferon-
742	26	59.1	1548	2	T04456	hypothetical prote	815	25	56.8	169	2	S76351	hypothetical prote
743	26	59.1	1607	2	G87259	conserved hypothet	816	25	56.8	172	2	F83037	conserved hypothet
744	26	59.1	1621	2	A82255	hypothetical prote	817	25	56.8	173	2	H81426	H+-transporting tw
745	26	59.1	1722	2	A88470	protein C28H8.3 {i	818	25	56.8	174	2	G69824	conserved hypothet
746	26	59.1	1758	2	T30560	resistance protein	819	25	56.8	175	2	H71896	hypothetical prote
747	26	59.1	1871	2	S27938	hypothetical prote	820	25	56.8	175	2	H96913	probable membrane
748	26	59.1	1900	2	AG2391	serine/threonine k	821	25	56.8	179	2	AD1917	hypothetical prote
749	26	59.1	2154	2	A84669	hypothetical prote	822	25	56.8	180	2	B83064	hypothetical prote
750	26	59.1	2479	1	MNVWRA	nonstructural poly	823	25	56.8	184	2	T25584	hypothetical prote
751	26	59.1	2549	2	A54340	FKBP-rapamycin-ass	824	25	56.8	184	2	T04396	RLCH5 protein - ba
752	26	59.1	2549	2	A54837	rapamycin/FKBP12 t	825	25	56.8	184	2	A12369	hypothetical prote
753	26	59.1	2610	2	T20968	hypothetical prote	826	25	56.8	185	2	JC7369	prenylated Rab acc
754	26	59.1	2818	2	B55282	neurofibromatosis-	827	25	56.8	188	2	AF1337	hypothetical prote
755	26	59.1	2820	2	JC5196	neurofibromin I -	828	25	56.8	188	2	AC1708	hypothetical prote
756	26	59.1	2825	2	I54352	neurofibromin - mo	829	25	56.8	188	2	C84787	hypothetical prote
757	26	59.1	4085	2	S28600	hypothetical prote	830	25	56.8	190	2	A96562	unknown protein {i
758	26	59.1	4466	1	S17231	dynein beta heavy	831	25	56.8	193	2	G70884	probable IS1602res
759	26	59.1	4466	1	S17653	dynein beta heavy	832	25	56.8	193	2	AI1904	hypothetical prote



833	25	56.8	194	2	P75210	indolepyruvate fer	906	25	56.8	293	2	A12626	transcription regu
834	25	56.8	194	2	AE2310	hypothetical prote	907	25	56.8	294	2	B72605	probable high-affi
835	25	56.8	195	2	G90902	probable transcrip	908	25	56.8	294	2	D64175	glycosyltransferas
836	25	56.8	196	1	F71246	probable indolepyr	909	25	56.8	294	2	AB0298	chelated iron tran
837	25	56.8	196	2	D90389	conserved hypotet	910	25	56.8	296	2	B53434	cell surface glyco
838	25	56.8	196	2	C95322	hypothetical prote	911	25	56.8	299	2	G95232	transcription regu
839	25	56.8	202	2	T36518	probable transcrip	912	25	56.8	299	2	A98097	transcription acti
840	25	56.8	202	2	G90207	conserved hypotet	913	25	56.8	299	2	T11682	transcription fact
841	25	56.8	208	2	I46985	Na+/myo-inositol c	914	25	56.8	299	2	H97408	probable transcrip
842	25	56.8	208	2	B84920	hypothetical prote	915	25	56.8	300	2	T20905	hypothetical prote
843	25	56.8	209	2	C70424	hypothetical prote	916	25	56.8	301	2	AE3195	dehydrogenase Atus
844	25	56.8	211	2	AH0874	probable membrane	917	25	56.8	301	2	AB1162	conserved hypotet
845	25	56.8	212	2	AC0421	conserved hypotet	918	25	56.8	304	2	T02911	hypothetical prote
846	25	56.8	213	2	T47382	hypothetical prote	919	25	56.8	305	2	E83890	sugar transport sy
847	25	56.8	220	2	AD3613	probable s-adenosy	920	25	56.8	305	2	F72316	hypothetical prote
848	25	56.8	222	2	F81124	conserved hypotet	921	25	56.8	311	2	G86324	hypothetical prote
849	25	56.8	224	1	PWPF6	H+-transporting tw	922	25	56.8	312	2	T39091	hypothetical prote
850	25	56.8	224	1	PWPF6Y	H+-transporting tw	923	25	56.8	312	2	E75329	probable acetyltra
851	25	56.8	224	2	T12882	conserved hypotet	924	25	56.8	312	2	S67052	hypothetical prote
852	25	56.8	227	2	T10991	H+-transporting tw	925	25	56.8	313	2	T20812	hypothetical prote
853	25	56.8	227	2	T37535	vacuolar atp synth	926	25	56.8	314	1	S48466	MOB1 protein [vali
854	25	56.8	228	2	B96961	cell division ATP-	927	25	56.8	314	2	D96703	hypothetical prote
855	25	56.8	230	2	C75301	rRNA methylase Spo	928	25	56.8	314	2	F85879	probable receptor
856	25	56.8	230	2	E69233	carbamoyl-phosphat	929	25	56.8	314	2	D91035	probable receptor
857	25	56.8	230	2	AC2192	hypothetical prote	930	25	56.8	314	2	A65011	probable receptor
858	25	56.8	232	2	D87623	conserved hypotet	931	25	56.8	315	2	C87293	hypothetical prote
859	25	56.8	235	2	T51968	proteasome endopep	932	25	56.8	315	2	T23824	hypothetical prote
860	25	56.8	237	2	B85714	hypothetical prote	933	25	56.8	316	2	H97664	hypothetical prote
861	25	56.8	238	2	S62809	type I restriction	934	25	56.8	316	2	AC3889	hypothetical prote
862	25	56.8	240	2	JB0011	DNA-directed RNA p	935	25	56.8	316	2	E83586	probable transcrip
863	25	56.8	241	2	J72226	conserved hypotet	936	25	56.8	316	2	AD2074	transposase all214
864	25	56.8	242	2	JC4300	galactin-3 - rabbi	937	25	56.8	317	2	AD0606	putrescine transpo
865	25	56.8	242	2	H83846	pseudouridylate sy	938	25	56.8	317	2	D85596	putrescine transpo
866	25	56.8	243	2	T14963	phage lambda-relat	939	25	56.8	317	2	H90745	permease of putres
867	25	56.8	244	2	A56847	glutathione transf	940	25	56.8	317	2	C45313	putrescine transpo
868	25	56.8	244	2	S71879	glutathione transf	941	25	56.8	317	2	T47953	hypothetical prote
869	25	56.8	244	2	AH0363	probable membrane	942	25	56.8	318	2	T35367	hypothetical prote
870	25	56.8	244	2	T47904	MADS-box protein A	943	25	56.8	319	2	B97296	phosphoribosylpyro
871	25	56.8	244	2	AE1318	hypothetical prote	944	25	56.8	319	2	G70373	Mg(2+) and Co(2+)
872	25	56.8	244	2	AE1690	hypothetical prote	945	25	56.8	319	2	AC2421	iron(III) diclrat
873	25	56.8	244	2	P82510	probable transcrip	946	25	56.8	319	2	T27116	hypothetical prote
874	25	56.8	246	2	T34067	hypothetical prote	947	25	56.8	321	2	S04253	quinatate 5-dehydrog
875	25	56.8	249	2	D69065	conserved hypotet	948	25	56.8	323	2	F83743	hypothetical prote
876	25	56.8	250	2	A35820	galactin 3 - human	949	25	56.8	323	2	C86384	unknown protein [i
877	25	56.8	250	2	T44227	hypothetical prote	950	25	56.8	324	2	T42656	hypothetical prote
878	25	56.8	250	2	JQ2165	glycoprotein GL pr	951	25	56.8	325	2	T41474	hypothetical prote
879	25	56.8	250	2	T44041	Glycoprotein L [im	952	25	56.8	325	2	A69830	conserved hypotet
880	25	56.8	250	2	A84871	probable protein k	953	25	56.8	325	2	C95371	conserved hypotet
881	25	56.8	250	2	S62838	hypothetical prote	954	25	56.8	326	1	WMV215	BiSR protein precu
882	25	56.8	251	2	H97744	cytochrome c1, hem	955	25	56.8	326	2	T37450	interleukin-1 beta
883	25	56.8	252	2	A69286	polysaccharide ABC	956	25	56.8	327	2	H85488	thiamin-binding pe
884	25	56.8	253	2	C81148	conserved hypotet	957	25	56.8	327	2	H90637	thiamin-binding pe
885	25	56.8	253	2	C81406	probable hemeolysi	958	25	56.8	327	2	D64728	G protein-coupled
886	25	56.8	257	2	H64003	hypothetical prote	959	25	56.8	328	2	IS5450	tryptophanyl-tRNA
887	25	56.8	258	2	A75140	hypothetical prote	960	25	56.8	329	2	E89867	DNA methyltransfer
888	25	56.8	261	2	D83859	hypothetical prote	961	25	56.8	330	2	S53990	thiamin monophosph
889	25	56.8	261	2	T30170	hypothetical prote	962	25	56.8	332	2	AE2438	thiamin biosynthes
890	25	56.8	264	2	E83284	probable enoyl-CoA	963	25	56.8	333	2	AF0455	cell surface glyco
891	25	56.8	264	2	D69811	hypothetical prote	964	25	56.8	335	2	A53434	cytochrome-c perox
892	25	56.8	265	2	T35325	probable hydroxyly	965	25	56.8	338	2	B75584	hypothetical prote
893	25	56.8	266	2	D87265	hypothetical prote	966	25	56.8	338	2	T28779	hypothetical prote
894	25	56.8	267	2	T32063	hypothetical prote	967	25	56.8	339	2	T41570	hypothetical prote
895	25	56.8	271	2	G85035	hypothetical prote	968	25	56.8	341	2	T42425	SEC24-like protein
896	25	56.8	279	2	T26166	hypothetical prote	969	25	56.8	343	2	A46475	melanoma-associate
897	25	56.8	281	2	S61201	hypothetical prote	970	25	56.8	343	2	D71341	probable exported
898	25	56.8	281	2	D24720	hypothetical prote	971	25	56.8	343	2	F83896	hypothetical prote
899	25	56.8	288	2	A05062	probable mbpy prot	972	25	56.8	344	2	H83928	hypothetical prote
900	25	56.8	289	1	I57010	purine-nucleoside	973	25	56.8	344	2	S72578	hypothetical prote
901	25	56.8	289	2	I76672	purine-nucleoside	974	25	56.8	345	2	A98251	hypothetical prote
902	25	56.8	292	2	T33987	hypothetical prote	975	25	56.8	345	2	AB3035	conserved hypotet
903	25	56.8	292	2	F81944	probable integral	976	25	56.8	346	2	T28730	hypothetical prote
904	25	56.8	293	2	T00099	glycosyltransferas	977	25	56.8	347	2	T38154	hypothetical prote
905	25	56.8	293	2	S47094	hypothetical prote	978	25	56.8	347	2	T20543	hypothetical prote

```

979      25  56.8      348  2  AF0193      dihydroorotase (BC
980      25  56.8      348  2  C26720      CAMP-regulated D2
981      25  56.8      349  2  T43920      xFuc protein limpo
982      25  56.8      350  2  T25172      hypothetical prote
983      25  56.8      351  2  A84827      hypothetical prote
984      25  56.8      353  1  JQ1946      core protein vp7 -
985      25  56.8      353  2  A83609      probable periplasm
986      25  56.8      353  2  AH3238      ATP-dependent DNA
987      25  56.8      354  2  T43507      DNA repair protein
988      25  56.8      355  1  B64489      hypothetical prote
989      25  56.8      358  1  ADWU      fructose-bisphosph
990      25  56.8      358  2  D85307      fructose-bisphosph
991      25  56.8      359  2  T47187      hypothetical prote
992      25  56.8      360  2  AG2645      flagellar biosynth
993      25  56.8      360  2  G97427      flhB protein (U951
994      25  56.8      360  2  F72094      UDP-3-O- (R-3-hydr
995      25  56.8      360  2  F85528      UDP glucosamine N-
996      25  56.8      361  2  H84949      peptide chain rele
997      25  56.8      361  2  A84015      hypothetical prote
998      25  56.8      361  2  I49594      homeobox protein -
999      25  56.8      363  2  AD0366      sulfate transport
1000     25  56.8      368  2  S67507      morphogen lefty pr

ALIGNMENTS

RESULT 1
T14337
RAD23 protein, isoform II - carrot
C:Species: Daucus carota (carrot)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-Oct-2004
C:Accession: T14337
R:Sturm, A.; Leinhard, S.
Plant J. 13, 815-821, 1998
A:Title: Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.
A:Reference number: Z17989; MUID:98345997; PMID:9681019
A:Accession: T14337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-379 <STU>
A:CROSS-references: UNIPROT:O03991; UNIPARC:UPI000009EEDA; EMBL:Y12014; NID:gl914684; PI
A:Experimental source: subspecies Queen Anne's Lace, isolate W001C
C:Genetics:
A:Gene: RAD23-2

Query Match      79.5%; Score 35; DB 2; Length 379;
Best Local Similarity 77.8%; Pred. No. 10;
Matches      7; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

QY      1  FLOLMEPV 9
DB      302  FLOLINEPV 310

RESULT 2
E95218
iron-compound ABC transporter, permease protein SP1870 [imported] - Streptococcus pneum
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: E95218
R:Tetrelín, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
non, T.; Hickey, E.K.; Holt, I.B.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95218
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <KUR>
A:CROSS-references: UNIPROT:Q97NY1; UNIPARC:UPI000004A8ED; GB:AE005672; PIDN:AAK75942.1;

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A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1870

Query Match      77.3%; Score 34; DB 2; Length 318;
Best Local Similarity 75.0%; Pred. No. 14;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      1  FLOLMEPV 8
DB      152  FLOVLMDP 159

RESULT 3
C98082
hypothetical protein fatC [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: C98082
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.,
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: C98082
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <KUR>
A:CROSS-references: UNIPROT:Q8DNJ4; UNIPARC:UPI00000E36D2; GB:AE007317; PIDN:AAL00488.1,
C:Genetics:
A:Gene: fatC

Query Match      77.3%; Score 34; DB 2; Length 318;
Best Local Similarity 75.0%; Pred. No. 14;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      1  FLOLMEPV 8
DB      152  FLOVLMDP 159

RESULT 4
T24897
hypothetical protein T13H5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24897
R:Lightning, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19950
A:Accession: T24897
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1254 <WIL>
A:CROSS-references: UNIPROT:Q22467; UNIPARC:UPI000017BBA2; EMBL:Z66524; PIDN:CRA91418.1,
A:Experimental source: clone T13H5
C:Genetics:
A:Gene: CESP:T13H5.2
A:Map position: 2
A:Introns: 63/1, 158/2, 200/3, 286/2, 404/3, 437/1, 539/3, 616/1, 688/3, 732/3, 778/3, 8

Query Match      77.3%; Score 34; DB 2; Length 1254;
Best Local Similarity 77.8%; Pred. No. 60;
Matches      7; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

QY      1  FLOLMEPV 9
DB      622  FLOLSVEPV 630

RESULT 5

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## H86296

F309.1 protein - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: H86296  
 R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: H86296

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-113 <STO>

A;Cross-references: UNIPROT:Q9SA20; UNIPARC:UPI00000A3C14; GB:AB005172; NID:g4966345; PT

C;Genetics:

A;Map position: 1

Query Match 75.0%; Score 33; DB 2; Length 113;

Best Local Similarity 87.5%; Pred. No. 8;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEP 8

|||||

Db 34 FLQLLMEP 41

## RESULT 6

G89845  
 hypothetical protein SA0689 [imported] - Staphylococcus aureus (strain N315)  
 C;Species: Staphylococcus aureus  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 05-Oct-2004  
 C;Accession: G89845

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun  
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: G89845

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-318 <KUR>

A;Cross-references: UNIPROT:Q99VP0; UNIPARC:UPI00000CAA00; GB:BA000018; PID:g13700625; E

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA0689

C;Superfamily: ferrichrome ABC transporter

Query Match 75.0%; Score 33; DB 2; Length 318;

Best Local Similarity 62.5%; Pred. No. 24;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEP 8

|||||

Db 151 FIQLIMDP 158

## RESULT 7

S44346  
 RAD23 protein homolog - human  
 N;Alternate names: p58/HR23B; XP-C repair complementing protein  
 C;Species: Homo sapiens (man)  
 C;Date: 25-Dec-1994 #sequence\_revision 01-Sep-1995 #text\_change 05-Oct-2004  
 C;Accession: S44346  
 R;Masutani, C.; Sugawara, K.; Yanagisawa, J.; Sonoyama, T.; Ui, M.; Enomoto, T.; Takio,  
 EMBO J. 13, 1831-1843, 1994

Query Match 75.0%; Score 33; DB 2; Length 2764;

Best Local Similarity 55.6%; Pred. No. 2.3e+02;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9

|||||

A;Title: Purification and cloning of a nucleotide excision repair complex involving the  
 A;Reference number: S44345; MUID:94222030; PMID:8168482  
 A;Accession: S44346  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-409 <WAS>  
 A;Cross-references: UNIPROT:P54727; UNIPARC:UPI0000132F6C; EMBL:D21090; NID:g498147; PI  
 F;1-80/Domains: ubiquitin homology <UBH>

Query Match 75.0%; Score 33; DB 2; Length 409;

Best Local Similarity 66.7%; Pred. No. 31;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9

|||||

Db 324 FIQMLNEPV 332

## RESULT 8

S07649  
 gene coi intron 1 protein - Neurospora crassa mitochondrion  
 C;Species: mitochondrion Neurospora crassa  
 C;Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 07-Dec-1999  
 C;Accession: S07649

R;Field, D.J.; Sommerfield, A.; Saville, B.J.; Collins, R.A.

Nucleic Acids Res. 17, 9087-9099, 1989

A;Title: A group II intron in the Neurospora mitochondrial coi gene: nucleotide sequence

A;Reference number: S07649; MUID:90067912; PMID:2531370

A;Accession: S07649

A;Molecule type: DNA

A;Residues: 1-908 <PIE>

A;Cross-references: UNIPARC:UPI00001787BD; EMBL:X14669

A;Experimental source: strain Adiopodoume

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC3

C;Superfamily: yeast mitochondrion oxi3 intron 1 protein

C;Keywords: mitochondrion

Query Match 75.0%; Score 33; DB 2; Length 908;

Best Local Similarity 75.0%; Pred. No. 71;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMEPV 9

|||||

Db 369 IQLVMEPV 376

## RESULT 9

T13949  
 neurofibromin - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: T13949

R;The, I.; Hannigan, G.E.; Cowley, G.S.; Reginald, S.; Zhong, Y.; Gusella, J.P.; Hariha

Science 276, 791-794, 1997

A;Title: Rescue of a Drosophila NF1 mutant phenotype by protein kinase A.

A;Reference number: Z17826; MUID:97277221; PMID:9115203

A;Accession: T13949

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-2764 <THE>

A;Cross-references: UNIPROT:O01399; UNIPARC:UPI000007CA4D; EMBL:L26502; NID:gl929432; P

C;Genetics:

A;Gene: NF1

A;Cross-references: FlyBase:FBgn0015269

Query Match 75.0%; Score 33; DB 2; Length 2764;

Best Local Similarity 55.6%; Pred. No. 2.3e+02;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1340 YLQMLLEPL 1348

RESULT 10  
T13945  
neurofibromin - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13945  
R:Bernards, A.  
submitted to the EMBL Data Library, April 1997  
A:Reference number: Z17824  
A:Accession: T13945  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2802 <BER>  
A:Cross-references: UNIPROT:O01397; UNIPARC:UPI0000081CF7; EMBL:L26500; NID:g1929428; P13945  
C:Genetics:  
A:Gene: NF1  
A:Cross-references: FlyBase:FBgn0015269  
A:Introns: 19/3; 67/3; 196/1; 243/2; 441/2; 548/3; 733/1; 912/2; 1443/1; 1645/2; 2430/3;  
Query Match 75.0%; Score 33; DB 2; Length 2802;  
Best Local Similarity 55.6%; Pred. No. 2.3e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
:|:|:|:  
Db 1340 YLQMLLEPL 1348

RESULT 11  
T13947  
neurofibromin - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13947  
R:The, I.; Hannigan, G.E.; Cowley, G.S.; Reginald, S.; Zhong, Y.; Gusella, J.F.; Harihar  
Science 276, 791-794, 1997  
A:Title: Rescue of a *Drosophila* NF1 mutant phenotype by protein kinase A.  
A:Reference number: Z17826; MUID:97277221; PMID:9115203  
A:Accession: T13947  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2802 <THE>  
A:Cross-references: UNIPROT:O01398; UNIPARC:UPI000007631A; EMBL:L26501; NID:g1929430; P13947  
C:Genetics:  
A:Gene: NF1  
A:Cross-references: FlyBase:FBgn0015269

Query Match 75.0%; Score 33; DB 2; Length 2802;  
Best Local Similarity 55.6%; Pred. No. 2.3e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
:|:|:|:  
Db 1340 YLQMLLEPL 1348

RESULT 12  
T14336  
RAD23 protein, isoform I - carrot  
C:Species: *Daucus carota* (carrot)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 05-Oct-2004  
C:Accession: T14336  
R:Sturm, A.; Leinhardt, S.  
Plant J. 13, 815-821, 1998  
A:Title: Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.  
A:Reference number: Z17989; MUID:98345997; PMID:9681019  
A:Accession: T14336  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-382 <STU>

A:Cross-references: UNIPROT:O03990; UNIPARC:UPI00000A023F; EMBL:Y12013; NID:g1914682; P14336  
A:Experimental source: subspecies Queen Anne's Lace, isolate W001C  
C:Genetics:  
A:Gene: RAD23-1

Query Match 72.7%; Score 32; DB 2; Length 382;  
Best Local Similarity 66.7%; Pred. No. 48;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
:|:|:|:  
Db 311 FLQLINEPM 319

RESULT 13  
A82042  
xanthine/uracil permease family protein VC2712 [imported] - *Vibrio cholerae* (strain N16)  
C:Species: *Vibrio cholerae*  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: A82042  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.  
I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: A82042  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-480 <HEI>  
A:Cross-references: UNIPROT:Q9KNM0; UNIPARC:UPI00000C3394; GB:AE004337; GB:AE003852; NID13942  
A:Experimental source: serogroup O1, strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC2712  
A:Map position: 1  
C:Superfamily: hypothetical protein b2882

Query Match 72.7%; Score 32; DB 2; Length 480;  
Best Local Similarity 66.7%; Pred. No. 60;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
:|:|:|:  
Db 371 FVQLIPEPV 379

RESULT 14  
T04076  
protoporphyrinogen oxidase (EC 1.3.3.4) IX, mitochondrial [validated] - common tobacco  
C:Species: *Nicotiana tabacum* (common tobacco)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04076  
R:Rimontova, I.; Kruse, E.; Mock, H.P.; Grimm, B.  
Proc. Natl. Acad. Sci. U.S.A. 94, 8895-8900, 1997  
A:Title: Cloning and characterization of a plastidal and a mitochondrial isoform of to:  
A:Reference number: Z15186; MUID:97385200; PMID:9238074  
A:Accession: T04076  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-504 <LER>  
A:Cross-references: UNIPROT:Q24164; UNIPARC:UPI00001320B8; EMBL:Y13466; NID:g2370334; P14336  
A:Experimental source: strain SR1  
C:Genetics:  
A:Gene: ppXII  
C:Function:  
A:Description: EC 1.3.3.4 [validated, MUID:97385200]  
A:Pathway: tetrapyrrole synthesis  
C:Keywords: mitochondrion; oxidoreductase

Query Match 72.7%; Score 32; DB 2; Length 504;  
Best Local Similarity 62.5%; Pred. No. 64;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLMPEPV 9  
 Db 128 LQMLLEPI 135

RESULT 15  
 hypothetical protein [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: F86251  
 R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 anesen, N.P.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: F86251  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-536 <STO>  
 A;Cross-references: UNIPROT:Q9SA99; UNIPARC:UPI0000048235; GB:AE005172; NID:g4835780; PI  
 C;Genetics:  
 A;Map position: 1  
 C;Superfamily: poppy reticuline oxidase

Query Match 72.7%; Score 32; DB 2; Length 536;  
 Best Local Similarity 55.6%; Pred. No. 68;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLOLMPEPV 9  
 Db 286 FMRLLQPV 294

RESULT 16  
 A41120  
 prostaglandin transporter - rat  
 N;Alternate names: matrix F/G  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 27-Mar-1992 #sequence\_revision 11-Aug-1995 #text\_change 09-Jul-2004  
 C;Accession: A41120  
 R;Hakes, D.J.; Berezney, R.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6186-6190, 1991  
 A;Title: Molecular cloning of matrix F/G: a DNA binding protein of the nuclear matrix th  
 A;Reference number: A41120; MUID:91296785; PMID:2068100  
 A;Accession: A41120  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-643 <HAK>  
 A;Cross-references: UNIPROT:Q00910; UNIPARC:UPI0000135445; GB:M64862  
 R;Note: the authors did not translate the codons for residues 1-99 in this reference  
 R;Kanai, N.; Lu, R.; Satriano, J.A.; Bao, Y.; Wolkoff, A.W.; Schuster, V.L.  
 Science 268, 866-869, 1995  
 A;Title: Identification and characterization of a prostaglandin transporter.  
 A;Reference number: A38955; MUID:95273959; PMID:7754369  
 A;Contents: annotation  
 C;Keywords: transmembrane protein

Query Match 72.7%; Score 32; DB 2; Length 643;  
 Best Local Similarity 66.7%; Pred. No. 82;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLOLMPEPV 9  
 Db 318 FLRLMNP 326

RESULT 17  
 B64126  
 transposase homolog HI1478 - Haemophilus influenzae (strain Rd KW20)  
 C;Species: Haemophilus influenzae  
 C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
 C;Accession: B64126  
 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,  
 Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,  
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
 Science 269, 496-512, 1995  
 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
 A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A;Reference number: A64000; MUID:95350630; PMID:7542800  
 A;Accession: B64126  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-687 <TIGR>  
 A;Cross-references: UNIPROT:O05069; UNIPARC:UPI00001372FE; GB:U32825; GB:L42023; NID:g3  
 C;Superfamily: phage Mu transposase

Query Match 72.7%; Score 32; DB 2; Length 687;  
 Best Local Similarity 66.7%; Pred. No. 88;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLOLMPEPV 9  
 Db 624 FLEMLPEPV 632

RESULT 18  
 S58108  
 hypothetical protein SPAC31A2.16 - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 13-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
 C;Accession: T38614; S58108  
 R;Devlin, K.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Walsh, S.V.  
 submitted to the EMBL Data Library, July 1995  
 A;Reference number: Z21731  
 A;Accession: T38614  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1101 <DE2>  
 A;Cross-references: UNIPROT:Q09733; UNIPARC:UPI0000139F65; EMBL:Z50113; NID:g914878; PI  
 A;Experimental source: strain 972h; cosmid c31A2  
 C;Genetics:  
 A;Gene: SPAC31A2.16  
 A;Map position: 1  
 A;Introns: 808/1; 884/1; 920/2  
 C;Superfamily: fission yeast protein SPAC31A2.16; CDC24 homology  
 F;230-431/Domain: CDC24 homology <CD24>

Query Match 72.7%; Score 32; DB 2; Length 1101;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QLIMEPV 9  
 Db 379 QLIMEPV 385

RESULT 19  
 T16927  
 hypothetical protein T23F2.2 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C;Accession: T16927  
 R;Du, Z.  
 submitted to the EMBL Data Library, October 1995  
 A;Description: The sequence of C. elegans cosmid T23F2.  
 A;Reference number: Z18608  
 A;Accession: T16927  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA

A;Residues: 1-1510 <DUZ>  
A;Cross-references: UNIPARC:UPI000017BBDD; EMBL:U39649; NID:g1049370; PID:g1049372; PIDN:  
C;Genetics:  
A;Gene: CESP-T23F2.2  
A;introns: 20/2; 81/1; 119/2; 211/3; 236/3; 290/2; 344/1; 396/3; 439/3; 465/3; 556/3; 60

Query Match 72.7%; Score 32; DB 2; Length 1510;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
|||:||||  
Db 429 YLQKMEPV 437

RESULT 20  
C36179  
gonadotropin II beta chain precursor - chum salmon  
C;Species: Oncorhynchus keta (chum salmon)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: C36179; S09344  
R;Sekine, S.; Saito, A.; Itoh, H.; Kawauchi, H.; Itoh, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8645-8649, 1989  
A;Title: Molecular cloning and sequence analysis of chum salmon gonadotropin cDNAs.  
A;Reference number: A36179; MUID:90046849; PMID:2813416  
A;Accession: C36179  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-142 <SEK>  
A;Cross-references: UNIPROT:P10256; UNIPARC:UPI000012BCCE; GB:M27154; NID:g213429; PIDN:  
R;Itoh, H.; Suzuki, K.; Kawauchi, H.  
Gen. Comp. Endocrinol. 71, 438-451, 1988  
A;Title: The complete amino acid sequences of beta-subunits of two distinct chum salmon  
A;Reference number: S07216; MUID:89053031; PMID:3192067  
A;Accession: S09344  
A;Molecule type: protein  
A;Residues: 24-72, 'I', 74-142 <ITO>  
A;Cross-references: UNIPARC:UPI000015BB63  
C;Superfamily: pituitary glycoprotein hormone beta chain  
C;Keywords: glycoprotein; heterodimer; hormone; pituitary  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-142/Product: gonadotropin II beta chain #status experimental <MAT>  
F;29-54, 43-77, 46-108, 58-130, 92-120, 110-113/Disulfide bonds: #status predicted  
F;33/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.5%; Score 31; DB 1; Length 142;  
Best Local Similarity 66.7%; Pred. No. 28;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
|||:||||  
Db 13 FLQILLEPV 21

RESULT 21  
I50143  
gonadotropin II beta chain - arctic cisco  
C;Species: Coregonus autumnalis (arctic cisco)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: I50143  
R;Trofimova, I.N.; Belikov, S.I.  
Mol. Biol. (Mosk.) 28, 1052-1056, 1994  
A;Title: Cloning and sequencing the cDNA for the beta-subunit of Baikal omul gonadotropin  
A;Reference number: I50143; MUID:95082790; PMID:7990827  
A;Accession: I50143  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-142 <TRO>  
A;Cross-references: UNIPROT:P48251; UNIPARC:UPI000012BCC8; GB:L23431; NID:g387920; PIDN:  
C;Genetics:  
A;Gene: GTH-II  
C;Superfamily: pituitary glycoprotein hormone beta chain

Query Match 70.5%; Score 31; DB 2; Length 142;  
Best Local Similarity 66.7%; Pred. No. 28;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
|||:||||  
Db 14 FLQILLEPV 22

RESULT 22  
A69939  
conserved hypothetical protein ypmR - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: A69939; I40004  
R;Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: A69939  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-255 <KUN>  
A;Cross-references: UNIPROT:P40766; UNIPARC:UPI00000605F6; GB:Z99115; GB:AL0009126; NID:  
A;Experimental source: strain 168  
R;Smith, H.; de Jong, A.; Bron, S.; Venema, G.  
Gene 70, 351-361, 1988  
A;Title: Characterization of signal-sequence-coding regions selected from the Bacillus  
A;Reference number: I39994; MUID:89108019; PMID:3145906  
A;Accession: I40004  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 'M', 4-56, 'QLGARVGYIELDPLESTAQA' <RES>  
A;Cross-references: UNIPARC:UPI000016S9A5; GB:M22910; NID:g143689; PIDN:AAA22826.1; PID  
C;Genetics:  
A;Gene: ypmR

Query Match 70.5%; Score 31; DB 2; Length 255;  
Best Local Similarity 75.0%; Pred. No. 52;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQILMEP 8  
|||:||||  
Db 130 FLQLTVEP 137

RESULT 23  
T29192  
hypothetical protein T03F1.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T29192  
R;Du, Z.; Le, T.T.  
submitted to the EMBL Data Library, February 1997  
A;Description: The sequence of C. elegans cosmid T03F1.  
A;Reference number: Z20586  
A;Accession: T29192  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-342 <DUZ>  
A;Cross-references: UNIPROT:P91421; UNIPARC:UPI000007943E; EMBL:U88169; PIDN:AA842234.1;

A;Experimental source: strain Bristol N2; clone T03F1

C;Genetics:

A;Gene: CESP:T03F1.6

A;Map position: 1

A;Introns: 65/1; 121/1; 147/3; 219/1; 303/3

C;Superfamily: Caenorhabditis elegans hypothetical protein T03F1.6

Query Match 70.5%; Score 31; DB 2; Length 342;

Best Local Similarity 77.8%; Pred. No. 70;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9

|||||

Db 310 FLALLNEPV 318

RESULT 24

T01001

hypothetical protein At2g39720 [imported] - Arabidopsis thaliana

N;Alternate names: RING-H2 finger protein RHC2a

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004

C;Accession: T01001; T51857; F84820

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, November 1997

A;Description: Arabidopsis thaliana chromosome II BAC T517 genomic sequence.

A;Reference number: Z14162

A;Accession: T01001

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-401 <ROU>

A;Cross-references: UNIPROT:O22283; UNIPARC:UPI00000A67F4; EMBL:AC003000; NID:g2642152;

A;Experimental source: Cultivar Columbia

R;Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.

FEBS Lett. 436, 283-7, 1998

A;Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the mo

A;Reference number: Z13771; MUID:98452956; PMID:9781696

A;Accession: T51857

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-401 <JEN>

A;Cross-references: UNIPARC:UPI00000A67F4; EMBL:AF079186; PIDN:AAC69860.1

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: F84820

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-401 <STO>

A;Cross-references: UNIPARC:UPI00000A67F4; GB:AE002093; NID:g2642154; PIDN:AAB87121.1; C

C;Genetics:

A;Gene: T517.2; At2g39720

A;Map position: 2

F;197-247/Domain: RING finger homology <RRN>

Query Match 70.5%; Score 31; DB 2; Length 401;

Best Local Similarity 55.6%; Pred. No. 83;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9

|||||

Db 30 FLELIQEPL 38

RESULT 25

S69677

hypothetical protein YDR393w - yeast (Saccharomyces cerevisiae)

C;Species: Saccharomyces cerevisiae

C;Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004

C;Accession: S69677

R;Dietrich, F.S.

submitted to the EMBL Data Library, July 1995

A;Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9926, 9461, and lambda

A;Reference number: S69665

A;Accession: S69677

A;Molecule type: DNA

A;Residues: 1-456 <DIE>

A;Cross-references: UNIPROT:Q04172; UNIPARC:UPI000006970E; EMBL:U32274; NID:g927313; PI

A;Gene: SGD:SHE9; MIPS:YDR393w

C;Genetics:

A;Cross-references: SGD:S0002801

A;Map position: 4R

Query Match 70.5%; Score 31; DB 2; Length 456;

Best Local Similarity 85.7%; Pred. No. 95;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLLMEP 8

|||||

Db 313 LQLLLEP 319

RESULT 26

T10626

reticuline oxidase homolog F21C20.190 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T10626

R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemck

submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16991

A;Accession: T10626

A;Molecule type: DNA

A;Residues: 1-539 <BEV>

A;Cross-references: UNIPROT:Q9SVG3; UNIPARC:UPI000004899E; EMBL:AL080254; GSPDB:GN000062

A;Experimental source: cultivar Columbia; BAC clone F21C20

C;Genetics:

A;Gene: ATSP:F21C20.190

A;Map position: 4

C;Superfamily: poppy reticuline oxidase

Query Match 70.5%; Score 31; DB 2; Length 539;

Best Local Similarity 55.6%; Pred. No. 1.1e+02;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9

|||||

Db 292 FLRMLIQPV 300

RESULT 27

A55019

muscarinic acetylcholine receptor, M3 isoform - chicken

C;Species: Gallus gallus (chicken)

C;Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 09-Jul-2004

C;Accession: A55019

R;Gadbut, A.P.; Galper, J.B.

J. Biol. Chem. 269, 25823-25829, 1994

A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and

A;Reference number: A55019; MUID:95014393; PMID:7929287

A;Accession: A55019

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-639 <GAD>

A;Cross-references: UNIPROT:P49578; UNIPARC:UPI00001252B4; GB:L10617; NID:g530097; PIDN

C;Superfamily: vertebrate rhodopsin

C;Keywords: neurotransmitter receptor

Query Match 70.5%; Score 31; DB 2; Length 639;

Best Local Similarity 55.6%; Pred. No. 1.4e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9





C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: E86201  
R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: E86201  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1760 <STO>  
A;Cross-references: UNIPROT:Q9SHK6, UNIPARC:UPI00000A3708; GB:AE005172; NID:96692694; PI  
C;Genetics:  
A;Gene: F12K11.4  
A;Map position: 1

Query Match 70.5%; Score 31; DB 2; Length 1760;  
Best Local Similarity 75.0%; Pred. No. 3.9e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEP 8  
||| |||:  
Db 927 FLQKMDP 934

RESULT 34  
E83533  
hypothetical protein PA0900 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: E83533  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: E83533  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-96 <STO>  
A;Cross-references: UNIPROT:O50176; UNIPARC:UPI00000CA933; GB:AE004524; GB:AE004091; NID  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA0900

Query Match 68.2%; Score 30; DB 2; Length 96;  
Best Local Similarity 75.0%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLMEPV 9  
||| |||:  
Db 71 LQLEMEPI 78

RESULT 35  
S56917  
hypothetical protein YJL135w - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein J0666  
C;Species: Saccharomyces cerevisiae  
C;Date: 08-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S56917; S71662  
R;Katsoulou, C.; Tzermia, M.; Alexandraki, D.  
submitted to the Protein Sequence Database, September 1995  
A;Reference number: S56912  
A;Accession: S56917  
A;Molecule type: DNA

A;Residues: 1-105 <KAT>  
A;Cross-references: UNIPROT:PA7012; UNIPARC:UPI000013B5F0; EMBL:Z49410; NID:g1008339; P  
R;Katsoulou, C.; Tzermia, M.; Tavernarakis, N.; Alexandraki, D.  
Yeast 12, 787-797, 1996  
A;Title: Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome X  
of chromosome XI.  
A;Reference number: S71643; MUID:96408771; PMID:8813765  
A;Accession: S71662  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-105 <KAW>  
A;Cross-references: UNIPARC:UPI000013B5F0; EMBL:X87371; NID:9854542; PIDN:CAA0820.1; P  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995  
C;Genetics:  
A;Cross-references: SGD:S0003671  
A;Map position: 10L  
C;Superfamily: Saccharomyces hypothetical protein YJL135w

Query Match 68.2%; Score 30; DB 2; Length 105;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEP 8  
||| |||:  
Db 2 FNQLLEP 9

RESULT 36  
S45797  
probable membrane protein YBL062w - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YBL0505  
C;Species: Saccharomyces cerevisiae  
C;Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: S45797  
R;Dubois, E.; El Bakoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45782  
A;Accession: S45797  
A;Molecule type: DNA  
A;Residues: 1-126 <DUB>  
A;Cross-references: UNIPROT:P38189; UNIPARC:UPI000013A32A; EMBL:Z35823; NID:g536095; PI  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: MIPS:YBL062w  
A;Cross-references: SGD:S0000158  
A;Map position: 2L  
C;Keywords: transmembrane protein  
F;8-28/Domain: transmembrane #status predicted <TM1>  
F;71-99/Domain: transmembrane #status predicted <TM2>

Query Match 68.2%; Score 30; DB 2; Length 126;  
Best Local Similarity 66.7%; Pred. No. 41;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9  
||| |||:  
Db 73 FLMLVSEPV 81

RESULT 37  
A25800  
gonadotropin beta chain precursor - chinook salmon  
C;Species: Oncorhynchus tshawytscha (chinook salmon)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A25800  
R;Trinh, K.Y.; Wang, N.C.; Hew, C.L.; Crim, L.W.  
Eur. J. Biochem. 159, 619-624, 1986  
A;Title: Molecular cloning and sequencing of salmon gonadotropin beta subunit.  
A;Reference number: A25800; MUID:87004682; PMID:2428617  
A;Accession: A25800  
A;Molecule type: mRNA  
A;Residues: 1-142 <TRI>  
A;Cross-references: UNIPROT:P07732; UNIPARC:UPI000012BCD0; GB:X04404; NID:g64202; PIDN:

C:Superfamily: pituitary glycoprotein hormone beta chain  
P:29-54,43-77,46-108,58-130,92-120,110-113/Dисульфide bonds: #status predicted

Query Match 68.2%; Score 30; DB 1; Length 142;  
Best Local Similarity 55.6%; Pred. No. 46;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9  
DB 13 FLCLILEPI 21  
||:|:|:

RESULT 38  
T29222  
hypothetical protein F55G1.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29222  
R:Murray, J.; Le, T.T.  
submitted to the EMBL Data Library, May 1996  
A:Description: The sequence of C. elegans cosmid F55G1.  
A:Reference number: Z20591  
A:Accession: T29222  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-307 <MUR>  
A:Cross-references: UNIPROT:Q20844; UNIPARC:UPI00000798A4; EMBL:U58750; PIDN:AA00641.1;  
A:Experimental source: strain Bristol N2; clone F55G1  
C:Genetics:  
A:Gene: CESP:F55G1.7  
A:Map position: 4  
A:Introns: 64/2; 160/2; 193/2; 250/2  
C:Superfamily: Caenorhabditis elegans hypothetical protein F55G1.7

Query Match 68.2%; Score 30; DB 2; Length 307;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEPV 8  
DB 21 FLQLMLP 28  
||:|:|:

RESULT 39  
G75117  
dipeptide abc transporter, ATP-binding protein (dppf) PAB1875 - Pyrococcus abyssi (strain  
C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: G75117  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure  
A:Reference number: A75001  
A:Accession: G75117  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-326 <RAW>  
A:Cross-references: UNIPROT:Q9V077; UNIPARC:UPI000006692A; GB:AJ248285; GB:AL096836; NID  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB1875  
C:Superfamily: inner membrane protein malk; ATP-binding cassette homology  
F:30-229/Domain: ATP-binding cassette homology <ABC>

Query Match 68.2%; Score 30; DB 2; Length 326;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLLMEPV 9  
DB 112 QIIMEPV 118  
||:|:|:

RESULT 40  
G71014  
probable dipeptide transport ATP-binding protein dppF - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 16-Aug-2004  
C:Accession: G71014  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki,  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: G71014  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-329 <RAW>  
A:Cross-references: UNIPROT:O50121; UNIPARC:UPI0000066797; GB:AP000006; NID:g3236133; P  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Note: PH1413  
C:Function:  
A:Description: probably responsible for energy-coupling to the transport system  
A:Keywords: ATP; binding protein-dependent transport system; membrane protein; nucleotid  
F:33-232/Domain: ATP-binding cassette homology <ABC>  
F:50-57/Region: nucleotide-binding motif A (P-loop)  
F:176-180/Region: nucleotide-binding motif B

Query Match 68.2%; Score 30; DB 2; Length 329;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLLMEPV 9  
DB 115 QIIMEPV 121  
||:|:|:

RESULT 41  
T34128  
hypothetical protein C33G8.12 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T34128  
R:Gattung, S.; Wu, X.  
submitted to the EMBL Data Library, March 1996  
A:Description: The sequence of C. elegans cosmid C33G8.  
A:Reference number: Z21481  
A:Accession: T34128  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-358 <GAT>  
A:Cross-references: UNIPROT:Q18392; UNIPARC:UPI0000082498; EMBL:U53154; PIDN:AA025856.1;  
A:Experimental source: strain Bristol N2; clone C33G8  
C:Genetics:  
A:Gene: CESP:C33G8.12  
A:Map position: 5  
A:Introns: 32/2; 80/1; 105/3; 277/1

Query Match 68.2%; Score 30; DB 2; Length 358;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLLMEPV 8  
DB 189 QLLMEPV 193  
||:|:|:

RESULT 42  
F96827  
protein P20B17.8 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 05-Oct-2004  
C:Accession: F96827  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96827  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-367 <STO>  
A:Cross-references: UNIPROT:Q9NA10; UNIPARC:UPI000009BA51; GB:AE005173; NID:97715605; PT  
C:Genetics:  
A:Gene: F20B17.8  
A:Map position: 1

Query Match 68.2%; Score 30; DB 2; Length 367;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEP 8  
|::|::|  
Db 288 FLQLVNEP 295

## RESULT 43

AE3356  
lipid-A-disaccharide synthase (EC 2.4.1.182) [imported] - Brucella melitensis (strain 16  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C:Accession: AE3356

R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
M.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AE3356

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-395 <KUR>  
A:Cross-references: UNIPROT:Q8YHG6; UNIPROT:Q8GOE6; UNIPARC:UPI0000057E2D; GB:AE008917;  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEI0835  
A:Map position: 1  
C:Superfamily: lipid A disaccharide synthase  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 68.2%; Score 30; DB 2; Length 395;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMEP 8  
|::|::|  
Db 212 IQLMEP 218

## RESULT 44

G86151  
F22M8.11 protein - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: G86151  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G86151  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-541 <STO>  
A:Cross-references: UNIPROT:Q9LPC3; UNIPARC:UPI00000481A1; GB:AE005172; NID:98570449; P  
C:Genetics:  
A:Map position: 1  
C:Superfamily: poppy reticuline oxidase

Query Match 68.2%; Score 30; DB 2; Length 541;  
Best Local Similarity 44.4%; Pred. No. 1.9e+02;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9  
|::|::|  
Db 291 FMELMLQPV 299

## RESULT 45

T08456  
hypothetical protein F22O6.190 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T08456

R;Quetier, P.; Parnelle, B.; Boutry, M.; Goffeau, A.; Salanoubat, M.; Mewes, H.W.; Maye  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16420  
A:Accession: T08456  
A:Molecule type: DNA  
A:Residues: 1-541 <QUE>

A:Cross-references: UNIPROT:Q8S745; UNIPARC:UPI000009D94F; EMBL:AL050300; GSPDB:GN000061  
A:Experimental source: cultivar Columbia; BAC clone F22O6  
C:Genetics:  
A:Gene: ATSP:F22O6.190  
A:Map position: 3  
A:Introns: 97/3

Query Match 68.2%; Score 30; DB 2; Length 541;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9  
|::|::|  
Db 387 FYQLLAEP 395

## RESULT 46

AI1855  
hypothetical protein all0394 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AI1855

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AI1855  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-606 <KUR>  
A:Cross-references: UNIPROT:Q8YZR3; UNIPARC:UPI000000CDD29; GB:BA000019; PIDN:BA072352.1  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all0394  
C:Superfamily: Escherichia coli plasmid ColV-K30 aerobactin biosynthesis protein iuca

Query Match 68.2%; Score 30; DB 2; Length 606;

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Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9
   |||: |||:
Db 439 YLQIYLEPI 447

RESULT 47
matrix metalloproteinase - Japanese newt
C:Species: Cynops pyrrhogaster (Japanese newt)
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: JC7776
R:Suzuki, A.S.; Tadano, Y.; Yamamoto, T.; Abe, S.I.; Tajima, T.
Biochem. Biophys. Res. Commun. 288, 380-384, 2001
A:Title: Expression of a novel matrix metalloproteinase gene during Cynops early embryogenesis
A:Reference number: JC7776; PMID:11606053
A:Contents: Embryo
A:Accession: JC7776
A:Molecule type: mRNA
A:Residues: 1-616 <SUZ>
A:Cross-references: UNIPROT:Q90YC2; UNIPARC:UPI000017CCA4; DDBJ:AB054185
C:Comment: This protein plays a role in gastrulation-related cell movement of Cynops embryos involved in neural induction via degradation of the extracellular matrix and activation of C:Genetics:
A:Gene: Cymmp
C:Keywords: embryo; mesoderm

Query Match 68.2%; Score 30; DB 2; Length 616;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9
   |||: |||:
Db 193 FLQMLAAPV 201

RESULT 48
A75055
DNA topoisomerase I (topa) PAB1430 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 31-Dec-2004
C:Accession: A75055
R:Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: A75055
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-685 <KAW>
A:Cross-references: UNIPROT:Q9UY58; UNIPARC:UPI0000345DE; GB:AJ248287; GB:AL096836; NID:
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1430
C:Superfamily: DNA topoisomerase type IA

Query Match 68.2%; Score 30; DB 2; Length 685;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLMEP 8
   |||: |||:
Db 399 FLALFMEP 406

RESULT 49
S35093
plakoglobin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S35093; S24636

```

```

R:Fouquet, B.; Zimbelmann, R.; Franke, W.W.
Differentiation 51, 187-194, 1992
A:Title: Identification of plakoglobin in oocytes and early embryos of Xenopus laevis: mRNA
A:Reference number: S35093; MUID:93093332; PMID:1459559
A:Accession: S35093
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-738 <FOU>
A:Cross-references: UNIPROT:P30998; UNIPARC:UPI0000131B9D; EMBL:M95593; NID:g214656; PID:
R:Demarais, A.A.
submitted to the EMBL Data Library, June 1992
A:Reference number: S24636
A:Accession: S24636
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 133-184, 'V', 186-225, 'T', 227-292 <DEM>
A:Cross-references: UNIPARC:UPI00001715CE; EMBL:X67078; NID:g65252; PID:g65253
C:Keywords: cytoskeleton

Query Match 68.2%; Score 30; DB 2; Length 738;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9
   |||: |||:
Db 585 FVQLLYSPV 593

RESULT 50
A33810
band 3 anion transport protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33810
R:Kudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 264, 8185-8192, 1989
A:Title: Primary structure of the rat kidney band 3 anion exchange protein deduced from
A:Reference number: A33810; MUID:89255254; PMID:2722777
A:Accession: A33810
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-848 <KUD>
A:Cross-references: UNIPROT:P23562; UNIPARC:UPI000002A4A3; GB:J04793; NID:g203092; PID:
C:Superfamily: band 3 anion transport protein
C:Keywords: alternative splicing; transmembrane protein

Query Match 68.2%; Score 30; DB 2; Length 848;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMEPV 9
   |||: |||:
Db 709 LSILMEPI 716

Search completed: May 9, 2006, 02:25:05
Job time : 31.4 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:25:44 ; Search time 25.2 Seconds  
(without alignments)  
29.527 Million cell updates/sec

Title: US-09-870-216C-3  
Perfect score: 44  
Sequence: 1 FLQLLMEPV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5 COMB.pep:\*

2: /cgn2\_6/prodata/1/iaa/6 COMB.pep:\*

3: /cgn2\_6/prodata/1/iaa/H COMB.pep:\*

4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep:\*

5: /cgn2\_6/prodata/1/iaa/RE COMB.pep:\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	77.3	318	2	US-09-583-110-2976
2	34	77.3	336	2	US-09-107-433-5076
3	33	75.0	305	2	US-09-710-279-1264
4	33	75.0	324	2	US-09-134-001C-5525
5	33	75.0	368	2	US-09-413-574-4
6	33	75.0	368	2	US-09-805-550-4
7	33	75.0	409	2	US-09-538-092-1214
8	33	75.0	409	2	US-09-949-016-6281
9	33	75.0	454	2	US-09-949-016-11120
10	33	75.0	2802	2	US-09-542-331-1
11	33	75.0	2802	2	US-09-510-791-1
12	32	72.7	107	2	US-09-328-352-5811
13	32	72.7	195	2	US-09-134-000C-4338
14	32	72.7	323	2	US-09-107-532A-5460
15	32	72.7	406	2	US-09-248-796A-17915
16	32	72.7	434	2	US-09-005-286B-2
17	32	72.7	434	2	US-09-227-718B-2
18	32	72.7	434	2	US-09-840-008A-2
19	32	72.7	484	2	US-09-949-016-7513
20	32	72.7	484	2	US-09-949-016-7514
21	32	72.7	484	2	US-09-949-016-7515
22	32	72.7	642	1	US-08-706-936-3
23	31	70.5	131	2	US-09-270-767-37595
24	31	70.5	131	2	US-09-270-767-52812
25	31	70.5	262	2	US-09-949-016-6584
26	31	70.5	375	2	US-09-252-149B-35
27	31	70.5	375	2	US-09-451-501-27

28	31	70.5	375	2	US-09-686-344-27	Sequence 27, Appl
29	31	70.5	375	2	US-09-626-896-18	Sequence 18, Appl
30	31	70.5	375	2	US-09-485-046-14	Sequence 14, Appl
31	31	70.5	375	2	US-10-278-803-27	Sequence 27, Appl
32	31	70.5	375	2	US-09-841-730-18	Sequence 18, Appl
33	31	70.5	1000	2	US-09-193-562D-30	Sequence 30, Appl
34	31	70.5	1000	2	US-10-055-412B-30	Sequence 30, Appl
35	31	70.5	1132	2	US-09-949-002-372	Sequence 372, App
36	31	70.5	1137	2	US-09-949-002-542	Sequence 542, App
37	31	70.5	1253	1	US-08-252-966B-12	Sequence 12, Appl
38	31	70.5	1261	1	US-08-252-966B-18	Sequence 18, Appl
39	30	68.2	103	2	US-09-302-628B-38	Sequence 38, Appl
40	30	68.2	116	2	US-09-252-991A-29715	Sequence 29715, A
41	30	68.2	327	2	US-09-252-991A-33067	Sequence 33067, A
42	30	68.2	475	2	US-09-248-796A-18640	Sequence 18640, A
43	30	68.2	515	2	US-09-434-840-63	Sequence 63, Appl
44	30	68.2	526	2	US-09-434-840-2	Sequence 2, Appl
45	30	68.2	540	2	US-09-252-991A-18305	Sequence 18305, A
46	30	68.2	541	2	US-09-434-840-55	Sequence 55, Appl
47	30	68.2	728	2	US-08-915-337-2	Sequence 2, Appl
48	30	68.2	857	2	US-09-949-016-7836	Sequence 7836, Ap
49	30	68.2	1332	2	US-09-252-991A-25772	Sequence 25772, A
50	30	68.2	1501	2	US-09-710-279-2850	Sequence 2850, Ap
51	30	68.2	1529	2	US-09-134-001C-3945	Sequence 3945, Ap
52	29	65.9	17	2	US-09-641-803-2	Sequence 2, Appl
53	29	65.9	17	2	US-09-641-801-2	Sequence 2, Appl
54	29	65.9	17	2	US-09-641-802-2	Sequence 2, Appl
55	29	65.9	17	2	US-10-281-652-2	Sequence 2, Appl
56	29	65.9	44	2	US-09-046-894-38	Sequence 38, Appl
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59	29	65.9	45	1	US-08-487-002-83	Sequence 83, Appl
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61	29	65.9	45	1	US-08-488-011B-83	Sequence 83, Appl
62	29	65.9	45	2	US-08-850-727-83	Sequence 83, Appl
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64	29	65.9	45	4	PCT-US95-10203-83	Sequence 83, Appl
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67	29	65.9	50	1	US-08-250-858-12	Sequence 12, Appl
68	29	65.9	50	1	US-08-446-915-12	Sequence 12, Appl
69	29	65.9	50	1	US-08-744-139-12	Sequence 12, Appl
70	29	65.9	50	2	US-08-779-599-12	Sequence 12, Appl
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72	29	65.9	51	1	US-08-691-814B-19	Sequence 19, Appl
73	29	65.9	51	2	US-09-248-796A-23706	Sequence 23706, A
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76	29	65.9	153	2	US-09-270-767-31788	Sequence 31788, A
77	29	65.9	153	2	US-09-270-767-47005	Sequence 47005, A
78	29	65.9	177	2	US-09-248-796A-27953	Sequence 27953, A
79	29	65.9	180	2	US-09-270-767-40016	Sequence 40016, A
80	29	65.9	180	2	US-09-270-767-55232	Sequence 55232, A
81	29	65.9	198	2	US-09-248-796A-17465	Sequence 17465, A
82	29	65.9	218	2	US-09-327-983-6	Sequence 6, Appl
83	29	65.9	218	2	US-09-549-827A-10	Sequence 10, Appl
84	29	65.9	227	2	US-09-543-681A-4555	Sequence 4555, Ap
85	29	65.9	246	2	US-09-270-767-44162	Sequence 44162, A
86	29	65.9	278	2	US-09-248-796A-26610	Sequence 26610, A
87	29	65.9	328	2	US-08-459-046-2	Sequence 2, Appl
88	29	65.9	328	2	US-08-513-974B-56	Sequence 56, Appl
89	29	65.9	328	2	US-08-513-974B-380	Sequence 380, App
90	29	65.9	328	2	US-09-102-710B-2	Sequence 2, Appl
91	29	65.9	328	2	US-09-461-436B-56	Sequence 56, Appl
92	29	65.9	328	2	US-09-745-842-18	Sequence 18, Appl
93	29	65.9	358	2	US-09-328-352-4988	Sequence 4988, Ap
94	29	65.9	363	2	US-09-538-092-1213	Sequence 1213, Ap
95	29	65.9	372	2	US-09-492-709A-375	Sequence 375, App
96	29	65.9	374	1	US-08-928-692-51	Sequence 51, Appl
97	29	65.9	374	2	US-09-339-972-51	Sequence 51, Appl
98	29	65.9	375	2	US-09-949-016-8374	Sequence 8374, Ap
99	29	65.9	406	2	US-09-491-577-38	Sequence 38, Appl
100	29	65.9	414	2	US-09-489-039A-10428	Sequence 10428, A

101	29	65.9	415	2	US-09-902-540-12194	Sequence 12194, A	174	28	63.6	375	2	US-09-686-344-23	Sequence 23, Appl
102	29	65.9	435	2	US-09-248-796A-19401	Sequence 19401, A	175	28	63.6	375	2	US-09-485-046-10	Sequence 10, Appl
103	29	65.9	438	2	US-09-716-964B-132	Sequence 132, App	176	28	63.6	375	2	US-10-278-803-23	Sequence 23, Appl
104	29	65.9	497	2	US-09-252-991A-31532	Sequence 31532, A	177	28	63.6	376	1	US-08-933-750C-31	Sequence 31, Appl
105	29	65.9	527	2	US-09-489-039A-14144	Sequence 14144, A	178	28	63.6	376	2	US-09-234-613-31	Sequence 31, Appl
106	29	65.9	648	2	US-09-252-991A-17619	Sequence 17619, A	179	28	63.6	376	2	US-09-311-021-80	Sequence 80, Appl
107	29	65.9	781	2	US-09-766-387-2	Sequence 2, Appli	180	28	63.6	379	2	US-09-252-991A-26924	Sequence 26924, A
108	29	65.9	781	2	US-09-766-387-4	Sequence 4, Appli	181	28	63.6	386	2	US-08-875-082-2	Sequence 2, Appli
109	29	65.9	781	2	US-09-417-039-10	Sequence 10, Appli	182	28	63.6	403	2	US-09-638-649-5	Sequence 5, Appli
110	29	65.9	781	2	US-09-538-092-1067	Sequence 1067, Ap	183	28	63.6	403	2	US-09-638-648-5	Sequence 5, Appli
111	29	65.9	901	1	US-08-884-681-5	Sequence 5, Appli	184	28	63.6	412	2	US-09-902-540-9713	Sequence 9713, Ap
112	29	65.9	901	2	US-09-258-643-5	Sequence 5, Appli	185	28	63.6	418	2	US-09-902-540-14023	Sequence 14023, A
113	29	65.9	952	2	US-09-949-016-7283	Sequence 7283, Ap	186	28	63.6	425	2	US-09-107-532A-6574	Sequence 6574, Ap
114	29	65.9	952	2	US-09-949-016-7284	Sequence 7284, Ap	187	28	63.6	446	2	US-09-328-352-7464	Sequence 7464, Ap
115	29	65.9	968	2	US-08-560-005-7	Sequence 7, Appli	188	28	63.6	472	2	US-09-385-219A-8	Sequence 8, Appli
116	29	65.9	968	2	US-09-418-540-7	Sequence 7, Appli	189	28	63.6	512	2	US-09-672-785-4	Sequence 4, Appli
117	29	65.9	968	2	US-09-969-528-7	Sequence 7, Appli	190	28	63.6	542	2	US-09-543-681A-6864	Sequence 6864, Ap
118	29	65.9	1005	1	US-08-089-986-3	Sequence 3, Appli	191	28	63.6	545	2	US-09-270-767-39221	Sequence 39221, A
119	29	65.9	1005	1	US-08-478-585-3	Sequence 3, Appli	192	28	63.6	545	2	US-09-270-767-54438	Sequence 54438, A
120	29	65.9	1005	1	US-08-717-312-3	Sequence 3, Appli	193	28	63.6	549	2	US-09-248-796A-20436	Sequence 20436, A
121	29	65.9	1005	1	US-08-266-408-3	Sequence 3, Appli	194	28	63.6	580	2	US-09-902-540-16677	Sequence 16677, A
122	29	65.9	1005	4	PCT-US94-07886-3	Sequence 3, Appli	195	28	63.6	590	2	US-09-538-052-967	Sequence 967, App
123	29	65.9	1396	1	US-08-804-227C-9	Sequence 9, Appli	196	28	63.6	590	2	US-09-826-509-517	Sequence 517, App
124	29	65.9	1396	1	US-08-804-198-3	Sequence 3, Appli	197	28	63.6	681	2	US-09-252-991A-25690	Sequence 25690, A
125	29	65.9	4545	1	US-08-804-227C-14	Sequence 14, Appli	198	28	63.6	740	2	US-09-489-039A-13001	Sequence 13001, A
126	29	65.9	4550	1	US-08-804-227C-8	Sequence 8, Appli	199	28	63.6	942	1	US-08-884-681-4	Sequence 4, Appli
127	29	65.9	4550	1	US-08-804-198-2	Sequence 2, Appli	200	28	63.6	942	2	US-08-560-005-6	Sequence 6, Appli
128	29	63.6	111	2	US-09-543-681A-6056	Sequence 6056, Ap	201	28	63.6	942	2	US-09-258-643-4	Sequence 4, Appli
129	28	63.6	126	2	US-09-513-999C-5595	Sequence 5595, Ap	202	28	63.6	942	2	US-09-418-540-6	Sequence 6, Appli
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133	28	63.6	142	2	US-10-104-047-2330	Sequence 2330, Ap	206	28	63.6	1289	2	US-09-949-016-7313	Sequence 7313, Ap
134	28	63.6	142	2	US-09-248-796A-28014	Sequence 28014, A	207	28	63.6	1399	2	US-09-388-221B-4	Sequence 4, Appli
135	28	63.6	151	2	US-09-540-236-2508	Sequence 2508, Ap	208	28	63.6	1424	2	US-09-388-221B-12	Sequence 12, Appli
136	28	63.6	162	2	US-09-270-767-31643	Sequence 31643, A	209	28	63.6	1429	2	US-10-029-347-3	Sequence 3, Appli
137	28	63.6	162	2	US-09-270-767-48680	Sequence 48680, A	210	28	63.6	1429	2	US-10-029-347-26	Sequence 26, Appli
138	28	63.6	178	2	US-09-270-767-33545	Sequence 33545, A	211	28	63.6	1429	2	US-10-183-770A-3	Sequence 3, Appli
139	28	63.6	178	2	US-09-270-767-48762	Sequence 48762, A	212	28	63.6	1429	2	US-10-183-770A-15	Sequence 15, Appli
140	28	63.6	202	2	US-09-252-991A-17114	Sequence 17114, A	213	28	63.6	1443	2	US-09-996-617-2	Sequence 2, Appli
141	28	63.6	214	2	US-09-134-000C-4828	Sequence 4828, Ap	214	28	63.6	1454	2	US-09-388-221B-6	Sequence 6, Appli
142	28	63.6	271	2	US-08-482-918-52	Sequence 52, Appl	215	28	63.6	1454	2	US-09-388-221B-10	Sequence 10, Appli
143	28	63.6	271	2	US-09-224-681-52	Sequence 52, Appl	216	28	63.6	1473	2	US-09-388-221B-2	Sequence 2, Appli
144	28	63.6	271	2	US-09-635-251-52	Sequence 52, Appl	217	28	63.6	2214	2	US-09-902-540-15988	Sequence 15988, A
145	28	63.6	271	2	US-09-224-683-52	Sequence 52, Appl	218	28	63.6	3854	2	US-09-943-016-7876	Sequence 7876, Ap
146	28	63.6	271	2	US-09-604-325A-52	Sequence 52, Appl	219	28	63.6	10	4	PCT-US96-01735-4	Sequence 4, Appli
147	28	63.6	290	2	US-09-655-908-6	Sequence 6, Appli	220	27	61.4	38	1	US-08-425-061-14	Sequence 14, Appl
148	28	63.6	290	2	US-09-655-908-8	Sequence 8, Appli	221	27	61.4	38	1	US-08-825-886-14	Sequence 14, Appl
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151	28	63.6	312	1	US-08-420-235B-11	Sequence 11, Appl	224	27	61.4	41	2	US-09-046-894-37	Sequence 37, Appl
152	28	63.6	312	4	PCT-US95-10194-11	Sequence 11, Appl	225	27	61.4	42	1	US-08-480-754-82	Sequence 82, Appl
153	28	63.6	312	4	PCT-US95-10194-11	Sequence 11, Appl	226	27	61.4	42	1	US-08-483-553-82	Sequence 82, Appl
154	28	63.6	331	2	US-09-543-681A-4749	Sequence 4749, Ap	227	27	61.4	42	1	US-08-487-002-82	Sequence 82, Appl
155	28	63.6	334	2	US-09-248-796A-17169	Sequence 17169, A	228	27	61.4	42	1	US-08-483-554B-82	Sequence 82, Appl
156	28	63.6	352	2	US-09-489-039A-7589	Sequence 7589, Ap	229	27	61.4	42	1	US-08-488-011B-82	Sequence 82, Appl
157	28	63.6	355	1	US-08-118-270-11	Sequence 11, Appl	230	27	61.4	42	2	US-08-850-727-82	Sequence 82, Appl
158	28	63.6	355	4	PCT-US93-08528-11	Sequence 11, Appl	231	27	61.4	42	2	US-09-199-637A-110	Sequence 110, App
159	28	63.6	358	2	US-09-107-532A-6033	Sequence 6033, Ap	232	27	61.4	42	4	PCT-US95-10202-82	Sequence 82, Appl
160	28	63.6	360	1	US-08-671-525B-6	Sequence 6, Appli	233	27	61.4	42	4	PCT-US95-10203-82	Sequence 82, Appl
161	28	63.6	360	1	US-08-672-109B-6	Sequence 6, Appli	234	27	61.4	42	4	PCT-US95-10220-82	Sequence 82, Appl
162	28	63.6	360	1	US-08-842-045-6	Sequence 6, Appli	235	27	61.4	48	1	US-08-691-814B-14	Sequence 14, Appl
163	28	63.6	360	1	US-08-842-238-6	Sequence 6, Appli	236	27	61.4	48	1	US-09-230-637-62	Sequence 62, Appl
164	28	63.6	360	1	US-08-780-749A-1	Sequence 1, Appli	237	27	61.4	49	2	US-09-949-016-6797	Sequence 6797, Ap
165	28	63.6	360	1	US-08-629-335B-6	Sequence 6, Appli	238	27	61.4	59	2	US-09-270-767-43958	Sequence 43958, A
166	28	63.6	360	2	US-08-870-511-1	Sequence 1, Appli	239	27	61.4	62	2	US-09-248-796A-28080	Sequence 28080, A
167	28	63.6	360	2	US-09-709-066-4	Sequence 4, Appli	240	27	61.4	63	1	US-08-425-061-15	Sequence 15, Appl
168	28	63.6	370	2	US-09-417-039-3	Sequence 3, Appli	241	27	61.4	63	1	US-08-825-886-15	Sequence 15, Appl
169	28	63.6	374	2	US-09-626-896-8	Sequence 8, Appli	242	27	61.4	63	2	US-08-989-890-15	Sequence 15, Appl
170	28	63.6	374	2	US-09-841-730-8	Sequence 8, Appli	243	27	61.4	63	2	US-09-902-540-15371	Sequence 15371, A
171	28	63.6	375	2	US-09-252-149B-34	Sequence 34, Appl	244	27	61.4	64	2	US-09-248-796A-23598	Sequence 23598, A
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249	27	61.4	81	1	US-08-425-886-17	Sequence 17, Appl	322	27	61.4	439	2	US-09-710-279-2408	Sequence 2408, Ap
250	27	61.4	80	2	US-08-989-890-17	Sequence 17, Appl	323	27	61.4	458	2	US-09-198-452A-209	Sequence 209, App
251	27	61.4	89	2	US-09-134-000C-6393	Sequence 6393, Ap	324	27	61.4	458	2	US-09-438-185A-192	Sequence 192, App
252	27	61.4	93	2	US-09-107-433-4137	Sequence 4137, Ap	325	27	61.4	459	2	US-09-134-001C-4856	Sequence 4856, Ap
253	27	61.4	100	2	US-09-230-196-3	Sequence 3, Appl	326	27	61.4	477	2	US-09-489-039A-8194	Sequence 8194, Ap
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256	27	61.4	106	2	US-09-270-767-32489	Sequence 32489, A	329	27	61.4	515	2	US-09-171-461-8	Sequence 8, Appl
257	27	61.4	106	2	US-09-270-767-47706	Sequence 47706, A	330	27	61.4	515	2	US-09-970-711-8	Sequence 8, Appl
258	27	61.4	123	1	US-08-768-796A-16271	Sequence 16271, A	331	27	61.4	517	2	US-09-540-236-2796	Sequence 2796, Ap
259	27	61.4	135	1	US-08-383-621-5	Sequence 5, Appl	332	27	61.4	525	2	US-09-328-352-4492	Sequence 4492, Ap
260	27	61.4	135	2	US-08-459-906-5	Sequence 5, Appl	333	27	61.4	525	2	US-10-104-047-3922	Sequence 3922, Ap
261	27	61.4	140	2	US-09-198-452A-888	Sequence 888, App	334	27	61.4	526	2	US-09-949-016-7634	Sequence 7634, Ap
262	27	61.4	157	2	US-09-270-767-33500	Sequence 33500, A	335	27	61.4	533	2	US-09-949-016-7634	Sequence 7634, Ap
263	27	61.4	158	2	US-09-248-796A-17085	Sequence 17085, A	336	27	61.4	540	2	US-09-248-796A-19351	Sequence 19351, A
264	27	61.4	161	2	US-09-328-352-7968	Sequence 7968, A	337	27	61.4	545	2	US-09-252-991A-18967	Sequence 18967, A
265	27	61.4	167	2	US-09-252-991A-19755	Sequence 19755, A	338	27	61.4	552	2	US-09-833-466-3	Sequence 3, Appl
266	27	61.4	200	2	US-09-107-532A-5055	Sequence 5055, Ap	339	27	61.4	552	2	US-10-104-047-3426	Sequence 3426, Ap
267	27	61.4	204	6	5187075-6	Patent No. 5187075	340	27	61.4	584	2	US-09-102-528-12	Sequence 12, Appl
268	27	61.4	214	2	US-09-328-352-6571	Sequence 6571, Ap	341	27	61.4	606	2	US-09-248-796A-14276	Sequence 14276, A
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272	27	61.4	241	2	US-08-483-101-12	Sequence 12, Appl	345	27	61.4	637	2	US-09-469-211A-4	Sequence 4, Appl
273	27	61.4	241	2	US-09-978-248A-11	Sequence 11, Appl	346	27	61.4	639	2	US-09-248-796A-20278	Sequence 20278, A
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275	27	61.4	255	1	US-08-576-156-2	Sequence 2, Appl	348	27	61.4	664	2	US-09-949-016-9005	Sequence 9005, Ap
276	27	61.4	256	2	US-08-659-188-2	Sequence 2, Appl	349	27	61.4	667	2	US-09-303-064-55	Sequence 55, Appl
277	27	61.4	256	2	US-08-655-227-2	Sequence 2, Appl	350	27	61.4	667	2	US-09-086-503-55	Sequence 55, Appl
278	27	61.4	256	2	US-08-655-241-2	Sequence 2, Appl	351	27	61.4	700	2	US-09-134-000C-6262	Sequence 6262, Ap
279	27	61.4	256	2	US-09-398-326-2	Sequence 2, Appl	352	27	61.4	765	1	US-08-425-061-19	Sequence 19, Appl
280	27	61.4	256	2	US-09-853-450-2	Sequence 2, Appl	353	27	61.4	765	1	US-08-825-886-19	Sequence 19, Appl
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284	27	61.4	299	2	US-09-134-000C-6675	Sequence 6675, Ap	357	27	61.4	808	2	US-09-438-185A-312	Sequence 312, App
285	27	61.4	300	1	US-08-592-214A-2	Sequence 2, Appl	358	27	61.4	834	1	US-08-861-464-4	Sequence 4, Appl
286	27	61.4	300	2	US-09-149-976-2	Sequence 2, Appl	359	27	61.4	834	1	US-08-396-001-4	Sequence 4, Appl
287	27	61.4	312	1	US-08-425-061-18	Sequence 18, Appl	360	27	61.4	834	2	US-09-323-433A-4	Sequence 4, Appl
288	27	61.4	312	1	US-08-825-886-18	Sequence 18, Appl	361	27	61.4	834	2	US-09-826-752-4	Sequence 4, Appl
289	27	61.4	312	2	US-08-989-890-18	Sequence 18, Appl	362	27	61.4	864	2	US-09-489-039A-12869	Sequence 12869, A
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291	27	61.4	326	2	US-09-830-230A-692	Sequence 692, App	364	27	61.4	900	1	US-08-825-886-20	Sequence 20, Appl
292	27	61.4	359	2	US-09-489-039A-7467	Sequence 7467, Ap	365	27	61.4	900	2	US-08-989-890-20	Sequence 20, Appl
293	27	61.4	359	2	US-09-830-230A-691	Sequence 691, App	366	27	61.4	914	1	US-08-425-061-21	Sequence 21, Appl
294	27	61.4	380	2	US-09-489-847-277	Sequence 277, App	367	27	61.4	914	1	US-08-825-886-21	Sequence 21, Appl
295	27	61.4	383	2	US-09-266-965-100	Sequence 100, App	368	27	61.4	914	1	US-08-989-890-21	Sequence 21, Appl
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297	27	61.4	392	2	US-09-461-240-2	Sequence 2, Appl	370	27	61.4	1033	2	US-09-902-540-12335	Sequence 12335, A
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299	27	61.4	403	2	US-09-431-577-10	Sequence 10, Appl	372	27	61.4	1095	2	US-09-489-039A-9267	Sequence 9267, Ap
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302	27	61.4	414	2	US-10-020-445A-466	Sequence 466, App	375	27	61.4	1098	1	US-08-954-418-2	Sequence 2, Appl
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305	27	61.4	426	2	US-08-826-246-4	Sequence 4, Appl	378	27	61.4	1202	2	US-08-989-890-22	Sequence 22, Appl
306	27	61.4	426	2	US-08-944-495-4	Sequence 4, Appl	379	27	61.4	1231	2	US-09-107-532A-5150	Sequence 5150, Ap
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313	27	61.4	426	2	US-08-825-486-4	Sequence 4, Appl	386	27	61.4	1634	2	US-09-949-016-6794	Sequence 6794, Ap
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315	27	61.4	426	2	US-09-885-722A-6	Sequence 6, Appl	388	27	61.4	1804	2	US-09-362-336A-4	Sequence 4, Appl
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317	27	61.4	428	2	US-08-301-162-18	Sequence 18, Appl	390	27	61.4	1852	1	US-08-825-886-24	Sequence 24, Appl
318	27	61.4	428	2	US-09-461-240-18	Sequence 18, Appl	391	27	61.4	1852	2	US-08-989-890-24	Sequence 24, Appl
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399	27	61.4	1863	1	US-08-798-691-2	Sequence 2, Appli	472	26	59.1	136	2	US-09-115-824-8	Sequence 8, Appli
400	27	61.4	1863	1	US-08-798-691-4	Sequence 4, Appli	473	26	59.1	145	2	US-09-107-532A-5389	Sequence 5389, Ap
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405	27	61.4	1863	1	US-08-825-487A-2	Sequence 2, Appli	478	26	59.1	164	2	US-09-107-532A-5100	Sequence 5100, Ap
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407	27	61.4	1863	2	US-08-825-487A-6	Sequence 6, Appli	480	26	59.1	179	2	US-09-270-767-43211	Sequence 43211, A
408	27	61.4	1863	2	US-09-074-476-2	Sequence 2, Appli	481	26	59.1	182	2	US-09-134-001C-5022	Sequence 5022, Ap
409	27	61.4	1863	2	US-09-074-476-4	Sequence 4, Appli	482	26	59.1	197	2	US-09-107-532A-5858	Sequence 5858, Ap
410	27	61.4	1863	2	US-09-074-476-6	Sequence 6, Appli	483	26	59.1	201	2	US-09-134-000C-4329	Sequence 4329, Ap
411	27	61.4	1863	2	US-09-099-753-2	Sequence 2, Appli	484	26	59.1	212	2	US-09-252-991A-28492	Sequence 28492, A
412	27	61.4	1863	2	US-08-850-727-2	Sequence 2, Appli	485	26	59.1	215	2	US-09-540-236-2807	Sequence 2807, Ap
413	27	61.4	1863	2	US-08-986-106-2	Sequence 2, Appli	486	26	59.1	217	2	US-09-902-540-16731	Sequence 16731, A
414	27	61.4	1863	2	US-09-007-678B-49	Sequence 49, Appl	487	26	59.1	219	2	US-09-294-298A-9	Sequence 9, Appli
415	27	61.4	1863	2	US-08-989-890-16	Sequence 16, Appl	488	26	59.1	220	2	US-09-489-039A-10333	Sequence 10333, A
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417	27	61.4	1863	2	US-09-462-401A-2	Sequence 2, Appli	490	26	59.1	231	2	US-09-013-881-7	Sequence 7, Appli
418	27	61.4	1863	2	US-09-538-092-1098	Sequence 1098, Ap	491	26	59.1	231	2	US-09-612-473-7	Sequence 7, Appli
419	27	61.4	1863	2	US-09-734-672A-2	Sequence 2, Appli	492	26	59.1	232	2	US-09-270-767-36511	Sequence 36511, A
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422	27	61.4	1863	2	US-09-923-327A-264	Sequence 264, App	495	26	59.1	239	2	US-09-540-236-3695	Sequence 3695, Ap
423	27	61.4	1863	2	US-09-923-327A-266	Sequence 266, App	496	26	59.1	248	2	US-09-134-000C-4356	Sequence 4356, Ap
424	27	61.4	1863	2	US-09-923-327A-268	Sequence 268, App	497	26	59.1	251	2	US-09-270-767-31717	Sequence 31717, A
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427	27	61.4	1863	4	PCT-US95-10220-2	Sequence 2, Appli	500	26	59.1	254	2	US-09-543-681A-4919	Sequence 4919, Ap
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429	27	61.4	2262	2	US-09-949-016-8849	Sequence 8849, Ap	502	26	59.1	255	2	US-09-107-433-4875	Sequence 4875, Ap
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434	27	61.4	4872	2	US-09-424-783-3	Sequence 3, Appli	507	26	59.1	267	2	US-09-107-532A-4931	Sequence 4931, App
435	27	61.4	4968	2	US-09-424-783-5	Sequence 5, Appli	508	26	59.1	275	2	US-09-949-016-11338	Sequence 11338, A
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438	26	59.1	48	2	US-09-205-658-174	Sequence 174, App	511	26	59.1	279	2	US-09-270-767-41981	Sequence 41981, A
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440	26	59.1	66	2	US-09-248-796A-21588	Sequence 21588, A	513	26	59.1	282	2	US-10-104-047-3069	Sequence 3069, Ap
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444	26	59.1	75	2	US-09-621-976-6348	Sequence 6348, Ap	517	26	59.1	285	2	US-09-270-767-33107	Sequence 33107, A
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461	26	59.1	126	1	US-08-118-906-2	Sequence 2, Appli	534	26	59.1	335	2	US-10-206-576-178	Sequence 178, App
462	26	59.1	126	1	US-08-486-196-2	Sequence 2, Appli	535	26	59.1	342	2	US-09-054-272-2	Sequence 2, Appli
463	26	59.1	126	1	US-08-488-135-2	Sequence 2, Appli	536	26	59.1	342	2	US-09-826-509-555	Sequence 555, App
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465	26	59.1	126	2	US-09-471-276-1569	Sequence 1569, Ap	538	26	59.1	347	2		



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545	26	59.1	374	2	US-09-270-767-4402	Sequence 4402, A	618	59.1	520	2	US-09-949-002-553	Sequence 553, App
546	26	59.1	378	2	US-09-902-540-10358	Sequence 10358, A	619	59.1	520	2	US-09-999-833A-614	Sequence 614, App
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557	26	59.1	395	2	US-09-198-452A-790	Sequence 790, App	630	59.1	564	2	US-09-252-991A-24049	Sequence 24049, A
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571	26	59.1	407	2	US-09-854-731-23	Sequence 23, Appl	644	59.1	626	1	US-07-938-782A-2	Sequence 2, Appli
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573	26	59.1	413	2	US-09-663-600A-198	Sequence 198, App	646	59.1	626	4	US-09-578-441-5	Sequence 5, Appli
574	26	59.1	413	2	US-09-248-796A-19337	Sequence 19337, A	647	59.1	633	2	PCT-US93-08131-2	Sequence 2, Appli
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590	26	59.1	437	4	PCT-US93-10442-6	Sequence 6, Appli	663	59.1	729	2	US-09-771-161A-268	Sequence 268, App
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597	26	59.1	452	2	US-09-248-796A-16171	Sequence 20180, A	670	59.1	819	4	PCT-US93-10442-20	Sequence 20, Appl
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602	26	59.1	481	2	US-09-592-018-3	Sequence 3, Appli	675	59.1	835	2	US-09-577-304A-243	Sequence 243, App
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605	26	59.1	491	2	US-08-942-012B-27	Sequence 27, Appl	678	59.1	842	2	US-09-758-282B-263	Sequence 263, App
606	26	59.1	497	2	US-09-252-991A-22575	Sequence 22575, A	679	59.1	842	2	US-09-577-304A-259	Sequence 259, App
607	26	59.1	504	1	US-08-457-274A-25	Sequence 25, Appl	680	59.1	842	2	US-09-577-304A-263	Sequence 263, App
608	26	59.1	504	1	PCT-US95-05758-25	Sequence 25, Appl	681	59.1	869	2	US-09-949-016-7012	Sequence 7012, Ap
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696	26	59.1	1147	2	US-09-949-016-8862	Sequence 8862, Ap	769	25	56.8	113	2	US-09-902-540-15040	Sequence 15040, A
697	26	59.1	1165	1	US-08-240-357-2	Sequence 862, Ap	770	25	56.8	120	2	US-09-583-110-5022	Sequence 5022, Ap
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702	26	59.1	1168	2	US-10-201-000-2	Sequence 11, Appl	775	25	56.8	138	2	US-09-248-796A-19394	Sequence 19394, A
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708	26	59.1	1512	2	US-09-697-898-2	Sequence 3, Appl	781	25	56.8	143	2	US-09-877-790-1	Sequence 172, App
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711	26	59.1	1809	2	US-09-012-504A-12	Sequence 12, Appl	784	25	56.8	144	2	US-09-269-833D-35	Sequence 35, Appl
712	26	59.1	1809	2	US-09-012-399A-12	Sequence 12, Appl	785	25	56.8	144	2	US-09-601-729-7	Sequence 7, Appl
713	26	59.1	1822	2	US-09-949-016-7999	Sequence 7999, Ap	786	25	56.8	145	1	US-09-001-944-10	Sequence 10, Appl
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715	26	59.1	1871	2	US-09-349-546-1	Sequence 1, Appl	788	25	56.8	145	2	US-09-601-729-6	Sequence 33, Appl
716	26	59.1	1871	2	US-09-502-831-1	Sequence 2, Appl	789	25	56.8	146	2	US-09-269-833D-33	Sequence 33, Appl
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847	25	56.8	219	2	US-09-602-787A-110	Sequence 110, App	920	25	56.8	328	2	US-08-513-974B-39	Sequence 39, Appl
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989 25 56.8 386 2 US-09-755-274-6 Sequence 6, Appli  
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995 25 56.8 395 2 US-09-247-155-113 Sequence 113, App  
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## ALIGNMENTS

RESULT 1  
US-09-583-110-2976  
; Sequence 2976, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; PRIORITY FILING DATE: 2000-05-26  
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; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 2976  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-2976  
Query Match 77.3%; Score 34; DB 2; Length 318;  
Best Local Similarity 75.0%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLOLMPEP 8  
Db 152 FLQVLMDF 159  
RESULT 2  
US-09-107-433-5076  
; Sequence 5076, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:

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; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
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; APPLICATION NUMBER: US/09/107,433  
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; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 5076:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 336 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...336  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5076:  
US-09-107-433-5076  
Query Match 77.3%; Score 34; DB 2; Length 336;  
Best Local Similarity 75.0%; Pred. No. 47;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLOLMPEP 8  
Db 170 FLQVLMDF 177  
RESULT 3  
US-09-710-279-1264  
; Sequence 1264, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1264  
; LENGTH: 305  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-1264

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Query Match 75.0%; Score 33; DB 2; Length 305;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 8
Db 138 FLQLIMP 145

RESULT 4
US-09-134-001C-5525
; Sequence 5525, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5525
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5525

Query Match 75.0%; Score 33; DB 2; Length 324;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 8
Db 157 FLQLIMP 164

RESULT 5
US-09-413-574-4
; Sequence 4, Application US/09413574
; Patent No. 6235972
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; APPLICANT: Tagliani, Laura
; TITLE OF INVENTION: Maize Rad23 Genes and Uses Thereof
; FILE REFERENCE: 0964
; CURRENT APPLICATION NUMBER: US/09/413,574
; CURRENT FILING DATE: 1999-10-06
; EARLIER APPLICATION NUMBER: 60/109,728
; EARLIER FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Zea mays
US-09-413-574-4

Query Match 75.0%; Score 33; DB 2; Length 368;
Best Local Similarity 87.5%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 8
Db 291 FLQLNEP 298

RESULT 6
US-09-805-550-4
; Sequence 4, Application US/09805550
```

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; Patent No. 6878809
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; APPLICANT: Tagliani, Laura
; TITLE OF INVENTION: Rad23 Genes and Uses Thereof
; FILE REFERENCE: 0964D
; CURRENT APPLICATION NUMBER: US/09/805,550
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 09/413,574
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/109,728
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Zea mays
US-09-805-550-4

Query Match 75.0%; Score 33; DB 2; Length 368;
Best Local Similarity 87.5%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 8
Db 291 FLQLNEP 298

RESULT 7
US-09-538-092-1214
; Sequence 1214, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurPatSeqFormatter Version 0.9
; SEQ ID NO 1214
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P54727
US-09-538-092-1214

Query Match 75.0%; Score 33; DB 2; Length 409;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 9
Db 324 FLQLNEP 332

RESULT 8
US-09-949-016-6281
; Sequence 6281, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6281  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6281

Query Match 75.0%; Score 33; DB 2; Length 409;  
Best Local Similarity 66.7%; Pred. No. 92;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
|:|:|:|  
Db 324 FIQMLNEPV 332

## RESULT 9

US-09-949-016-11120  
; Sequence 11120, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11120  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11120

Query Match 75.0%; Score 33; DB 2; Length 454;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
|:|:|:|  
Db 369 FIQMLNEPV 377

## RESULT 10

US-09-542-331-1  
; Sequence 1, Application US/09542331  
; Patent No. 6261761  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Yi  
; APPLICANT: Guo, Hui-Fu  
; TITLE OF INVENTION: NF1 Protein and Its Role in Activation  
; TITLE OF INVENTION: of Adenylyl Cyclase by PACAP38-Like Neuropeptides  
; FILE REFERENCE: 1314.1047003  
; CURRENT APPLICATION NUMBER: US/09/542,331  
; CURRENT FILING DATE: 2000-04-04  
; EARLIER APPLICATION NUMBER: US 09/046,745

; EARLIER FILING DATE: 1998-03-24  
; EARLIER APPLICATION NUMBER: US 60/041,469  
; EARLIER FILING DATE: 1997-03-24  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2802  
; TYPE: PRT  
; ORGANISM: Drosophila  
US-09-542-331-1

Query Match 75.0%; Score 33; DB 2; Length 2802;  
Best Local Similarity 55.6%; Pred. No. 7e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
|:|:|:|  
Db 1340 YLQMLLEPL 1348

## RESULT 11

US-09-510-791-1  
; Sequence 1, Application US/09510791  
; Patent No. 6365126  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Yi  
; APPLICANT: Guo, Hui-Fu  
; APPLICANT: Tong, Jiayuan  
; TITLE OF INVENTION: Improvement of Learning and Short Term  
; TITLE OF INVENTION: Memory Defects with Neurofibromatosis 1 (NF1) Expression  
; FILE REFERENCE: 1314.1047-002  
; CURRENT APPLICATION NUMBER: US/09/510,791  
; CURRENT FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: US 09/046,745  
; PRIOR FILING DATE: 1998-03-24  
; PRIOR APPLICATION NUMBER: US 60/041,469  
; PRIOR FILING DATE: 1997-03-24  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2802  
; TYPE: PRT  
; ORGANISM: Drosophila  
US-09-510-791-1

Query Match 75.0%; Score 33; DB 2; Length 2802;  
Best Local Similarity 55.6%; Pred. No. 7e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
|:|:|:|  
Db 1340 YLQMLLEPL 1348

## RESULT 12

US-09-328-352-5811  
; Sequence 5811, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5811  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5811

Query Match 72.7%; Score 32; DB 2; Length 107;

Best Local Similarity 66.7%; Pred. No. 36;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9  
Db 2 YLEKLMFV 10

RESULT 13  
US-09-134-000C-4338  
; Sequence 4338, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4338  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-4338

Query Match 72.7%; Score 32; DB 2; Length 195;  
Best Local Similarity 62.5%; Pred. No. 68;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLMEP 8  
Db 27 FLQVMDP 34

RESULT 14  
US-09-107-532A-5460  
; Sequence 5460, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arianello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GFC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 5460:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 323 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (B) LOCATION 1...323  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5460:  
US-09-107-532A-5460

Query Match 72.7%; Score 32; DB 2; Length 323;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLMEP 8  
Db 155 FLQVMDP 162

RESULT 15  
US-09-248-796A-17915  
; Sequence 17915, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 17915  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (403)  
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk  
US-09-248-796A-17915

Query Match 72.7%; Score 32; DB 2; Length 406;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9  
Db 38 FLQLSHPI 46

RESULT 16  
US-09-005-286B-2  
; Sequence 2, Application US/09005286B  
; Patent No. 6756491  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, RONALD M.  
; APPLICANT: BLUMBERG, BRUCE  
; TITLE OF INVENTION: NOVEL STEROID-ACTIVATED NUCLEAR RECEPTORS AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 088802-5201  
; CURRENT APPLICATION NUMBER: US/09/005,286B  
; CURRENT FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-005-286B-2

Query Match 72.7%; Score 32; DB 2; Length 434;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
Db 315 FOQLLLEPM 323

RESULT 17  
US-09-227-718B-2  
; Sequence 2, Application US/09227718B  
; Patent No. 6809178  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, RONALD M.  
; TITLE OF INVENTION: NOVEL STEROID-ACTIVATED NUCLEAR RECEPTORS AND USES  
; FILE REFERENCE: 088802-5202  
; CURRENT APPLICATION NUMBER: US/09/227,718B  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 09/005,286  
; PRIOR FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-227-718B-2

Query Match 72.7%; Score 32; DB 2; Length 434;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
Db 315 FOQLLLEPM 323

RESULT 18  
US-09-840-008A-2  
; Sequence 2, Application US/09840008A  
; Patent No. 6911537  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, RONALD M.  
; TITLE OF INVENTION: XENOBIOTIC COMPOUND MODULATED EXPRESSION SYSTEMS AND USES THEREOF  
; FILE REFERENCE: 088802-5211  
; CURRENT APPLICATION NUMBER: US/09/840,008A  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 09/227,718  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 09/458,366  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 09/005,286  
; PRIOR FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-840-008A-2

Query Match 72.7%; Score 32; DB 2; Length 434;

Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLOLLMEPV 9  
Db 315 FOQLLLEPM 323

RESULT 19  
US-09-949-016-7513  
; Sequence 7513, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7513  
; LENGTH: 484  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7513

Query Match 72.7%; Score 32; DB 2; Length 484;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
Db 365 FOQLLLEPM 373

RESULT 20  
US-09-949-016-7514  
; Sequence 7514, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7514  
; LENGTH: 484  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7514

Query Match 72.7%; Score 32; DB 2; Length 484;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
Db 365 FOQLLLEPM 373



Db 365 FQQLLEPM 373

RESULT 21

US-09-949-016-7515

Sequence 7515, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: Fast-Seq for Windows Version 4.0

SEQ ID NO 7515

LENGTH: 484

TYPE: PRT

ORGANISM: Human

US-09-949-016-7515

Query Match 72.7%; Score 32; DB 2; Length 484;

Best Local Similarity 66.7%; Pred. No. 1.8e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLLEPM 9

Db 365 FQQLLEPM 373

RESULT 22

US-08-706-936-3

Sequence 3, Application US/08706936

Patent No. 5792851

GENERAL INFORMATION:

APPLICANT: VICTOR L. SCHUSTER AND RUN LU

TITLE OF INVENTION: HUMAN PROSTAGLANDIN TRANSPORTER

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN

STREET: 90 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: U.S.A.

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,936

FILING DATE: SEPTEMBER 3, 1996

ATTORNEY/AGENT INFORMATION:

NAME: CRAIG J. ARNOLD

REGISTRATION NUMBER: 34,287

REFERENCE/DOCKET NUMBER: 96700/406

TELEPHONE: (212) 697-5995

TELEFAX: (212) 286-0854 or 286-0082

TELEX: TWX 710-581-4766

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 642

TYPE: AMINO ACID

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PROTEIN

DESCRIPTION: YES

HYPOTHETICAL: YES

ORIGINAL SOURCE: RAT

ORGANISM: RAT

INDIVIDUAL ISOLATE: PROSTAGLANDIN TRANSPORTER

US-08-706-936-3

Query Match 72.7%; Score 32; DB 1; Length 642;

Best Local Similarity 66.7%; Pred. No. 2.4e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLMEPV 9

Db 317 FLRLMNP 325

RESULT 23

US-09-270-767-37595

Sequence 37595, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 37595

LENGTH: 131

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-37595

Query Match 70.5%; Score 31; DB 2; Length 131;

Best Local Similarity 44.4%; Pred. No. 71;

Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLMEPV 9

Db 90 FVQILVQPI 98

RESULT 24

US-09-270-767-52812

Sequence 52812, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 52812

LENGTH: 131

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-52812

Query Match 70.5%; Score 31; DB 2; Length 131;

Best Local Similarity 44.4%; Pred. No. 71;

Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLMEPV 9

Db 90 FVQILVQPI 98

```
RESULT 25
US-09-949-016-6564
; Sequence 6564, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6564
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6564

Query Match          70.5%; Score 31; DB 2; Length 262;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLQLMEPV 9
DB      10 FLSLSPV 18

RESULT 26
US-09-252-149B-35
; Sequence 35, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; VERTEBRATE SUBJECTS
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-252-149B-35

Query Match          70.5%; Score 31; DB 2; Length 375;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLMEPV 9
DB      13 FMQILVHPV 21

RESULT 27
US-09-451-501-27
; Sequence 27, Application US/09451501
; Patent No. 6468535
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee et al.,
```

```
;
;
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,501
; FILING DATE: 30-NO. 6468535-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,071
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/US94/03019
; FILING DATE: 18-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/105001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: Turkey GDF-8
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..376
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-451-501-27

Query Match          70.5%; Score 31; DB 2; Length 375;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLMEPV 9
DB      13 FMQILVHPV 21

RESULT 28
US-09-686-344-27
; Sequence 27, Application US/09686344
; Patent No. 6607884
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/686,344
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
```

; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Meleagris gallopavo  
US-09-686-344-27

Query Match 70.5%; Score 31; DB 2; Length 375;  
Best Local Similarity 55.6%; Pred. No. 2.1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLOLLMEPV 9  
Db 13 FMOILVHPV 21

RESULT 29  
US-09-626-896-18  
; Sequence 18, Application US/09626896  
; Patent No. 6656475  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS.  
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME  
; FILE REFERENCE: JHU1470-2  
; CURRENT APPLICATION NUMBER: US/09/626,896  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 09/485,046  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: PCT/US98/15598  
; PRIOR FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 60/054,461  
; PRIOR FILING DATE: 1997-08-01  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Meleagris gallopavo  
US-09-626-896-18

Query Match 70.5%; Score 31; DB 2; Length 375;  
Best Local Similarity 55.6%; Pred. No. 2.1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLOLLMEPV 9  
Db 13 FMOILVHPV 21

RESULT 30  
US-09-485-046-14  
; Sequence 14, Application US/09485046  
; Patent No. 6696260  
; GENERAL INFORMATION:  
; APPLICANT: The Johns Hopkins University School of Medicine  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra  
; TITLE OF INVENTION: METHODS TO IDENTIFY GROWTH DIFFERENTIATION FACTOR (GDF) RECEPTORS  
; FILE REFERENCE: JHU1470-1  
; CURRENT APPLICATION NUMBER: US/09/485,046  
; CURRENT FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: PCT/US98/15598  
; PRIOR FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: US 06/054,461  
; PRIOR FILING DATE: 1997-08-01  
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Meleagris gallopavo  
US-09-485-046-14

Query Match 70.5%; Score 31; DB 2; Length 375;  
Best Local Similarity 55.6%; Pred. No. 2.1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLOLLMEPV 9  
Db 13 FMOILVHPV 21

RESULT 31  
US-10-278-803-27  
; Sequence 27, Application US/10278803  
; Patent No. 6858208  
; GENERAL INFORMATION:  
; APPLICANT: Se-Jin Lee et al.,  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/278,803  
; FILING DATE: 22-Oct-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/451,501  
; FILING DATE: 30-No. 6858208-1999  
; APPLICATION NUMBER: 08/795,071  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/US94/03019  
; FILING DATE: 18-March-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lisa A. Haile, Ph.D.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07265/105001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; IMMEDIATE SOURCE:  
; CLONE: Turkey GDF-8  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..376  
; OTHER INFORMATION:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-10-278-803-27

Query Match 70.5%; Score 31; DB 2; Length 375;  
Best Local Similarity 55.6%; Pred. No. 2.1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 FLQLLMEPV 9
      |:|:|:|
Db      13 FMQILVHPV 21

RESULT 32
US-09-841-730-18
; Sequence 18, Application US/09841730
; Patent No. 6891082
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHUI470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-841-730-18

Query Match      70.5%; Score 31; DB 2; Length 375;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLLMEPV 9
      |:|:|:|
Db      13 FMQILVHPV 21

RESULT 33
US-09-193-562D-30
; Sequence 30, Application US/09193562D
; Patent No. 6309857
; GENERAL INFORMATION:
; APPLICANT: Pauli, Benedicht U.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
; TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
; FILE REFERENCE: 18617.0052
; CURRENT APPLICATION NUMBER: US/09/193,562D
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US/60/065,922
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 30
; LENGTH: 1000
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-562D-30

Query Match      70.5%; Score 31; DB 2; Length 1000;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLQLLMEPV 9
      |:|:|:|
Db      10 FLSLLSPPV 18

RESULT 34
US-10-055-412B-30
```

```
; Sequence 30, Application US/10055412B
; Patent No. 6692939
; GENERAL INFORMATION:
; APPLICANT: Pauli, Benedicht U.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
; TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
; FILE REFERENCE: 18617.0058
; CURRENT APPLICATION NUMBER: US/10/055,412B
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US/09/193,562
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US/60/065,922
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 30
; LENGTH: 1000
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-412B-30

Query Match      70.5%; Score 31; DB 2; Length 1000;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLQLLMEPV 9
      |:|:|:|
Db      10 FLSLLSPPV 18

RESULT 35
US-09-949-002-372
; Sequence 372, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-372

Query Match      70.5%; Score 31; DB 2; Length 1132;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 QLLMEPV 9
      |:|:|:|
Db      547 QLLMQPV 553

RESULT 36
US-09-949-002-542
; Sequence 542, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
```

; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 542  
; LENGTH: 1137  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-002-542

Query Match 70.5%; Score 31; DB 2; Length 1137;  
Best Local Similarity 85.7%; Pred. No. 6.9e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QLLMEPV 9  
Db 552 QLLMQPV 558

RESULT 37  
US-08-252-966B-12  
; Sequence 12, Application US/08252966B  
; Patent No. 5624818  
; GENERAL INFORMATION:  
; APPLICANT: Eisenman, Robert N.  
; APPLICANT: Hurlin, Peter J.  
; TITLE OF INVENTION: Regulatory Proteins that Dimerize with  
; TITLE OF INVENTION: Mad or Max  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessPLLC  
; STREET: 1420 Fifth Ave., Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/252,966B  
; FILING DATE: 01-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shelton, Dennis K.  
; REGISTRATION NUMBER: 26,997.  
; REFERENCE/DOCKET NUMBER: PHCR17694  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682-8100  
; TELEFAX: (206) 224-0779  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1253 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: translation of msina cdna; see Figure 23  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
US-08-252-966B-12

Query Match 70.5%; Score 31; DB 1; Length 1253;  
Best Local Similarity 66.7%; Pred. No. 7.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQILMEPV 9  
Db 1233 FLQILXSPV 1241

RESULT 38  
US-08-252-966B-18  
; Sequence 18, Application US/08252966B  
; Patent No. 5624818  
; GENERAL INFORMATION:  
; APPLICANT: Eisenman, Robert N.  
; APPLICANT: Hurlin, Peter J.  
; APPLICANT: Ayer, Donald E.  
; TITLE OF INVENTION: Regulatory Proteins that Dimerize with  
; TITLE OF INVENTION: Mad or Max  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessPLLC  
; STREET: 1420 Fifth Ave., Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/252,966B  
; FILING DATE: 01-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shelton, Dennis K.  
; REGISTRATION NUMBER: 26,997.  
; REFERENCE/DOCKET NUMBER: PHCR17694  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682-8100  
; TELEFAX: (206) 224-0779  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1261 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: translation of msina9 cdna; see Figure 29A, B, C, D  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
US-08-252-966B-18

Query Match 70.5%; Score 31; DB 1; Length 1261;  
Best Local Similarity 66.7%; Pred. No. 7.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQILMEPV 9  
Db 1242 FLQILXSPV 1250

RESULT 39  
US-09-302-626B-38  
; Sequence 38, Application US/09302626B  
; Patent No. 6709660  
; GENERAL INFORMATION:  
; APPLICANT: Scalato, Enzo  
; APPLICANT: Masignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizzi, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Meningococcal Antigens  
; FILE REFERENCE: CHIR0159  
; CURRENT APPLICATION NUMBER: US/09/302,626B  
; CURRENT FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: PCT/IB99/00103  
; PRIOR FILING DATE: 1999-01-14

Query Match 70.5%; Score 31; DB 1; Length 1261;  
Best Local Similarity 66.7%; Pred. No. 7.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQILMEPV 9  
Db 1242 FLQILXSPV 1250

; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-302-626B-38

Query Match 68.2%; Score 30; DB 2; Length 103;  
Best Local Similarity 66.7%; Pred. No. 88;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9  
|||:|:  
Db 26 FLTLNPNV 34

RESULT 40  
US-09-252-991A-29715  
; Sequence 29715, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29715  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29715

Query Match 68.2%; Score 30; DB 2; Length 116;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMEPV 9  
|||:|:  
Db 91 LQLEMEPI 98

RESULT 41  
US-09-252-991A-33067  
; Sequence 33067, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 33067  
; LENGTH: 327  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-33067

Query Match 68.2%; Score 30; DB 2; Length 327;  
Best Local Similarity 85.7%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLME 7  
|||:|:  
Db 210 FLQLLE 216

RESULT 42  
US-09-248-796A-18640  
; Sequence 18640, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18640  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-18640

Query Match 68.2%; Score 30; DB 2; Length 475;  
Best Local Similarity 62.5%; Pred. No. 4.4e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMEPV 9  
|||:|:  
Db 98 LELLVEPI 105

RESULT 43  
US-09-434-840-63  
; Sequence 63, Application US/09434840  
; Patent No. 6620985  
; GENERAL INFORMATION:  
; APPLICANT: Glazebrook, Jane  
; APPLICANT: Jirage, Dayadevi  
; APPLICANT: Tootle, Tina L  
; APPLICANT: Zhou, Nan  
; TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR  
; FILE REFERENCE: 043503.0009  
; CURRENT APPLICATION NUMBER: US/09/434,840  
; CURRENT FILING DATE: 1999-11-04  
; EARLIER APPLICATION NUMBER: 09/190,733  
; EARLIER FILING DATE: 1998-11-12  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 515  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-434-840-63

Query Match 68.2%; Score 30; DB 2; Length 515;  
Best Local Similarity 66.7%; Pred. No. 4.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9  
|||:|:  
Db 387 FYQLLAEP 395

RESULT 44  
US-09-434-840-2  
; Sequence 2, Application US/09434840

; Patent No. 6620985  
; GENERAL INFORMATION:  
; APPLICANT: Glazebrook, Jane  
; APPLICANT: Jitage, Davadevi  
; APPLICANT: Tootle, Tina L  
; APPLICANT: Zhou, Nan  
; APPLICANT: Feys, Bart  
; TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR  
; FILE REFERENCE: 043503.0009  
; CURRENT APPLICATION NUMBER: US/09/434,840  
; CURRENT FILING DATE: 1999-11-04  
; EARLIER APPLICATION NUMBER: 09/190,733  
; EARLIER FILING DATE: 1998-11-12  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 526  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-434-840-2

Query Match 68.2%; Score 30; DB 2; Length 526;  
Best Local Similarity 66.7%; Pred. No. 4.9e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9  
| | | | |  
Db 372 FYQLLAEP 380

RESULT 45  
US-09-252-991A-18305  
; Sequence 18305, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18305  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18305

Query Match 68.2%; Score 30; DB 2; Length 540;  
Best Local Similarity 66.7%; Pred. No. 5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9  
| | | | |  
Db 163 FLPLQOPV 171

RESULT 46  
US-09-434-840-55  
; Sequence 55, Application US/09434840  
; Patent No. 6620985  
; GENERAL INFORMATION:  
; APPLICANT: Glazebrook, Jane  
; APPLICANT: Jitage, Davadevi  
; APPLICANT: Tootle, Tina L  
; APPLICANT: Zhou, Nan  
; APPLICANT: Feys, Bart  
; TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR  
; FILE REFERENCE: 043503.0009

; CURRENT APPLICATION NUMBER: US/09/434,840  
; CURRENT FILING DATE: 1999-11-04  
; EARLIER APPLICATION NUMBER: 09/190,733  
; EARLIER FILING DATE: 1998-11-12  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-434-840-55

Query Match 68.2%; Score 30; DB 2; Length 541;  
Best Local Similarity 66.7%; Pred. No. 5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9  
| | | | |  
Db 387 FYQLLAEP 395

RESULT 47  
US-08-915-337-2  
; Sequence 2, Application US/08915337  
; Patent No. 6287802  
; GENERAL INFORMATION:  
; APPLICANT: Deng, Fan & Xia  
; TITLE OF INVENTION: EXT2 Gene  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/915,337  
; FILING DATE: August 21, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: China - 96121928.9  
; FILING DATE: October 21, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATG50019  
; TELEPHONE: (610) 270-5219  
; TELEFAX: (610) 270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 728 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
US-08-915-337-2

Query Match 68.2%; Score 30; DB 2; Length 728;  
Best Local Similarity 85.7%; Pred. No. 6.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 QLLMEPV 9  
Db 391 QLFMEPV 397

## RESULT 48

US-09-949-016-7836 Application US/09949016

; Sequence 7836

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7836

; LENGTH: 857

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7836

Query Match

Best Local Similarity 44.4%; Score 30; DB 2; Length 857;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9  
Db 288 FQLILDPI 296

## RESULT 49

US-09-252-991A-25772

; Sequence 25772, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 25772

; LENGTH: 1332

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25772

Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 1332;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMEPV 9  
Db 327 LQALLEPV 334

## RESULT 50

US-09-710-279-2850

; Sequence 2850, Application US/09710279

; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2850  
; LENGTH: 1501  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-2850

Query Match 68.2%; Score 30; DB 2; Length 1501;

Best Local Similarity 75.0%; Pred. No. 1.5e+03;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLMEPV 8

Db 297 FLSLAMEP 304

Search completed: May 9, 2006, 02:28:24

Job time : 34.2 secs



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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:25:44 ; Search time 80.8 Seconds  
(without alignments)  
46.540 Million cell updates/sec

Title: US-09-870-216C-3  
Perfect score: 44  
Sequence: 1 FLQLMEPV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	3	US-09-870-216C-3
2	44	100.0	9	4	US-10-017-327-3
3	35	79.5	67	3	US-09-764-869-1075
4	35	79.5	67	4	US-10-091-504-1075
5	35	79.5	67	4	US-10-227-577-1075
6	35	79.5	329	4	US-10-478-551-2
7	35	79.5	363	4	US-10-424-599-170467
8	35	79.5	363	4	US-10-424-599-219691
9	34	77.3	79	4	US-10-425-115-349203
10	34	77.3	180	4	US-10-437-963-114660
11	34	77.3	274	4	US-10-437-963-132856
12	34	77.3	307	3	US-09-799-848-3
13	34	77.3	307	3	US-09-781-712B-3
14	34	77.3	307	5	US-10-679-761-8
15	34	77.3	307	5	US-10-943-194-8
16	34	77.3	307	6	US-11-005-069-3
17	34	77.3	307	6	US-11-001-386-3
18	34	77.3	318	4	US-10-415-478A-5
19	34	77.3	318	5	US-10-472-928-3880
20	34	77.3	336	5	US-10-617-320-5076
21	34	77.3	504	4	US-10-425-114-45949
22	34	77.3	770	4	US-10-437-963-163658
23	34	77.3	798	4	US-10-425-115-200455
24	33	75.0	80	4	US-10-425-115-319897
25	33	75.0	117	3	US-09-864-408A-7182
26	33	75.0	138	4	US-10-425-115-223947
27	33	75.0	174	4	US-10-425-115-223948

28	33	75.0	193	4	US-10-767-701-35283	Sequence 35283, A
29	33	75.0	324	4	US-10-724-972A-7247	Sequence 7247, Ap
30	33	75.0	349	4	US-10-425-115-223949	Sequence 223949, A
31	33	75.0	368	3	US-09-805-550-4	Sequence 4, Appli
32	33	75.0	1234	4	US-10-437-963-138501	Sequence 138501, A
33	33	75.0	2764	6	US-11-097-143-27893	Sequence 27893, A
34	33	75.0	2802	6	US-11-097-143-18159	Sequence 18159, A
35	32	72.7	55	4	US-10-425-115-307557	Sequence 307557, A
36	32	72.7	73	4	US-10-767-701-56147	Sequence 56147, A
37	32	72.7	79	4	US-10-425-115-358291	Sequence 358291, A
38	32	72.7	104	4	US-10-767-701-62832	Sequence 62832, A
39	32	72.7	169	4	US-10-425-115-360733	Sequence 360733, A
40	32	72.7	189	4	US-10-424-599-245981	Sequence 245981, A
41	32	72.7	198	4	US-10-424-599-196742	Sequence 196742, A
42	32	72.7	269	4	US-10-424-599-234629	Sequence 234629, A
43	32	72.7	272	4	US-10-425-114-53064	Sequence 53064, A
44	32	72.7	276	4	US-10-425-115-367551	Sequence 367551, A
45	32	72.7	290	5	US-10-775-678-54	Sequence 54, Appli
46	32	72.7	334	4	US-10-437-963-108157	Sequence 108157, A
47	32	72.7	362	5	US-10-739-930-9255	Sequence 9255, Ap
48	32	72.7	420	4	US-10-425-115-365824	Sequence 365824, A
49	32	72.7	434	3	US-09-143-828-2	Sequence 2, Appli
50	32	72.7	434	3	US-09-227-718-2	Sequence 2, Appli
51	32	72.7	434	3	US-09-840-008-2	Sequence 2, Appli
52	32	72.7	434	4	US-10-081-555C-2	Sequence 2, Appli
53	32	72.7	434	4	US-10-642-322-10	Sequence 10, Appli
54	32	72.7	434	4	US-10-222-679-10	Sequence 10, Appli
55	32	72.7	434	4	US-10-478-551-4	Sequence 4, Appli
56	32	72.7	464	3	US-09-005-286-2	Sequence 2, Appli
57	32	72.7	466	4	US-10-090-090B-2	Sequence 2, Appli
58	32	72.7	473	3	US-09-143-828-4	Sequence 4, Appli
59	32	72.7	473	4	US-10-090-090B-18	Sequence 18, Appli
60	32	72.7	544	4	US-10-424-599-234633	Sequence 234633, A
61	32	72.7	592	4	US-10-437-963-179064	Sequence 179064, A
62	32	72.7	850	5	US-10-732-923-22359	Sequence 22359, A
63	32	72.7	51	4	US-10-425-115-228042	Sequence 228042, A
64	31	70.5	89	4	US-10-424-599-191540	Sequence 191540, A
65	31	70.5	89	4	US-10-425-115-188361	Sequence 188361, A
66	31	70.5	101	4	US-10-437-963-161997	Sequence 161997, A
67	31	70.5	112	3	US-09-764-868-996	Sequence 996, App
68	31	70.5	148	4	US-10-424-599-240480	Sequence 240480, A
69	31	70.5	270	4	US-10-425-114-53335	Sequence 53335, A
70	31	70.5	270	4	US-10-425-114-53365	Sequence 53365, A
71	31	70.5	291	3	US-09-764-868-898	Sequence 898, App
72	31	70.5	296	4	US-10-296-115-906	Sequence 906, App
73	31	70.5	369	4	US-10-437-963-161952	Sequence 161952, A
74	31	70.5	375	3	US-09-859-211-27	Sequence 27, Appli
75	31	70.5	375	3	US-09-841-730-18	Sequence 18, Appli
76	31	70.5	375	3	US-09-872-856-27	Sequence 27, Appli
77	31	70.5	375	3	US-10-074-152-35	Sequence 35, Appli
78	31	70.5	375	4	US-10-278-803-27	Sequence 27, Appli
79	31	70.5	375	4	US-10-463-973-27	Sequence 27, Appli
80	31	70.5	375	4	US-10-456-852-14	Sequence 14, Appli
81	31	70.5	382	4	US-10-282-122A-61153	Sequence 61153, A
82	31	70.5	392	4	US-10-424-599-256719	Sequence 256719, A
83	31	70.5	400	4	US-10-424-599-256715	Sequence 256715, A
84	31	70.5	424	4	US-10-437-963-131867	Sequence 131867, A
85	31	70.5	425	4	US-10-425-114-54716	Sequence 54716, A
86	31	70.5	433	4	US-10-425-114-45576	Sequence 45576, A
87	31	70.5	498	6	US-11-097-143-13059	Sequence 13059, A
88	31	70.5	515	4	US-10-424-599-278530	Sequence 278530, A
89	31	70.5	544	5	US-10-846-374B-176	Sequence 176, App
90	31	70.5	879	4	US-10-437-963-184438	Sequence 184438, A
91	31	70.5	1000	4	US-10-055-412B-30	Sequence 30, Appli
92	31	70.5	1000	5	US-10-779-949-30	Sequence 30, Appli
93	31	70.5	1016	3	US-09-738-626-4363	Sequence 4363, Ap
94	31	70.5	1019	5	US-10-487-092-11	Sequence 11, Appli
95	31	70.5	1039	4	US-10-408-765A-2259	Sequence 2259, Ap
96	31	70.5	46	4	US-10-425-115-205765	Sequence 205765, A
97	30	68.2	47	4	US-10-425-115-201838	Sequence 201838, A
98	30	68.2	49	4	US-10-424-599-189407	Sequence 189407, A
99	30	68.2	57	4	US-10-767-701-49297	Sequence 49297, A
100	30	68.2				

101	30	68.2	59	4	US-10-425-115-339894	Sequence 339894,	174	29	65.9	86	4	US-10-425-115-350109	Sequence 350109,
102	30	68.2	67	4	US-10-437-963-198423	Sequence 198423,	175	29	65.9	89	4	US-10-276-774-2423	Sequence 2423, Ap
103	30	68.2	76	4	US-10-425-115-280492	Sequence 280492,	176	29	65.9	93	4	US-10-425-115-345695	Sequence 345695,
104	30	68.2	98	4	US-10-425-115-368502	Sequence 368502,	177	29	65.9	94	4	US-10-425-115-334925	Sequence 334925,
105	30	68.2	103	4	US-10-695-499-38	Sequence 38, Appl	178	29	65.9	96	4	US-10-425-115-319633	Sequence 319633,
106	30	68.2	141	4	US-10-425-114-71262	Sequence 71262, A	179	29	65.9	100	4	US-10-425-115-321896	Sequence 321896,
107	30	68.2	164	4	US-10-425-115-281390	Sequence 281390,	180	29	65.9	102	4	US-10-425-115-341702	Sequence 341702,
108	30	68.2	180	3	US-09-811-284-192	Sequence 192, App	181	29	65.9	103	4	US-10-437-963-110524	Sequence 110524,
109	30	68.2	187	4	US-10-264-049-2383	Sequence 2383, Ap	182	29	65.9	112	4	US-10-424-599-202348	Sequence 202348,
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114	30	68.2	365	5	US-10-739-930-10418	Sequence 10418, A	187	29	65.9	136	4	US-10-437-963-126309	Sequence 126309,
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394	29	65.9	576	4	US-10-369-493-3203	Sequence 3203, Ap	467	28	63.6	76	4	US-10-424-599-230284	Sequence 230284,
395	29	65.9	582	4	US-10-437-963-147204	Sequence 147204,	468	28	63.6	77	4	US-10-437-963-138470	Sequence 138470,
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397	29	65.9	642	4	US-10-437-963-140313	Sequence 140313,	470	28	63.6	79	4	US-10-425-115-232572	Sequence 232572,
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399	29	65.9	652	6	US-11-097-143-20208	Sequence 20208, A	472	28	63.6	85	5	US-10-926-386-8	Sequence 8, Appl1
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403	29	65.9	691	6	US-11-097-143-13293	Sequence 13293, A	476	28	63.6	97	4	US-10-767-701-59721	Sequence 59721, A
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417	29	65.9	781	4	US-10-221-278-287	Sequence 287, App	490	28	63.6	143	4	US-10-080-170-589	Sequence 589, App
418	29	65.9	781	4	US-10-302-812-64	Sequence 64, Appl	491	28	63.6	143	4	US-10-468-356-599	Sequence 589, App
419	29	65.9	781	4	US-10-723-608-16	Sequence 16, Appl	492	28	63.6	145	4	US-10-437-963-176086	Sequence 176086,
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437	29	65.9	883	3	US-09-812-350-1	Sequence 1, Appl1	510	28	63.6	211	4	US-10-389-566-395	Sequence 395, App
438	29	65.9	883	5	US-10-732-923-6937	Sequence 6937, Ap	511	28	63.6	215	3	US-09-764-868-1004	Sequence 1004, Ap
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441	29	65.9	968	3	US-09-969-528-7	Sequence 7, Appl1	514	28	63.6	228	5	US-10-617-316-236	Sequence 236, App
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454	28	63.6	17	5	US-10-979-183-375	Sequence 375, App	527	28	63.6	270	5	US-10-957-135-87	Sequence 87, Appl
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461	28	63.6	62	4	US-10-102-808-527	Sequence 527, App	534	28	63.6	277	4	US-10-036-542-134	Sequence 134, App
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547	28	63.6	309	4	US-10-278-536-120	Sequence 120, App	620	28	63.6	470	4	US-10-408-765A-2813	Sequence 2813, Ap
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581	28	63.6	370	5	US-10-972-078-6	Sequence 6, Appli	654	28	63.6	594	5	US-10-450-763-34282	Sequence 34282, A
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592	28	63.6	375	5	US-10-665-374-6	Sequence 6, Appli	665	28	63.6	693	4	US-10-264-237-2727	Sequence 2727, Ap
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596	28	63.6	376	4	US-10-437-963-152511	Sequence 152511, A	669	28	63.6	758	4	US-10-221-278-240	Sequence 240, App
597	28	63.6	378	4	US-10-108-260A-2777	Sequence 2777, Ap	670	28	63.6	764	4	US-10-407-866-92	Sequence 92, Appl
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602	28	63.6	395	4	US-10-032-585-7810	Sequence 7810, Ap	675	28	63.6	814	5	US-10-357-819-14	Sequence 14, Appl
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607	28	63.6	423	6	US-11-097-143-32397	Sequence 32397, A	680	28	63.6	858	4	US-10-282-122A-50780	Sequence 50780, A
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609	28	63.6	428	4	US-10-156-761-12984	Sequence 12984, A	682	28	63.6	894	4	US-10-437-963-174765	Sequence 174765, A
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687	28	63.6	930	4	US-10-437-963-117719	Sequence 117719,	760	27	61.4	89	4	US-10-425-599-156399	Sequence 156399,
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707	28	63.6	1408	4	US-10-369-493-22183	Sequence 22183, A	780	27	61.4	116	4	US-10-424-599-200501	Sequence 200501,
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713	28	63.6	1429	4	US-10-029-347-26	Sequence 3, Appli	786	27	61.4	120	4	US-10-296-115-863	Sequence 863, App
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723	28	63.6	1429	6	US-11-107-572-15	Sequence 15, Appl	796	27	61.4	141	4	US-10-437-963-202570	Sequence 202570,
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736	27	61.4	24	3	US-09-999-220B-108	Sequence 108, App	809	27	61.4	163	3	US-10-424-599-165065	Sequence 165065,
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835	27	61.4	235	4	US-10-425-114-66298	Sequence 66298, A	908	27	61.4	381	4	US-10-369-493-12930	Sequence 12930, A
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837	27	61.4	241	3	US-09-978-248-11	Sequence 11, Appl	910	27	61.4	383	4	US-10-267-255-100	Sequence 2, Appl
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842	27	61.4	251	5	US-10-732-923-16211	Sequence 16211, A	915	27	61.4	395	5	US-10-739-930-8158	Sequence 8158, Ap
843	27	61.4	251	5	US-10-732-923-16215	Sequence 16215, A	916	27	61.4	395	5	US-10-450-763-38076	Sequence 38076, A
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858	27	61.4	270	4	US-10-369-493-11918	Sequence 11918, A	931	27	61.4	414	3	US-09-978-189-466	Sequence 466, App
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862	27	61.4	278	5	US-10-504-582-140	Sequence 140, App	935	27	61.4	414	3	US-09-978-403A-466	Sequence 466, App
863	27	61.4	279	4	US-10-369-493-1942	Sequence 1942, Ap	936	27	61.4	414	3	US-09-978-564A-466	Sequence 466, App
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874	27	61.4	309	4	US-10-425-114-45938	Sequence 45938, A	947	27	61.4	414	3	US-09-978-643A-466	Sequence 466, App
875	27	61.4	312	4	US-10-424-599-260604	Sequence 260604, A	948	27	61.4	414	3	US-09-978-375A-466	Sequence 466, App
876	27	61.4	314	4	US-10-097-065-305	Sequence 305, App	949	27	61.4	414	3	US-09-978-298A-466	Sequence 466, App
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880	27	61.4	326	5	US-10-994-726-692	Sequence 726, App	953	27	61.4	414	3	US-09-999-829A-466	Sequence 466, App
881	27	61.4	328	4	US-10-425-114-63636	Sequence 63636, A	954	27	61.4	414	3	US-09-978-299A-466	Sequence 466, App
882	27	61.4	328	4	US-10-767-701-44362	Sequence 44362, A	955	27	61.4	414	3	US-09-978-544A-466	Sequence 466, App
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884	27	61.4	330	4	US-10-424-599-271829	Sequence 271829, A	957	27	61.4	414	3	US-09-978-802A-466	Sequence 466, App
885	27	61.4	333	4	US-10-435-226-14	Sequence 14, Appl	958	27	61.4	414	3	US-09-999-831A-466	Sequence 466, App
886	27	61.4	336	4	US-10-425-115-362664	Sequence 362664, A	959	27	61.4	414	3	US-09-978-824-466	Sequence 466, App
887	27	61.4	340	4	US-10-282-122A-46441	Sequence 46441, A	960	27	61.4	414	4	US-10-028-072-418	Sequence 418, App
888	27	61.4	341	4	US-10-424-599-175916	Sequence 175916, A	961	27	61.4	414	4	US-10-140-808-418	Sequence 418, App
889	27	61.4	343	4	US-10-425-115-271254	Sequence 271254, A	962	27	61.4	414	4	US-10-121-049-418	Sequence 418, App
890	27	61.4	344	4	US-10-424-599-285022	Sequence 285022, A	963	27	61.4	414	4	US-10-123-904-418	Sequence 418, App
891	27	61.4	345	4	US-10-282-122A-49421	Sequence 49421, A	964	27	61.4	414	4	US-10-140-470-418	Sequence 418, App
892	27	61.4	348	4	US-10-282-122A-43220	Sequence 43220, A	965	27	61.4	414	4	US-10-175-746-418	Sequence 418, App
893	27	61.4	348	4	US-10-424-599-181709	Sequence 181709, A	966	27	61.4	414	4	US-10-176-918-418	Sequence 418, App
894	27	61.4	349	4	US-10-282-122A-46257	Sequence 46257, A	967	27	61.4	414	4	US-10-176-921-418	Sequence 418, App
895	27	61.4	350	4	US-10-425-114-46691	Sequence 46691, A	968	27	61.4	414	4	US-10-137-865-418	Sequence 418, App
896	27	61.4	350	4	US-10-437-963-186328	Sequence 186328, A	969	27	61.4	414	4	US-10-140-474-418	Sequence 418, App
897	27	61.4	351	3	US-09-764-864-926	Sequence 926, App	970	27	61.4	414	4	US-10-142-431-418	Sequence 418, App
898	27	61.4	351	3	US-10-369-493-9708	Sequence 9708, Ap	971	27	61.4	414	4	US-10-143-114-418	Sequence 418, App
899	27	61.4	351	4	US-10-425-114-56672	Sequence 56672, A	972	27	61.4	414	4	US-10-080-110-12	Sequence 12, Appl
900	27	61.4	353	4	US-10-424-599-162000	Sequence 162000, A	973	27	61.4	414	4	US-10-142-419-418	Sequence 418, App
901	27	61.4	355	4	US-10-425-114-65280	Sequence 65280, A	974	27	61.4	414	4	US-10-017-081A-466	Sequence 466, App
902	27	61.4	359	5	US-10-994-726-691	Sequence 691, App	975	27	61.4	414	4	US-10-123-262-418	Sequence 418, App
903	27	61.4	362	3	US-09-729-674-18	Sequence 18, Appl	976	27	61.4	414	4	US-10-142-423-418	Sequence 418, App



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977 27 61.4 414 4 US-10-121-050-418 Sequence 418, App
978 27 61.4 414 4 US-10-141-755-418 Sequence 418, App
979 27 61.4 414 4 US-10-167-743-466 Sequence 466, App
980 27 61.4 414 4 US-10-143-032-418 Sequence 418, App
981 27 61.4 414 4 US-10-013-921A-466 Sequence 466, App
982 27 61.4 414 4 US-10-123-108-418 Sequence 418, App
983 27 61.4 414 4 US-10-123-236-418 Sequence 418, App
984 27 61.4 414 4 US-10-123-261-418 Sequence 418, App
985 27 61.4 414 4 US-10-140-921-418 Sequence 418, App
986 27 61.4 414 4 US-10-140-928-418 Sequence 418, App
987 27 61.4 414 4 US-10-013-929A-466 Sequence 466, App
988 27 61.4 414 4 US-10-016-177A-466 Sequence 466, App
989 27 61.4 414 4 US-10-121-045-418 Sequence 418, App
990 27 61.4 414 4 US-10-123-292-418 Sequence 418, App
991 27 61.4 414 4 US-10-123-903-418 Sequence 418, App
992 27 61.4 414 4 US-10-124-819-418 Sequence 418, App
993 27 61.4 414 4 US-10-124-822-418 Sequence 418, App
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995 27 61.4 414 4 US-10-160-498-418 Sequence 418, App
996 27 61.4 414 4 US-10-124-824-418 Sequence 418, App
997 27 61.4 414 4 US-10-127-829A-418 Sequence 418, App
998 27 61.4 414 4 US-10-127-835A-418 Sequence 418, App
999 27 61.4 414 4 US-10-127-839A-418 Sequence 418, App
1000 27 61.4 414 4 US-10-127-839A-418 Sequence 418, App

ALIGNMENTS

RESULT 1
US-09-870-216C-3
; Sequence 3, Application US/09870216C
; Publication No. US20040138135A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881210100
; CURRENT APPLICATION NUMBER: US/09/870,216C
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/209,391
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/226,256
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/257,008
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-216C-3

Query Match 100.0%; Score 44; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9
Db 1 FLQLLMEPV 9

RESULT 2
US-10-017-327-3
; Sequence 3, Application US/10017327
; Publication No. US20020155471A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND
; FILE REFERENCE: GZ 2101.20
; CURRENT APPLICATION NUMBER: US/10/017,327
; CURRENT FILING DATE: 2001-12-06

US-10-017-327-3
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-327-3

Query Match 100.0%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9
Db 1 FLQLLMEPV 9

RESULT 3
US-09-764-869-1075
; Sequence 1075, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1075
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-869-1075

Query Match 79.5%; Score 35; DB 3; Length 67;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9
Db 7 FLQLLTPV 15

RESULT 4
US-10-091-504-1075
; Sequence 1075, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1075
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; NAME/KEY: misc_feature
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-091-504-1075

Query Match          79.5%; Score 35; DB 4; Length 67;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9
    |||||: ||
Db 7 FLQLLTPEV 15

RESULT 5
US-10-227-577-1075
; Sequence 1075, Application US/10227577
; Publication No. US20040005575A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C2
; CURRENT APPLICATION NUMBER: US/10/227,577
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/091,504
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,869
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1075
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-227-577-1075

Query Match          79.5%; Score 35; DB 4; Length 67;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9
    |||||: ||
Db 7 FLQLLTPEV 15

RESULT 6
US-10-478-551-2
; Sequence 2, Application US/10478551
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; Publication No. US20040171811A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; APPLICANT: Steven Anthony Kliewer
; APPLICANT: Jodi Marie Maglich
; APPLICANT: John Tomlin Moore
; APPLICANT: Linda Becker Moore
; APPLICANT: Timothy Mark Willson
; TITLE OF INVENTION: NONHUMAN PREGNANE X RECEPTOR SEQUENCES
; TITLE OF INVENTION: FOR USE IN COMPARITIVE PHARMACOLOGY
; FILE REFERENCE: PU3855WO
; CURRENT APPLICATION NUMBER: US/10/478,551
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/293,380
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Canine
US-10-478-551-2

Query Match          79.5%; Score 35; DB 4; Length 329;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9
    |||||: ||
Db 210 FQQLLEPV 218

RESULT 7
US-10-424-599-170467
; Sequence 170467, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 170467
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(363)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_124948C.1.pap
US-10-424-599-170467

Query Match          79.5%; Score 35; DB 4; Length 363;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9
    |||||: ||
Db 286 FLQLLEPV 294

RESULT 8
US-10-424-599-219691
; Sequence 219691, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219691
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40409C.1.pap
US-10-424-599-219691

Query Match          79.5%; Score 35; DB 4; Length 363;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1  FLQLLMEPV 9
      ||||: |||
Db      286  FLQLINEPV 294

RESULT 9
US-10-425-115-349203
; Sequence 349203, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 349203
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_81639C.1.pap
US-10-425-115-349203

Query Match          77.3%; Score 34; DB 4; Length 79;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1  FLQLLMEPV 9
      :|||::|||
Db      66  YLQLLKPV 74

RESULT 10
US-10-437-963-114660
; Sequence 114660, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114660
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(180)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18329C.1.pap
US-10-437-963-114660

Query Match          77.3%; Score 34; DB 4; Length 180;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  FLQLLMEPV 9
      ||||| ||
Db      169  FCQLLMHPV 177

RESULT 11
US-10-437-963-132856
; Sequence 132856, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 132856
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(274)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34784C.1.pap
US-10-437-963-132856

Query Match          77.3%; Score 34; DB 4; Length 274;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  FLQLLMEPV 9
      ||||| ||
Db      184  FCQLLMHPV 192

RESULT 12
US-09-799-848-3
; Sequence 3, Application US/09799848
; Patent No. US20010044145A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett
; APPLICANT: Cook, Phillip
```

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; APPLICANT: Crooke, Stanley
; APPLICANT: Wu, Hongjiang
; APPLICANT: Lima, Walter
; TITLE OF INVENTION: METHODS OF USING MAMMALIAN RNASE H AND COMPOSITIONS THEREOF
; FILE REFERENCE: ISPH-0521
; CURRENT APPLICATION NUMBER: US/09/799,848
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: US 09/453,514
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 09/144,611
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 08/861,306
; PRIOR FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: US 08/244,993
; PRIOR FILING DATE: 1994-06-21
; PRIOR APPLICATION NUMBER: US 07/814,961
; PRIOR FILING DATE: 1991-12-24
; PRIOR APPLICATION NUMBER: US 09/462,280
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/13966
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/889,296
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 08/411,734
; PRIOR FILING DATE: 1995-04-03
; PRIOR APPLICATION NUMBER: US 08/007,996
; PRIOR FILING DATE: 1993-10-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-799-848-3

Query Match 77.3%; Score 34; DB 3; Length 307;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9
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Db 227 FLQLSVEPV 235

RESULT 13
US-09-781-712B-3
; Sequence 3, Application US/09781712B
; Publication No. US20040180433A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T
; APPLICANT: Lima, Walter
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
; FILE REFERENCE: ISPH-0520
; CURRENT APPLICATION NUMBER: US/09/781,712B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 39
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-781-712B-3

Query Match 77.3%; Score 34; DB 3; Length 307;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9
    ||||:||||
Db 227 FLQLSVEPV 235

RESULT 14
US-10-679-761-8
; Sequence 8, Application US/10679761
; Publication No. US20040248145A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Lima, Walter
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
; FILE REFERENCE: ISPH-0790
; CURRENT APPLICATION NUMBER: US/10/679,761
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US 10/358,439
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 09/992,738
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/781,712
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/861,205
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: US 60/248,950
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/497,412
; PRIOR FILING DATE: 2003-08-21
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-10-679-761-8

Query Match 77.3%; Score 34; DB 5; Length 307;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9
    ||||:||||
Db 227 FLQLSVEPV 235

RESULT 15
US-10-943-194-8
; Sequence 8, Application US/10943194
; Publication No. US20050164234A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Lima, Walter
```

```
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
; FILE REFERENCE: ISPH-0874
; CURRENT APPLICATION NUMBER: US/10/943,194
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US PCT/US2004/027348
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 10/358,439
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 09/861,205
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 09/781,712
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-943-194-8

Query Match          77.3%; Score 34; DB 5; Length 307;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLMEPV 9
Db      227 FLQLSVEPV 235
      ||||| :|||

RESULT 16
US-11-005-069-3
; Sequence 3, Application US/11005069
; Publication No. US20050153340A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T
; APPLICANT: Lima, Walter
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
; FILE REFERENCE: ISPH-0520
; CURRENT APPLICATION NUMBER: US/11/005,069
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US/09/781,712
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-11-005-069-3

Query Match          77.3%; Score 34; DB 6; Length 307;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLMEPV 9
Db      227 FLQLSVEPV 235
      ||||| :|||

us-09-870-216c-3.rapbm
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
; FILE REFERENCE: ISPH-0874
; CURRENT APPLICATION NUMBER: US/10/943,194
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US PCT/US2004/027348
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 10/358,439
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 09/861,205
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 09/781,712
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-943-194-8

Query Match          77.3%; Score 34; DB 5; Length 307;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLMEPV 9
Db      227 FLQLSVEPV 235
      ||||| :|||

RESULT 17
US-11-001-386-3
; Sequence 3, Application US/11001386
; Publication No. US20050153921A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett
; APPLICANT: Cook, Phillip
; APPLICANT: Crooke, Stanley
; APPLICANT: Wu, Hongjiang
; APPLICANT: Lima, Walter
; TITLE OF INVENTION: METHODS OF USING MAMMALIAN RNASE H AND COMPOSITIONS THEREOF
; FILE REFERENCE: ISPH-0521
; CURRENT APPLICATION NUMBER: US/11/001,386
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US/09/799,848
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: US 09/453,514
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 09/144,611
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 08/861,306
; PRIOR FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: US 08/244,993
; PRIOR FILING DATE: 1994-06-21
; PRIOR APPLICATION NUMBER: US 07/814,961
; PRIOR FILING DATE: 1991-12-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-11-001-386-3

Query Match          77.3%; Score 34; DB 6; Length 307;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLMEPV 9
Db      227 FLQLSVEPV 235
      ||||| :|||

us-10-415-478A-5
; Sequence 5, Application US/10415478A
; Publication No. US20040116661A1
; GENERAL INFORMATION:
; APPLICANT: Jeremy Stuart Brown
; APPLICANT: David William Holden
; TITLE OF INVENTION: Streptococcal Genes
; FILE REFERENCE: GJB-6571
; CURRENT APPLICATION NUMBER: US/10/415,478A
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: PCT/GB01/04749
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 0026231.1
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 00028345.7
; PRIOR FILING DATE: 2000-11-21
```

;; PRIOR APPLICATION NUMBER: 0102666.5  
;; PRIOR FILING DATE: 2001-02-02  
;; PRIOR APPLICATION NUMBER: 60/288,118  
;; PRIOR FILING DATE: 2001-05-02  
;; NUMBER OF SEQ ID NOS: 91  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 5  
;; LENGTH: 318  
;; TYPE: PRT  
;; ORGANISM: Salmonella pneumoniae  
US-10-415-478A-5

Query Match 77.3%; Score 34; DB 4; Length 318;  
Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLLMEP 8  
Db 152 FLQVLMDF 159

RESULT 19  
US-10-472-928-3880  
;; Sequence 3880, Application US/10472928  
;; Publication No. US20050020813A1  
;; GENERAL INFORMATION:  
;; APPLICANT: CHIRON SpA  
;; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS  
;; FILE REFERENCE: P026926WO  
;; CURRENT APPLICATION NUMBER: US/10/472,928  
;; CURRENT FILING DATE: 2003-09-26  
;; PRIOR APPLICATION NUMBER: GB-0107658.7  
;; PRIOR FILING DATE: 2001-03-27  
;; NUMBER OF SEQ ID NOS: 4979  
;; SOFTWARE: SeqWin99, version 1.03  
;; SEQ ID NO 3880  
;; LENGTH: 318  
;; TYPE: PRT  
;; ORGANISM: Streptococcus pneumoniae  
;; FEATURE:  
;; OTHER INFORMATION: iron-compound ABC transporter, permease protein  
;; OTHER INFORMATION: Cellular location: membrane  
;; OTHER INFORMATION: Similar to strain R6 sequence 15903727 (e-173)  
US-10-472-928-3880

Query Match 77.3%; Score 34; DB 5; Length 318;  
Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLLMEP 8  
Db 152 FLQVLMDF 159

RESULT 20  
US-10-617-320-5076  
;; Sequence 5076, Application US/10617320  
;; Publication No. US20050136404A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Lynn A Doucette-Stamm and David Bush  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
;; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
;; THERAPEUTICS  
;; NUMBER OF SEQUENCES: 5206  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
;; STREET: 100 Beaver Street  
;; CITY: Waltham  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02354  
;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: CD-ROM ISO9660  
;; COMPUTER: <Unknown>  
;; OPERATING SYSTEM: <Unknown>  
;; SOFTWARE: <Unknown>  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/617,320  
;; FILING DATE: 10-Jul-2003  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/107,433  
;; FILING DATE: 30-Jun-1998  
;; APPLICATION NUMBER: 60/ 085131  
;; FILING DATE: May 12, 1998  
;; APPLICATION NUMBER: 60/051553  
;; FILING DATE: July 2, 1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ariniello, Pamela Deneke  
;; REGISTRATION NUMBER: 40,489  
;; REFERENCE/DOCKET NUMBER: GTC-011  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (781)893-5007  
;; TELEFAX: (781)893-8277  
;; INFORMATION FOR SEQ ID NO: 5076:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 336 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: YES  
;; ORIGINAL SOURCE:  
;; ORGANISM: Streptococcus pneumoniae  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (B) LOCATION 1...336  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5076:  
US-10-617-320-5076

Query Match 77.3%; Score 34; DB 5; Length 336;  
Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLLMEP 8  
Db 170 FLQVLMDF 177

RESULT 21  
US-10-425-114-45949  
;; Sequence 45949, Application US/10425114  
;; Publication No. US20040034888A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Liu, Jingdong  
;; APPLICANT: Zhou, Yihua  
;; APPLICANT: Kovalic, David K.  
;; APPLICANT: Screen, Steven E  
;; APPLICANT: Tabaska, Jack E  
;; APPLICANT: Cao, Yongwei  
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(53313)B  
;; CURRENT APPLICATION NUMBER: US/10/425,114  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 73128  
;; SEQ ID NO 45949  
;; LENGTH: 504  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: LIB3594-024-A4\_FLI.pep  
US-10-425-114-45949

Query Match 77.3%; Score 34; DB 4; Length 504;  
Best Local Similarity 77.8%; Pred. No. 3.3e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
| | | | |  
Db 67 FCQLLMHPV 75

RESULT 22  
US-10-437-963-163658  
; Sequence 163658, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 163658  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(770)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_62633C.1.pep  
US-10-437-963-163658

Query Match 77.3%; Score 34; DB 4; Length 770;  
Best Local Similarity 77.8%; Pred. No. 5.2e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
| | | | |  
Db 187 FCQLLMHPV 195

RESULT 23  
US-10-425-115-200455  
; Sequence 200455, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 200455  
; LENGTH: 798  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(798)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_114401C.1.pep  
US-10-425-115-200455

Query Match 77.3%; Score 34; DB 4; Length 798;  
Best Local Similarity 77.8%; Pred. No. 5.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
| | | | |  
Db 224 FCQLLMHPV 232

RESULT 24  
US-10-425-115-319897  
; Sequence 319897, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 319897  
; LENGTH: 80  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_54815C.1.pep  
US-10-425-115-319897

Query Match 75.0%; Score 33; DB 4; Length 80;  
Best Local Similarity 66.7%; Pred. No. 78;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
| | | | |  
Db 54 FLNLLMHP 62

RESULT 25  
US-09-864-408A-7182  
; Sequence 7182, Application US/09864408A  
; Publication No. US20040009474A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Shimkets, Richard A.  
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enco  
; FILE REFERENCE: 21402-012  
; CURRENT APPLICATION NUMBER: US/09/864,408A  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: 60/206,690  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 9068  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7182  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-864-408A-7182

Query Match 75.0%; Score 33; DB 3; Length 117;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 8  
| | | | |  
Db 67 FLQLLNEP 74

RESULT 26  
US-10-425-115-223947

; Sequence 223947, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 223947  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_135825C.1.pep  
US-10-425-115-223947

Query Match 75.0%; Score 33; DB 4; Length 138;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 8  
| | | | |  
DB 61 FLQLMPEP 68

RESULT 27  
US-10-425-115-223948  
; Sequence 223948, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 223948  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(174)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_135826C.1.pep  
US-10-425-115-223948

Query Match 75.0%; Score 33; DB 4; Length 174;  
Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 8  
| | | | |  
DB 97 FLQLMPEP 104

RESULT 28  
US-10-767-701-35283  
; Sequence 35283, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 35283  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(193)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C6308\_1.pep  
US-10-767-701-35283

Query Match 75.0%; Score 33; DB 4; Length 193;  
Best Local Similarity 87.5%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 8  
| | | | |  
DB 116 FLQLMPEP 123

RESULT 29  
US-10-724-972A-7247  
; Sequence 7247, Application US/10724972A  
; Publication No. US20040147734A1  
; GENERAL INFORMATION:  
; APPLICANT: Doucette-Stamm, Lynn  
; APPLICANT: Bush, David  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: PATH03-16  
; CURRENT APPLICATION NUMBER: US/10/724,972A  
; CURRENT FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: 09/450,969  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/134,001  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 7544  
; SEQ ID NO 7247  
; LENGTH: 324  
; TYPE: PRT  
; ORGANISM: S.epidermidis  
US-10-724-972A-7247

Query Match 75.0%; Score 33; DB 4; Length 324;  
Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMPEP 8  
| | | | |  
DB 157 FLQLMNP 164

RESULT 30  
US-10-425-115-223949  
; Sequence 223949, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei

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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 223949
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(349)
; FEATURE:
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_135827C.1.pap
US-10-425-115-223949

Query Match          75.0%; Score 33; DB 4; Length 349;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMNP 8
Db 297 FLQLMNP 304

RESULT 31
US-09-805-550-4
; Sequence 4, Application US/09805550
; Patent No. US20020026045A1
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; APPLICANT: Tagliani, Laura
; FILE REFERENCE: 0964D
; CURRENT APPLICATION NUMBER: US/09/805,550
; CURRENT FILING DATE: 2001-03-13
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/413,574
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/109,728
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Zea mays
US-09-805-550-4

Query Match          75.0%; Score 33; DB 3; Length 368;
Best Local Similarity 87.5%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMNP 8
Db 291 FLQLMNP 298

RESULT 32
US-10-437-963-138501
; Sequence 138501, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
```

```
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138501
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39884C.1.pap
US-10-437-963-138501

Query Match          75.0%; Score 33; DB 4; Length 1224;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLMNPV 9
Db 257 FLQLVIQPI 265

RESULT 33
US-11-097-143-27693
; Sequence 27693, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27693
; LENGTH: 2764
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-27693

Query Match          75.0%; Score 33; DB 6; Length 2764;
Best Local Similarity 55.6%; Pred. No. 3.1e+03;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLMNPV 9
Db 1340 VLQMLLEPL 1348

RESULT 34
US-11-097-143-18159
; Sequence 18159, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
```



```
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18159
; LENGTH: 2802
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-18159

Query Match 75.0%; Score 33; DB 6; Length 2802;
Best Local Similarity 55.6%; Pred. No. 3.1e+03;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9
|:|:|:|:|
Db 1340 YLQMLLEPL 1348

RESULT 35
US-10-425-115-307557
; Sequence 307557, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 307557
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_43561C.1.pep
US-10-425-115-307557

Query Match 72.7%; Score 32; DB 4; Length 55;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9
|:|:|:|:|
Db 37 FCQMLHPV 45
```

```
RESULT 36
US-10-767-701-56147
; Sequence 56147, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 56147
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30937978.pep
US-10-767-701-56147

Query Match 72.7%; Score 32; DB 4; Length 73;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 8
|:|:|:|:|
Db 55 FIQLVLEP 62

RESULT 37
US-10-425-115-358291
; Sequence 358291, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 358291
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_8992C.1.pep
US-10-425-115-358291

Query Match 72.7%; Score 32; DB 4; Length 79;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9
|:|:|:|:|
Db 64 FLQMLAKEV 72

RESULT 38
US-10-767-701-62832
; Sequence 62832, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 62832  
; LENGTH: 104  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 18066026.pep  
US-10-767-701-62832

Query Match 72.7%; Score 32; DB 4; Length 104;  
Best Local Similarity 87.5%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLLMEPV 9  
Db 64 LQLLCEPV 71

RESULT 39  
US-10-425-115-360733  
; Sequence 360733, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 360733  
; LENGTH: 169  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(169)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_92170C.1.pep  
US-10-425-115-360733

Query Match 72.7%; Score 32; DB 4; Length 169;  
Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLLMEPV 9  
Db 56 LQMLIEPV 63

RESULT 40  
US-10-424-599-245981  
; Sequence 245981, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 245981

; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_64151C.1.pep  
US-10-424-599-245981

Query Match 72.7%; Score 32; DB 4; Length 189;  
Best Local Similarity 55.6%; Pred. No. 3e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9  
Db 22 FMRLLLQPV 30

RESULT 41  
US-10-424-599-196742  
; Sequence 196742, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 196742  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_19685C.1.pep  
US-10-424-599-196742

Query Match 72.7%; Score 32; DB 4; Length 198;  
Best Local Similarity 87.5%; Pred. No. 3.2e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLLMEPV 9  
Db 132 LQLLMEPV 139

RESULT 42  
US-10-424-599-234629  
; Sequence 234629, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 234629  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(269)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_53899C.1.pep

US-10-424-599-234629

Query Match 72.7%; Score 32; DB 4; Length 269;  
Best Local Similarity 55.6%; Pred. No. 4.4e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9  
Db 59 FMRLLQPV 67

RESULT 43

US-10-425-114-53064  
; Sequence 53064, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 53064  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3158-004-D4\_FLI.pcp  
US-10-425-114-53064

Query Match 72.7%; Score 32; DB 4; Length 272;  
Best Local Similarity 66.7%; Pred. No. 4.4e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9  
Db 113 FYQLLVEPL 121

RESULT 44

US-10-425-115-367551  
; Sequence 367551, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 367551  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_98378C.1.pcp  
US-10-425-115-367551

Query Match 72.7%; Score 32; DB 4; Length 276;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9

Db 117 FYQLLVEPL 125  
| | | | |

RESULT 45

US-10-775-678-54  
; Sequence 54, Application US/10775678  
; Publication No. US20040229250A1  
; GENERAL INFORMATION:  
; APPLICANT: Transkaryotic Therapies, Inc.  
; APPLICANT: von Figura, Kurt  
; APPLICANT: Schmidt, Bernhard  
; APPLICANT: Dierks, Thomas  
; APPLICANT: Heartlein, Michael W.  
; APPLICANT: Cosma, Maria P.  
; APPLICANT: Ballabio, Andrea  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MULTIPLE SULFATASE DEFICIENCIES  
; FILE OF INVENTION: OTHER SULFATASE DEFICIENCIES  
; FILE REFERENCE: 0403  
; CURRENT APPLICATION NUMBER: US/10/775,678  
; CURRENT FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: US 60/447,747  
; PRIOR FILING DATE: 2003-02-11  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 54  
; LENGTH: 290  
; TYPE: PRT  
; ORGANISM: Anopheles gambiae  
US-10-775-678-54

Query Match 72.7%; Score 32; DB 5; Length 290;  
Best Local Similarity 77.8%; Pred. No. 4.7e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9  
Db 84 FQQLLSEPV 92

RESULT 46

US-10-437-963-108157  
; Sequence 108157, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 108157  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_12438C.1.pcp  
US-10-437-963-108157

Query Match 72.7%; Score 32; DB 4; Length 334;  
Best Local Similarity 66.7%; Pred. No. 5.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLLMEPV 9  
| | | | |

Db 180 FYQLLVEPL 188

## RESULT 47

US-10-739-930-9255  
; Sequence 9255, Application US/10739930  
; Publication No. US20040216190A1

; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 9255  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-C573\_22.p  
US-10-739-930-9255

Query Match 72.7%; Score 32; DB 5; Length 362;

Best Local Similarity 87.5%; Pred. No. 5.9e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLLMEPV 9

Db 132 LQLLMEPV 139

## RESULT 48

US-10-425-115-365824  
; Sequence 365824, Application US/10425115  
; Publication No. US20040214272A1

; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 365824  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(420)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_96797C.1.pep  
US-10-425-115-365824

Query Match 72.7%; Score 32; DB 4; Length 420;

Best Local Similarity 66.7%; Pred. No. 6.9e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9

Db 262 FYQLLVEPL 270

## RESULT 49

US-09-143-828-2  
; Sequence 2, Application US/09143828  
; Publication No. US20030032790A1  
; GENERAL INFORMATION:

; APPLICANT: Pharmacia & Upjohn  
; TITLE OF INVENTION: No. US20030032790A1el Vitamin D Receptor Related Polypeptides, N  
; FILE OF INVENTION: Acid Sequence Encoding the Same and Uses Thereof  
; FILE REFERENCE: 10806-65  
; CURRENT APPLICATION NUMBER: US/09/143,828  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: [Deduced amino  
; OTHER INFORMATION: acid sequence of vitamin D receptor related gamma  
; OTHER INFORMATION: (VDRRG)]  
US-09-143-828-2

Query Match 72.7%; Score 32; DB 3; Length 434;

Best Local Similarity 66.7%; Pred. No. 7.2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9

Db 315 FOQLLLEPM 323

## RESULT 50

US-09-227-718-2  
; Sequence 2, Application US/09227718A  
; Publication No. US20030044888A1  
; GENERAL INFORMATION:

; APPLICANT: Evans, Ronald M.  
; APPLICANT: Blumberg, Bruce  
; TITLE OF INVENTION: NOVEL STEROID-ACTIVATED NUCLEAR  
; FILE OF INVENTION: RECEPTORS AND USES THEREFOR  
; FILE REFERENCE: SALK2270-1  
; CURRENT APPLICATION NUMBER: US/09/227,718A  
; CURRENT FILING DATE: 1999-01-08  
; EARLIER APPLICATION NUMBER: US 09/005,286  
; EARLIER FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Xaa is threonine  
US-09-227-718-2

Query Match 72.7%; Score 32; DB 3; Length 434;

Best Local Similarity 66.7%; Pred. No. 7.2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9

Db 315 FOQLLLEPM 323

Search completed: May 9, 2006, 02:35:32  
Job time : 95.8 secs

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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:05:23 ; Search time 98.4 Seconds  
(without alignments)  
40.187 Million cell updates/sec

Title: US-09-870-216C-5

Perfect score: 44

Sequence: 1 FLQLEFDV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003s.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	5	Abb08362 Synthetic
2	44	100.0	9	7	AbR82214 Human ant
3	44	100.0	352	5	Abb08367 Human can
4	37	84.1	1278	4	AbB62030 Recombina
5	35	79.5	282	6	Adb06652 Alloiooc
6	35	79.5	285	6	Adb06654 Alloiooc
7	35	79.5	654	8	Adn26780 Bacterial
8	35	79.5	680	8	AdS28720 Bacterial
9	35	79.5	1612	4	AbB59769 Drosophil
10	34	77.3	254	8	AdR09173 Human pro
11	33	75.0	217	7	ABM74402 DNA clone
12	33	75.0	374	8	Adp98863 C. albica
13	33	75.0	388	8	AdS23723 Bacterial
14	32	72.7	72	5	ABP06827 Human ORF
15	32	72.7	173	6	ABU70578 Human adi
16	32	72.7	225	6	ABU21843 Protein e
17	32	72.7	274	6	ABU24075 Protein e
18	32	72.7	415	7	AdD27919 Human PCO
19	32	72.7	419	7	ABO78318 Pseudomon
20	32	72.7	440	9	AdZ59939 Human COX
21	32	72.7	489	9	AdW72143 Human COX
22	32	72.7	514	7	ADD12559 Human ENZ
23	32	72.7	537	9	AdZ59941 Human COX
24	32	72.7	551	7	AdC24201 Human NOV

25	32	72.7	551	7	ADD12554	Adl12554 Human ENZ
26	32	72.7	551	8	ADS85251	AdS85251 Human cyc
27	32	72.7	552	2	AAy29648	AAy29648 Sheep pro
28	32	72.7	552	7	ADD12555	Adl12555 Human ENZ
29	32	72.7	562	5	ABB09701	Abb09701 Amino aci
30	32	72.7	562	9	ADZ51367	AdZ51367 Amino aci
31	32	72.7	574	9	ADZ59937	AdZ59937 Human COX
32	32	72.7	580	7	ADD27944	AdD27944 COX-1 ami
33	32	72.7	580	7	ADD27968	AdD27968 COX-1 ami
34	32	72.7	594	9	ADZ59943	AdZ59943 Human COX
35	32	72.7	599	2	AAr21690	AAr21690 Prostagla
36	32	72.7	599	5	ABG56403	ABG56403 Human ova
37	32	72.7	599	6	ABR42249	ABr42249 Human cyc
38	32	72.7	599	7	ADC24199	AdC24199 Human NOV
39	32	72.7	599	7	ADD27936	AdD27936 Human COX
40	32	72.7	599	8	ADN05626	AdN05626 Antipsori
41	32	72.7	599	8	ADZ59945	AdZ59945 Wild type
42	32	72.7	599	9	ADZ51365	AdZ51365 Amino aci
43	32	72.7	600	1	AAp91008	AAp91008 Prostagla
44	32	72.7	600	7	ADD27937	AdD27937 Ovine COX
45	32	72.7	602	5	ABB57303	Abb57303 Mouse isc
46	32	72.7	602	6	ABR42251	ABr42251 Mouse cyc
47	32	72.7	602	7	ADD27941	AdD27941 Rat COX-1
48	32	72.7	602	7	ADD27940	AdD27940 Murine CO
49	32	72.7	603	7	ADD27938	AdD27938 Canine CO
50	32	72.7	606	7	ADD27939	AdD27939 Rabbit CO
51	32	72.7	608	5	ABB07241	Abb07241 Canine cy
52	32	72.7	608	5	ABB07243	Abb07243 Human cyc
53	32	72.7	629	7	ADD27929	AdD27929 Human hCO
54	32	72.7	630	8	ADR38436	ADR38436 Human cyc
55	32	72.7	630	8	ADR38434	ADR38434 Human cyc
56	32	72.7	633	5	ABG30579	ABg30579 Dog prost
57	32	72.7	633	8	ADQ52596	AdQ52596 Dog COX-1
58	32	72.7	634	7	ADD27916	AdD27916 Human COX
59	32	72.7	641	8	ADN26161	AdN26161 Bacterial
60	32	72.7	756	8	ADS28088	AdS28088 Bacterial
61	32	72.7	2889	2	AAW14987	AAw14987 Protein d
62	31	70.5	129	4	AAU56952	AAu56952 Propionib
63	31	70.5	129	6	ABM53471	ABm53471 Propionib
64	31	70.5	129	6	ABR43995	ABr43995 Canine MU
65	31	70.5	188	4	ABG66790	ABg66790 Mouse ZAL
66	31	70.5	188	6	ABR43993	ABr43993 Canine MU
67	31	70.5	188	7	ADFI18581	AdFI18581 Mouse zal
68	31	70.5	190	4	AAW78656	AAw78656 Human pro
69	31	70.5	190	4	AAAB66792	AAb66792 Variant Z
70	31	70.5	190	4	AAAB66789	AAb66789 Human ZAL
71	31	70.5	190	7	ADFI18579	AdFI18579 Human zal
72	31	70.5	190	7	ADFI18583	AdFI18583 Zalpha29
73	31	70.5	195	4	ABBI2318	ABb12318 Human sec
74	31	70.5	195	4	AAW79640	AAw79640 Human pro
75	31	70.5	210	2	AAW10528	AAw10528 Saccharom
76	31	70.5	278	6	ABU40853	ABu40853 Protein e
77	31	70.5	287	7	ADP06974	AdP06974 Bacterial
78	31	70.5	390	6	ABU26413	ABu26413 Protein e
79	31	70.5	394	6	ABM68786	ABm68786 Phototrab
80	31	70.5	524	7	ABO68964	ABo68964 Pseudomon
81	31	70.5	608	4	ABB67704	ABb67704 Drosophil
82	31	70.5	641	4	ABG08043	ABg08043 Novel hum
83	31	70.5	654	8	ADN26504	AdN26504 Bacterial
84	31	70.5	803	7	ABO66225	ABo66225 Klebsiell
85	31	70.5	826	7	ADCS8116	AdC58116 Caenorhab
86	30	68.2	84	4	ABG08377	ABg08377 Novel hum
87	30	68.2	104	2	AAy41017	AAy41017 Drosophil
88	30	68.2	130	2	AAy41008	AAy41008 Drosophil
89	30	68.2	143	8	ADY22843	AdY22843 Plant ful
90	30	68.2	145	6	ADA54519	AdA54519 Human pro
91	30	68.2	193	4	AAm82094	AAm82094 Human hae
92	30	68.2	194	7	ADM26474	AdM26474 Hyperther
93	30	68.2	229	7	ADC00897	AdC00897 Enterohae
94	30	68.2	237	2	AAy38578	AAy38578 Neisseria
95	30	68.2	237	3	AAy74980	AAy74980 Neisseria
96	30	68.2	237	9	ABE49004	ABe49004 N. mening
97	30	68.2	272	6	ABU49547	ABu49547 Protein e

98	30	68.2	300	2	AAV16108	Aay16108 A formate	171	29	65.9	57	3	AAG03256	Aag03256 Human sec
99	30	68.2	301	7	ADC01231	Adc01231 Enterohae	172	29	65.9	80	4	ADM19701	Adm19701 Protein e
100	30	68.2	306	6	ABj25871	Abj25871 Aspergill	173	29	65.9	80	5	ABP05494	Abp05494 Human ORF
101	30	68.2	326	6	ABJ26471	Abj26471 Aspergill	174	29	65.9	87	3	AB226156	Ab226156 B. cereus
102	30	68.2	334	8	AD080861	Ad080861 Human pro	175	29	65.9	122	9	ABW91659	Abw91659 Human pol
103	30	68.2	370	4	AAU36760	Aau36760 Staphyloc	176	29	65.9	127	4	AAO02629	Aao02629 Mus muscu
104	30	68.2	370	4	AAU34032	Aau34032 Staphyloc	177	29	65.9	130	2	AAW62622	Aaw62622 Mus muscu
105	30	68.2	370	4	AAU34032	Aau34032 Staphyloc	178	29	65.9	141	2	AAW01466	Aay01466 Polypepti
106	30	68.2	370	4	AAU34032	Aau34032 Staphyloc	179	29	65.9	141	2	AAW01466	Aay01466 Polypepti
107	30	68.2	370	4	AAU34032	Aau34032 Staphyloc	180	29	65.9	141	7	ABO23428	Ab023428 Amino aci
108	30	68.2	370	5	ABP38558	Abp38558 Staphyloc	181	29	65.9	141	7	ABO23428	Ab023428 Amino aci
109	30	68.2	370	6	ABU42763	Abu42763 Protein e	182	29	65.9	141	8	AD020222	Ad020222 Human PRO
110	30	68.2	370	6	ABU42763	Abu42763 Protein e	183	29	65.9	141	8	AD020222	Ad020222 Human PRO
111	30	68.2	370	6	ABU42763	Abu42763 Protein e	184	29	65.9	141	8	AD020222	Ad020222 Human PRO
112	30	68.2	370	8	AD062339	Ad062339 Staphyloc	185	29	65.9	141	8	ADP55186	Adp55186 Human PRO
113	30	68.2	438	4	AAU393706	Aau393706 Human pro	186	29	65.9	141	8	ADP55186	Adp55186 Human PRO
114	30	68.2	452	8	ADQ66264	Adq66264 Novel hum	187	29	65.9	141	8	ADP55186	Adp55186 Human PRO
115	30	68.2	457	6	ABU19106	Abu19106 Protein e	188	29	65.9	152	6	ABM70101	Abm70101 Photorhab
116	30	68.2	463	9	ADW18234	Adw18234 E grandis	189	29	65.9	152	6	ABM70101	Abm70101 Photorhab
117	30	68.2	472	4	AAU79088	Aau79088 Coryneb	190	29	65.9	157	4	ABM70101	Abm70101 Photorhab
118	30	68.2	472	4	AAU79088	Aau79088 Coryneb	191	29	65.9	163	3	ABM70101	Abm70101 Photorhab
119	30	68.2	480	4	AAU75431	Aau75431 Human col	192	29	65.9	178	2	AAW04279	Aay04279 Borrelia
120	30	68.2	504	8	ABG08378	Abg08378 Novel hum	193	29	65.9	181	3	AAW04279	Aay04279 Borrelia
121	30	68.2	525	3	AAU18429	Aau18429 Amino aci	194	29	65.9	185	7	ABO62926	Ab062926 Klebsiell
122	30	68.2	585	7	ADM26755	Adm26755 Hyperther	195	29	65.9	185	7	ABO62926	Ab062926 Klebsiell
123	30	68.2	604	3	AAU343581	Aau343581 Human can	196	29	65.9	203	3	AAG46893	Aag46893 Arabidops
124	30	68.2	619	3	AAU343581	Aau343581 Human can	197	29	65.9	203	3	AAG46893	Aag46893 Arabidops
125	30	68.2	638	5	ABF65552	Abf65552 Bifidobac	198	29	65.9	205	5	ABB93357	Abb93357 Herbicida
126	30	68.2	700	6	ABU34375	Abu34375 Protein e	199	29	65.9	205	5	ABB93357	Abb93357 Herbicida
127	30	68.2	700	6	ABU34375	Abu34375 Protein e	200	29	65.9	209	3	AAG13209	Aag13209 Arabidops
128	30	68.2	706	4	AAU34375	Aau34375 Protein e	201	29	65.9	209	3	AAG13209	Aag13209 Arabidops
129	30	68.2	706	4	AAU34375	Aau34375 Protein e	202	29	65.9	209	3	AAG13209	Aag13209 Arabidops
130	30	68.2	806	4	AAU34375	Aau34375 Protein e	203	29	65.9	212	6	ADA36198	Ada36198 Acinetoba
131	30	68.2	818	8	ADG27352	Adg27352 Novel hum	204	29	65.9	220	6	ABU41552	Abu41552 Protein e
132	30	68.2	818	8	ADG27352	Adg27352 Novel hum	205	29	65.9	225	8	ADT57617	Adt57617 Plant pol
133	30	68.2	881	8	ADG27352	Adg27352 Novel hum	206	29	65.9	228	8	ADT57617	Adt57617 Plant pol
134	30	68.2	881	8	ADG27352	Adg27352 Novel hum	207	29	65.9	240	9	ADX84916	Adx84916 TBC conse
135	30	68.2	881	8	ADG27352	Adg27352 Novel hum	208	29	65.9	240	9	ADX84916	Adx84916 TBC conse
136	30	68.2	928	8	ADG27352	Adg27352 Novel hum	209	29	65.9	240	9	ADX84916	Adx84916 TBC conse
137	30	68.2	928	8	ADG27352	Adg27352 Novel hum	210	29	65.9	240	9	ADX84916	Adx84916 TBC conse
138	30	68.2	976	8	ADG27352	Adg27352 Novel hum	211	29	65.9	241	3	AAG34976	Aag34976 Arabidops
139	30	68.2	1092	8	ADN20021	Adn20021 Bacterial	212	29	65.9	241	3	AAG34976	Aag34976 Arabidops
140	30	68.2	1176	4	AAU70151	Aau70151 DNA encod	213	29	65.9	242	2	AAW31730	Aaw31730 Mycobacte
141	30	68.2	1176	4	AAU70151	Aau70151 DNA encod	214	29	65.9	242	2	AAW31730	Aaw31730 Mycobacte
142	30	68.2	1176	4	AAU70151	Aau70151 DNA encod	215	29	65.9	246	3	AAW31730	Aaw31730 Mycobacte
143	30	68.2	1350	8	ADU13084	Adu13084 Human ste	216	29	65.9	246	3	AAW31730	Aaw31730 Mycobacte
144	30	68.2	1378	8	ADU13084	Adu13084 Human ste	217	29	65.9	246	3	AAW31730	Aaw31730 Mycobacte
145	30	68.2	1429	8	ABM83575	Abm83575 Human dia	218	29	65.9	257	9	ABM92350	Abm92350 M. xanthu
146	30	68.2	1455	7	ADU70264	Adu70264 Human dia	219	29	65.9	257	9	ABM92350	Abm92350 M. xanthu
147	30	68.2	1626	7	ADU70264	Adu70264 Human dia	220	29	65.9	258	3	AAG16701	Aag16701 Arabidops
148	30	68.2	1626	7	ADU70264	Adu70264 Human dia	221	29	65.9	258	3	AAG16701	Aag16701 Arabidops
149	30	68.2	1633	8	ABM83574	Abm83574 Human dia	222	29	65.9	258	3	AAG16701	Aag16701 Arabidops
150	30	68.2	1634	9	AAU080028	Aau080028 Cyclin-de	223	29	65.9	263	3	AAG24080	Aag24080 Arabidops
151	30	68.2	1649	4	AAU080028	Aau080028 Cyclin-de	224	29	65.9	263	3	AAG24080	Aag24080 Arabidops
152	30	68.2	1649	4	AAU080028	Aau080028 Cyclin-de	225	29	65.9	276	3	AAG24079	Aag24079 Arabidops
153	30	68.2	1649	4	AAU080028	Aau080028 Cyclin-de	226	29	65.9	276	3	AAG24079	Aag24079 Arabidops
154	30	68.2	1649	4	AAU080028	Aau080028 Cyclin-de	227	29	65.9	280	8	ADJ49299	Adj49299 Oil-assoc
155	30	68.2	1651	5	AAU11781	Aau11781 Human kin	228	29	65.9	316	8	ADL05781	Adl05781 M. catarr
156	30	68.2	1662	5	AAU11781	Aau11781 Human kin	229	29	65.9	316	8	ADL05781	Adl05781 M. catarr
157	30	68.2	1662	5	AAU11781	Aau11781 Human kin	230	29	65.9	324	3	AAG16700	Aag16700 Arabidops
158	30	68.2	1662	8	ADN38385	Adn38385 Novel hum	231	29	65.9	324	3	AAG16700	Aag16700 Arabidops
159	30	68.2	2270	7	ADJ68994	Adj68994 Human hea	232	29	65.9	324	4	AAE01920	Aae01920 Arabidops
160	30	68.2	2259	4	ABM62745	Abm62745 Drosophil	233	29	65.9	324	4	AAE01920	Aae01920 Arabidops
161	30	68.2	2559	4	ABM62745	Abm62745 Drosophil	234	29	65.9	324	4	AAE01920	Aae01920 Arabidops
162	30	68.2	2871	5	AAU71325	Aau71325 Human MHC	235	29	65.9	324	4	AAE01920	Aae01920 Arabidops
163	29	65.9	9	5	AAU71325	Aau71325 Human MHC	236	29	65.9	324	4	AAE01920	Aae01920 Arabidops
164	29	65.9	9	5	AAU71325	Aau71325 Human MHC	237	29	65.9	324	4	AAE01920	Aae01920 Arabidops
165	29	65.9	9	5	AAU71325	Aau71325 Human MHC	238	29	65.9	324	4	AAE01920	Aae01920 Arabidops
166	29	65.9	9	5	AAU71325	Aau71325 Human MHC	239	29	65.9	324	4	AAE01920	Aae01920 Arabidops
167	29	65.9	10	5	AAU71325	Aau71325 Human MHC	240	29	65.9	324	4	AAE01920	Aae01920 Arabidops
168	29	65.9	10	5	AAU71325	Aau71325 Human MHC	241	29	65.9	324	4	AAE01920	Aae01920 Arabidops
169	29	65.9	10	5	AAU71325	Aau71325 Human MHC	242	29	65.9	324	4	AAE01920	Aae01920 Arabidops
170	29	65.9	44	4	AAU71325	Aau71325 Human MHC	243	29	65.9	427	7	ADP59642	Adp59642 Human pol

244	29	65.9	427	7	ABO70866	AbO70866 Pseudomon	317	28	63.6	93	4	AAM34378	Aam34378 Peptide #
245	29	65.9	450	2	AAW71507	Aaw71507 Helicobac	318	28	63.6	93	4	AAW74266	Aam74266 Human bon
246	29	65.9	450	6	ABU30694	Abu30694 Protein e	319	28	63.6	93	4	AAW61474	Aam61474 Human bra
247	29	65.9	450	8	ADU05537	Adu05537 H. pylori	320	28	63.6	93	4	ABG56066	Abg56066 Human liv
248	29	65.9	451	9	ADX84853	Adx84853 Inositol	321	28	63.6	93	5	ABG44204	Abg44204 Human pep
249	29	65.9	461	6	ABU30106	Abu30106 Protein e	322	28	63.6	95	5	ABB99028	Abb99028 Human zin
250	29	65.9	467	7	ADC96559	Adc96559 E. faeciu	323	28	63.6	99	6	ABM63998	Abm63998 Propionib
251	29	65.9	483	4	AAU23275	Aau23275 Novel hum	324	28	63.6	99	6	AAU67479	Aau67479 Propionib
252	29	65.9	501	6	ABU29962	Abu29962 Protein e	325	28	63.6	100	2	AAW75205	Aaw75205 Human sec
253	29	65.9	512	7	ADC97621	Adc97621 E. faeciu	326	28	63.6	100	5	AAE26968	Aae26968 Human gen
254	29	65.9	547	8	ADY07361	Ady07361 Plant ful	327	28	63.6	100	5	AAE27106	Aae27106 Human gen
255	29	65.9	553	8	ADX96602	Adx96602 Plant ful	328	28	63.6	100	6	ABU64979	Abu64979 Human sec
256	29	65.9	557	8	ADR85992	Adr85992 Aspergill	329	28	63.6	100	8	ADG89788	Adg89788 Human pro
257	29	65.9	628	8	ADY04303	Ady04303 Plant ful	330	28	63.6	101	3	AAE65396	Aay65396 Human 5'
258	29	65.9	639	5	ABB97389	Abb97389 Novel hum	331	28	63.6	101	8	ADU72960	Adu72960 Signal pe
259	29	65.9	642	7	ABO70640	AbO70640 Pseudomon	332	28	63.6	101	8	ADV89018	Adv89018 Streptoco
260	29	65.9	654	5	ABP35619	Abp35619 Fungal ZB	333	28	63.6	101	8	ADV82394	Adv82394 Streptoco
261	29	65.9	680	2	AAO7453	Aao7453 First ope	334	28	63.6	101	8	ADV80271	Adv80271 Streptoco
262	29	65.9	680	2	AAW46516	Aaw46516 Saccharom	335	28	63.6	101	9	ADZ73951	Adz73951 Human com
263	29	65.9	734	8	ADN20364	Adn20364 Bacterial	336	28	63.6	106	2	AAZ35987	Aay35987 Extended
264	29	65.9	759	5	ABP66048	Abp66048 Bifidobac	337	28	63.6	106	2	AAZ36184	Aay36184 Human sec
265	29	65.9	769	8	ABO59732	AbO59732 Human gen	338	28	63.6	106	2	AAZ36137	Aay36137 Human sec
266	29	65.9	769	8	ADS30443	AdS30443 Bacterial	339	28	63.6	106	5	ABB97399	Abb97399 Novel hum
267	29	65.9	783	9	ABM92624	Abm92624 M. xanthu	340	28	63.6	106	7	ADJ46036	Adj46036 Novel hum
268	29	65.9	790	6	ABU22946	Abu22946 Protein e	341	28	63.6	106	7	ADJ45942	Adj45942 Novel hum
269	29	65.9	801	4	ABG00798	Abg00798 Novel tyr	342	28	63.6	106	8	ADP19445	Adp19445 Human sec
270	29	65.9	832	3	AAZ85663	Aaz85663 Human tyr	343	28	63.6	106	8	ADP19295	Adp19295 Human sec
271	29	65.9	924	5	AAU71093	Aau71093 Human can	344	28	63.6	119	4	AAZ64660	Aag64660 Hydroxyin
272	29	65.9	924	5	ABG70909	Abg70909 R. obamen	345	28	63.6	119	4	ADO70984	Ado70984 Stenotrop
273	29	65.9	924	7	ADF61934	Adf61934 R. obamen	346	28	63.6	133	8	ADJ49763	Adj49763 Oii-assoc
274	29	65.9	928	4	ABM63382	Abm63382 Drosophil	347	28	63.6	136	3	AAZ23474	Aag23474 Arabidops
275	29	65.9	1024	2	AAW19604	Aaw19604 Mycoplasma	348	28	63.6	143	6	ADB07558	Adb07558 Alloicoc
276	29	65.9	1049	8	ADU69762	Adu69762 S agalact	349	28	63.6	153	4	AAZ97829	Aab97829 Mouse pro
277	29	65.9	1049	8	ADU69581	Adu69581 S agalact	350	28	63.6	154	6	ABU24597	Abu24597 Protein e
278	29	65.9	1049	8	ADU69756	Adu69756 S agalact	351	28	63.6	155	6	ABJ38699	Abj38699 Human nuc
279	29	65.9	1049	8	ADV87847	Adv87847 Streptoco	352	28	63.6	166	8	ADO19564	Ado19564 Human PRO
280	29	65.9	1049	8	ADV79100	Adv79100 Streptoco	353	28	63.6	166	8	ADP54625	Adp54625 Human PRO
281	29	65.9	1049	8	ADV82666	Adv82666 Streptoco	354	28	63.6	183	3	ABM40381	Aab40381 Human ORF
282	29	65.9	1049	8	ADV81299	Adv81299 Streptoco	355	28	63.6	183	3	ABP06895	Abp06895 Human ORF
283	29	65.9	1049	8	ADV82607	Adv82607 Streptoco	356	28	63.6	188	7	ADF04952	Adf04952 Bacterial
284	29	65.9	1078	6	ABU20969	Abu20969 Protein e	357	28	63.6	188	7	ADO67118	Ado67118 Klebsiell
285	29	65.9	1088	8	ADT04695	Adt04695 Soybean D	358	28	63.6	198	7	ADD29473	Add29473 Mouse cae
286	29	65.9	1112	5	ABG92095	Abg92095 Human rec	359	28	63.6	201	9	ABE40704	Aeb40704 L. pneumo
287	29	65.9	1157	4	ABE61471	Abb61471 Drosophil	360	28	63.6	205	9	ABE37386	Aeb37386 L. pneumo
288	29	65.9	1198	4	ABG06391	Abg06391 Novel hum	361	28	63.6	212	4	ABG00118	Abg00118 Novel hum
289	29	65.9	1234	8	ADS24254	AdS24254 Bacterial	362	28	63.6	212	5	AAO22790	Aao22790 Protein o
290	29	65.9	1590	4	ABM66698	Abm66698 Drosophil	363	28	63.6	215	4	AAU53203	Aau53203 Propionib
291	29	65.9	1590	4	ABM62575	Abm62575 Drosophil	364	28	63.6	215	6	ABM49722	Abm49722 Propionib
292	29	65.9	1596	5	AAO17113	Aao17113 Murine Gl	365	28	63.6	227	7	ABO80435	AbO80435 Pseudomon
293	29	65.9	1596	5	AAO17114	Aao17114 Human sof	366	28	63.6	229	7	ADH87318	Adh87318 Enterococ
294	29	65.9	1596	8	ADQ17743	Adq17743 Human sof	367	28	63.6	236	5	ABP02921	Abp02921 Human ORF
295	29	65.9	1597	9	AEA27510	Aea27510 Human zin	368	28	63.6	249	3	AAZ23473	Aag23473 Arabidops
296	29	65.9	1597	9	AEA30113	Aea30113 Glioblast	369	28	63.6	259	8	ADS24825	AdS24825 Bacterial
297	29	65.9	1601	8	ADQ37057	Adq37057 Cell prol	370	28	63.6	264	7	ABO75173	AbO75173 Pseudomon
298	29	65.9	2000	6	ABR53389	AbR53389 Protein s	371	28	63.6	274	8	ADK16707	Adk16707 Nanoarcha
299	29	65.9	2000	7	ADK62088	Adk62088 Disease t	372	28	63.6	287	9	ABE42519	Aeb42519 L. pneumo
300	28.5	64.8	451	6	ABU23211	Abu23211 Protein e	373	28	63.6	305	3	AAZ58593	Aay58593 Sorangium
301	28.5	64.8	463	8	ADS41850	AdS41850 Bacterial	374	28	63.6	319	6	ABU50413	Abu50413 Protein e
302	28.5	64.8	464	8	ADN18588	Adn18588 Bacterial	375	28	63.6	325	4	AAU42000	Aau42000 Propionib
303	28	63.6	52	2	AAU12357	Aau12357 Human 5'	376	28	63.6	325	6	ABM38519	Abm38519 Propionib
304	28	63.6	62	4	AAU60122	Aau60122 Propionib	377	28	63.6	328	1	AAZ70274	Aap70274 Sequence
305	28	63.6	62	6	ABM56641	Abm56641 Propionib	378	28	63.6	328	2	AAZ41528	Aar41528 S.lividan
306	28	63.6	64	4	AAU48047	Aau48047 Propionib	379	28	63.6	328	2	AAR80286	Aar80286 galt gene
307	28	63.6	64	6	ABM44566	Abm44566 Propionib	380	28	63.6	335	4	ABG00743	Abg00743 Novel hum
308	28	63.6	66	9	ABM92065	Abm92065 M. xanthu	381	28	63.6	337	6	ABU30010	Abu30010 Protein e
309	28	63.6	72	2	AAZ36182	Aay36182 Human sec	382	28	63.6	361	2	AAW70837	Aaw70837 Arabidops
310	28	63.6	72	2	AAZ36135	Aay36135 Human sec	383	28	63.6	361	5	ABB91076	Abb91076 Herbicida
311	28	63.6	72	4	ABG16320	Abg16320 Novel hum	384	28	63.6	361	7	ABO69886	AbO69886 Pseudomon
312	28	63.6	72	7	ADJ46034	Adj46034 Novel hum	385	28	63.6	361	8	ADN72581	Adn72581 Thale cre
313	28	63.6	72	7	ADJ45940	Adj45940 Novel hum	386	28	63.6	361	9	ADZ44935	Adz44935 A thalian
314	28	63.6	72	8	ADP19443	Adp19443 Human sec	387	28	63.6	361	8	ADY04487	Ady04487 Plant ful
315	28	63.6	82	5	ABP25785	Abp25785 Streptoco	388	28	63.6	368	8	ADS44116	AdS44116 Bacterial
316	28	63.6	93	4	ABB40617	Abb40617 Peptide #	389	28	63.6	370	8	ADS44330	AdS44330 Bacterial

390	28	63.6	372	8	ADO02844	Ado02844	Thalecres	463	28	63.6	3133	8	ADS29884	Ads29884	Bacterial
391	28	63.6	378	7	ADC94150	Adc94150	E. faeciu	464	28	63.6	3500	8	AUQ74675	Auq74675	Streptomy
392	28	63.6	387	9	AEA26335	Aea26335	Stress co	465	28	63.6	5024	4	AG822935	Ag822935	S. epider
393	28	63.6	388	9	AEV09284	Aev09284	B. pendul	466	28	63.6	5836	8	ADK16042	Adk16042	Streptomy
394	28	63.6	400	4	AAU34975	Aau34975	Enterococ	467	28	63.6	6641	6	ABU42656	Abu42656	Protein e
395	28	63.6	400	6	AAU32937	Aau32937	Protein e	468	28	63.6	10182	5	ABP43814	Abp43814	Staphyloc
396	28	63.6	401	7	ADH86525	Adh86525	Enterococ	469	28	63.6	10203	8	ADO84851	Ado84851	S. epiderm
397	28	63.6	410	7	ADM25749	Adm25749	Hyperther	470	28	63.6	10203	8	ADO84803	Ado84803	Staphyloc
398	28	63.6	410	8	ADX95524	Adx95524	Plant ful	471	27.5	62.5	259	5	AAU82361	Aau82361	C. albica
399	28	63.6	414	3	AAAB10995	Aab10995	H. tuberc	472	27.5	62.5	259	5	ABP73764	Abp73764	Aspergill
400	28	63.6	414	4	AAAB10995	Aab10995	H. tuberc	473	27.5	62.5	847	8	ADP86343	Adp86343	Aspergill
401	28	63.6	415	3	AAAB10977	Aab10977	H. tuberc	474	27	61.4	11	2	AAW99720	Aaw99720	p65 trans
402	28	63.6	415	4	AAAB10897	Aab10897	H. tuberc	475	27	61.4	11	6	ABG76157	Abg76157	Human p65
403	28	63.6	415	4	AAAB11145	Aab11145	H. tuberc	476	27	61.4	12	2	ABG76157	Abg76157	Human p65
404	28	63.6	426	9	AE839445	Aeb39445	L. pneumo	477	27	61.4	12	2	ABG76157	Abg76157	Human p65
405	28	63.6	426	9	AE836016	Aeb36016	L. pneumo	478	27	61.4	13	2	AAW99728	Aaw99728	p65 trans
406	28	63.6	428	8	ADK66099	Adk66099	Plant ful	479	27	61.4	13	6	ABG76165	Abg76165	Human p65
407	28	63.6	439	3	AAV79185	Aay79185	Haematopo	480	27	61.4	28	5	AAE28293	Aae28293	Human Din
408	28	63.6	456	8	ADT60266	Adt60266	Plant pol	481	27	61.4	63	3	ABK56756	Abk56756	Human pro
409	28	63.6	462	7	ADC61141	Adc61141	Baeyer-Vi	482	27	61.4	86	5	ADK36963	Adk36963	Novel hum
410	28	63.6	465	9	AEW93294	Abm93294	M. xanthu	483	27	61.4	87	2	AAW54382	Aaw54382	Actinomad
411	28	63.6	471	9	AEW93249	Abm93249	M. xanthu	484	27	61.4	87	2	ABG01396	Abg01396	Novel hum
412	28	63.6	489	6	ABU49517	Abu49517	Protein e	485	27	61.4	87	5	ABK54875	Abk54875	Lactococc
413	28	63.6	493	8	ADT60625	Adt60625	Plant pol	486	27	61.4	92	8	ABO60160	Ab060160	Human gen
414	28	63.6	538	4	ABK66928	Abk66928	Drosophil	487	27	61.4	96	4	AAW90450	Aaw90450	Human imm
415	28	63.6	540	8	ADN22465	Adn22465	Bacterial	488	27	61.4	99	5	ABB81754	Abb81754	Tumour ne
416	28	63.6	542	8	ADS43287	Adn43287	Bacterial	489	27	61.4	103	7	ADP07666	Adp07666	Bacterial
417	28	63.6	585	2	AAU06297	Aay06297	Human tra	490	27	61.4	106	4	ABG10675	Abg10675	Novel hum
418	28	63.6	591	5	ABG92868	Aab92868	Clock pro	491	27	61.4	111	4	AAW83900	Aaw83900	Human imm
419	28	63.6	591	4	AAU16186	Aau16186	Human nov	492	27	61.4	112	5	ABP60738	Abp60738	Chlamydom
420	28	63.6	591	6	ABU55255	Abu55255	Human nov	493	27	61.4	116	8	ADK73447	Adk73447	Plant ful
421	28	63.6	599	5	ABG92867	Abg92867	Clock pro	494	27	61.4	117	4	ABB68515	Abb68515	Drosophil
422	28	63.6	602	3	AAV79162	Aay79162	Aryl hydr	495	27	61.4	128	2	AAW74943	Aaw74943	Human sec
423	28	63.6	602	8	ABU56486	Abu56486	Lung canc	496	27	61.4	128	5	ABG95399	Abg95399	Human nov
424	28	63.6	602	8	ADK52095	Adk52095	Human ato	497	27	61.4	128	6	ABO34593	Ab034593	Region of
425	28	63.6	602	8	ADL14099	Adl14099	Human sar	498	27	61.4	128	7	ADT23254	Adt23254	Novel hum
426	28	63.6	602	8	ADN04976	Adn04976	Human sar	499	27	61.4	128	8	ADH74256	Adh74256	Human sec
427	28	63.6	602	9	ADY17746	Ady17746	PRO polyp	500	27	61.4	134	3	AAW9817	Aaw9817	Arabidops
428	28	63.6	622	5	ABG92866	Abg92866	Clock pro	501	27	61.4	134	9	ADZ221350	Adz221350	Nuclear f
429	28	63.6	636	5	ABG92879	Abg92879	EMAL2 (br	502	27	61.4	135	4	AAO02596	Aao02596	Human pol
430	28	63.6	636	5	ABG92865	Abg92865	Clock pro	503	27	61.4	137	2	AAV37516	Aav37516	Protein w
431	28	63.6	673	2	AAV85953	Aay85953	S. pneumo	504	27	61.4	139	3	AAW9816	Aaw9816	Arabidops
432	28	63.6	690	8	ADN23403	Adn23403	Bacterial	505	27	61.4	142	2	AAV37322	Aav37322	Amino aci
433	28	63.6	703	6	ABU35605	Abu35605	Protein e	506	27	61.4	148	3	AAW9815	Aaw9815	Arabidops
434	28	63.6	703	7	ABO64303	Ab064303	Klebsiell	507	27	61.4	150	2	AAV35501	Aav35501	Chlamydia
435	28	63.6	737	8	ADO01496	Ado01496	N. bentha	508	27	61.4	157	4	ABB61010	Abb61010	Drosophil
436	28	63.6	845	8	ADN23684	Adn23684	Bacterial	509	27	61.4	157	8	ADK73573	Adk73573	Plant ful
437	28	63.6	870	8	ADT55671	Adt55671	Plant pol	510	27	61.4	160	3	AAW9816	Aaw9816	Arabidops
438	28	63.6	903	5	ABG30986	Abg30986	Zebrafish	511	27	61.4	161	7	ADK64272	Adk64272	Disease t
439	28	63.6	925	9	ADY25781	Ady25781	MRAC MCP2	512	27	61.4	162	4	AAW00029	Aaw00029	GDP-4-ket
440	28	63.6	1042	7	ABM87416	Abm87416	Rice abio	513	27	61.4	162	9	ABM91163	Abm91163	M. xanthu
441	28	63.6	1046	8	ADH56195	Adh56195	Arabidops	514	27	61.4	164	7	ABO82761	Ab082761	Pseudomon
442	28	63.6	1048	8	ADK62526	Adk62526	Protein s	515	27	61.4	166	2	AAW9816	Aaw9816	Arabidops
443	28	63.6	1048	7	ADK62526	Adk62526	Disease t	516	27	61.4	166	3	AAW9816	Aaw9816	Arabidops
444	28	63.6	1056	2	AAV24308	Aay24308	Cyclotell	517	27	61.4	168	6	AAU35760	Aau35760	Helicobac
445	28	63.6	1067	8	ADN23681	Adn23681	Bacterial	518	27	61.4	168	4	AAU37082	Aau37082	Protein e
446	28	63.6	1081	8	ADH56193	Adh56193	Arabidops	519	27	61.4	168	8	ADY24616	Ady24616	Plant ful
447	28	63.6	1081	8	ADT04690	Adt04690	Thale cre	520	27	61.4	170	4	ADM20136	Adm20136	Protein e
448	28	63.6	1128	3	AAW929155	Aag929155	Arabidops	521	27	61.4	172	4	ADM19897	Adm19897	Protein e
449	28	63.6	1206	3	AAW929154	Aag929154	Arabidops	522	27	61.4	175	9	ADY65214	Ady65214	S. manso
450	28	63.6	1241	9	AEA27508	Aea27508	Human zin	523	27	61.4	176	3	AAW97814	Aaw97814	Arabidops
451	28	63.6	1241	9	AEA30111	Aea30111	Glioblast	524	27	61.4	177	7	ADP05028	Adp05028	Bacterial
452	28	63.6	1258	5	ABG33067	Abg33067	Human Gli	525	27	61.4	177	8	ADK43073	Adk43073	Bacterial
453	28	63.6	1293	3	AAW929153	Aag929153	Arabidops	526	27	61.4	178	6	ABU36162	Abu36162	Protein e
454	28	63.6	1357	8	ADN22522	Adn22522	Bacterial	527	27	61.4	183	4	AAW90385	Aaw90385	Human unc
455	28	63.6	1413	8	ADN23439	Adn23439	Bacterial	528	27	61.4	183	4	AAW39504	Aaw39504	Human pol
456	28	63.6	1735	9	ADY72592	Ady72592	A. orient	529	27	61.4	187	3	AAW92624	Aaw92624	Arabidops
457	28	63.6	1921	9	ADY72598	Ady72598	A. orient	530	27	61.4	188	4	AAU16162	Aau16162	Human nov
458	28	63.6	2000	6	ABK53461	Abk53461	Protein s	531	27	61.4	188	6	ABU55231	Abu55231	Human nov
459	28	63.6	2000	7	ADK64602	Adk64602	Disease t	532	27	61.4	194	4	ABG24406	Abg24406	Novel hum
460	28	63.6	2034	6	AAE36121	Aae36121	Streptomy	533	27	61.4	194	6	ABU30285	Abu30285	Protein e
461	28	63.6	2049	9	ADZ51729	Adz51729	PKS PscF,	534	27	61.4	218	3	AAW92624	Aaw92624	Arabidops
462	28	63.6	2066	4	AAE10146	Aae10146	Streptomy	535	27	61.4	219	8	ADL04947	Adl04947	M. catarr



536	27	61.4	229	4	AAE02232	Aae02232 Staphyloc	609	27	61.4	315	9	ADY17772	Ady17772 PRO polyp
537	27	61.4	229	5	ABB80681	Abb80681 Human tra	610	27	61.4	317	8	ADR5897	Adr5897 Novel S.
538	27	61.4	229	8	ADL26978	Adl26978 Protein o	611	27	61.4	317	9	AEA59767	Aea59767 Streptoco
539	27	61.4	229	8	ADZ74037	Adz74037 Staphyloc	612	27	61.4	328	6	ABM73167	Abm73167 Staphyloc
540	27	61.4	231	2	AAZ43385	Aaz43385 Product o	613	27	61.4	328	8	ADT07484	Adt07484 Human col
541	27	61.4	232	3	AAZ43385	Aaz43385 Product o	614	27	61.4	329	8	ADP81119	Adp81119 Protein o
542	27	61.4	232	3	AAZ43385	Aaz43385 Product o	615	27	61.4	332	3	AAG36394	Aag36394 Arabidops
543	27	61.4	235	8	ADH22547	Adh22547 Human tra	616	27	61.4	332	3	AAG37924	Aag37924 Arabidops
544	27	61.4	237	2	AAW19739	Aaw19739 Sugar bio	617	27	61.4	332	7	ADB31807	Adb31807 Plant (A.
545	27	61.4	237	2	AAW99391	Aaw99391 S. erythra	618	27	61.4	332	7	ADD30588	Add30588 Plant yie
546	27	61.4	237	3	AAZ38579	Aaz38579 Neisseria	619	27	61.4	332	8	ADI44043	Adi44043 Plant tra
547	27	61.4	237	3	AAZ38579	Aaz38579 Neisseria	620	27	61.4	332	8	ADQ02265	Adq02265 Thalecres
548	27	61.4	237	9	ABE44906	Abu44906 N. gonorr	621	27	61.4	332	8	ADT56428	Adt56428 Plant pol
549	27	61.4	239	6	ABU44443	Abu44443 Protein e	622	27	61.4	333	8	ADY05282	Ady05282 Plant ful
550	27	61.4	240	9	ADW74664	Adw74664 Novel act	623	27	61.4	334	8	ADS43267	Ads43267 Bacterial
551	27	61.4	241	6	ABP78385	Abp78385 N. gonorr	624	27	61.4	335	8	ADS43434	Ads43434 Bacterial
552	27	61.4	246	4	AAZ83028	Aaz83028 S. epider	625	27	61.4	336	8	ABO62683	Abog62683 Klebsiell
553	27	61.4	246	6	ABM70343	Abm70343 Photorhab	626	27	61.4	339	8	ADM48179	Adm48179 Polypepti
554	27	61.4	253	4	ABP62923	Abp62923 Drosophil	627	27	61.4	341	4	AAZ89991	Aaz89991 C. glutami
555	27	61.4	256	5	ABP40626	Abp40626 Staphyloc	628	27	61.4	341	5	AAU79517	Aau79517 C. glutam
556	27	61.4	256	8	ADS07845	Ads07845 Staphyloc	629	27	61.4	344	8	ADX91400	Adx91400 Plant ful
557	27	61.4	260	7	ADL33592	Adl33592 Transcrip	630	27	61.4	348	2	AAZ40973	Aaz40973 recA gene
558	27	61.4	260	8	ADM72633	Adm72633 p65 prote	631	27	61.4	349	4	AAG75571	Aag75571 Human col
559	27	61.4	260	8	ADP70965	Adp70965 Novel zin	632	27	61.4	349	4	ABG09229	Abg09229 Novel hum
560	27	61.4	260	9	ADV39069	Adv39069 Human p65	633	27	61.4	349	4	ABG15957	Abg15957 Novel hum
561	27	61.4	262	3	AAZ23154	Aaz23154 Arabidops	634	27	61.4	357	6	ABO70461	Abog70461 Pseudomon
562	27	61.4	262	8	ADN73679	Adn73679 Thale cre	635	27	61.4	358	7	ABU39478	Abu39478 Protein e
563	27	61.4	263	3	AAZ43771	Aaz43771 Zea mays	636	27	61.4	369	3	AGA43769	Aag43769 Zea mays
564	27	61.4	263	7	ADC52118	Adc52118 Aeropyrum	637	27	61.4	376	9	AEZ39217	Aeb39217 L. pneumo
565	27	61.4	263	7	ADD19026	Add19026 Human dis	638	27	61.4	378	7	ADL33707	Adl33707 Zinc fing
566	27	61.4	263	8	ADS44399	Ads44399 Bacterial	639	27	61.4	378	7	ADL33662	Adl33662 Zinc fing
567	27	61.4	269	5	ABBS4124	Abbs4124 Lactococc	640	27	61.4	378	7	ADL33680	Adl33680 Zinc fing
568	27	61.4	269	5	AAO19278	Aao19278 Human p65	641	27	61.4	378	7	ADL33666	Adl33666 Zinc fing
569	27	61.4	269	5	AAO19278	Aao19278 Human p65	642	27	61.4	379	9	AEBA4168	Aeb4168 L. pneumo
570	27	61.4	272	4	AAZ41290	Aaz41290 Human pol	643	27	61.4	380	9	AEZ37861	Aeb37861 L. pneumo
571	27	61.4	276	8	ADS23506	Ads23506 Bacterial	644	27	61.4	382	7	ADL33668	Adl33668 Zinc fing
572	27	61.4	280	3	AAZ23153	Aaz23153 Arabidops	645	27	61.4	382	7	ADL33664	Adl33664 Zinc fing
573	27	61.4	281	6	ADB09612	Adb09612 Alloiococ	646	27	61.4	386	8	ADU66618	Adu66618 Human kin
574	27	61.4	281	6	ADB09612	Adb09612 Alloiococ	647	27	61.4	389	4	ABG15761	Abg15761 Novel hum
575	27	61.4	284	3	AAZ43770	Aaz43770 Zea mays	648	27	61.4	389	9	ABM92903	Abm92903 M. xanthu
576	27	61.4	284	4	ABB60998	Abb60998 Drosophil	649	27	61.4	390	9	AEBA42333	Aeb42333 L. pneumo
577	27	61.4	288	4	AAZ79831	Aaz79831 Corynebac	650	27	61.4	390	9	AEZ37227	Aeb37227 L. pneumo
578	27	61.4	288	4	AAZ79874	Aaz79874 Corynebac	651	27	61.4	392	8	ADI61501	Adi61501 A. thalia
579	27	61.4	289	6	ABU23304	Abu23304 Protein e	652	27	61.4	392	8	ADO02523	Ado02523 Thalecres
580	27	61.4	293	3	AAZ37926	Aaz37926 Arabidops	653	27	61.4	398	9	AEZ35767	Aeb35767 L. pneumo
581	27	61.4	293	3	AAZ36396	Aaz36396 Arabidops	654	27	61.4	402	6	ADB10718	Adb10718 Alloiococ
582	27	61.4	293	8	ADK46497	Adk46497 Streptoco	655	27	61.4	405	8	ADX79320	Adx79320 Plant ful
583	27	61.4	293	8	ADK66523	Adk66523 Plant ful	656	27	61.4	406	8	ADX79327	Adx79327 Plant ful
584	27	61.4	297	8	ADR95110	Adr95110 Novel S.	657	27	61.4	410	4	ABB63090	Abb63090 Drosophil
585	27	61.4	297	9	AEA58980	Aea58980 Streptoco	658	27	61.4	410	7	ADD01213	Add01213 Human nuc
586	27	61.4	298	7	ABM73844	Abm73844 DNA clone	659	27	61.4	410	7	ADM05645	Adm05645 Human pro
587	27	61.4	300	7	ADC24091	Adc24091 Protein s	660	27	61.4	416	7	ABO74654	Abog74654 Pseudomon
588	27	61.4	300	8	ADH36192	Adh36192 Chemical	661	27	61.4	416	8	ADX68779	Adx68779 Plant ful
589	27	61.4	300	8	ADG93891	Adg93891 Nitrilase	662	27	61.4	418	5	ABB80924	Abb80924 L. lactis
590	27	61.4	300	8	ADI62490	Adi62490 Nitrilase	663	27	61.4	424	2	AAW79959	Aaw79959 Campyloba
591	27	61.4	300	8	ADI64611	Adi64611 Nitrilase	664	27	61.4	425	7	ABO84328	Abog84328 Pseudomon
592	27	61.4	301	4	ABB57921	Abb57921 Drosophil	665	27	61.4	431	2	AAZ85858	Aaz85858 WD-40 dom
593	27	61.4	301	8	ADO89738	Ado89738 Antagonis	666	27	61.4	431	2	ABM82259	Abm82259 Tumour-as
594	27	61.4	306	4	AAU38064	Aau38064 Streptoco	667	27	61.4	431	9	ADX05948	Adx05948 Cyclin-de
595	27	61.4	306	6	ABU02741	Abu02741 S. pneumo	668	27	61.4	437	6	ADB10716	Adb10716 Alloiococ
596	27	61.4	306	6	ABU02741	Abu02741 S. pneumo	669	27	61.4	437	8	ADY24524	Ady24524 Plant ful
597	27	61.4	306	8	ADM92274	Adm92274 S. pneumo	670	27	61.4	437	8	ADY24525	Ady24525 Plant ful
598	27	61.4	308	8	ADK47854	Adk47854 Streptoco	671	27	61.4	438	4	AAZ88523	Aaz88523 Haemophil
599	27	61.4	310	4	AAU00095	Aau00095 GDP-4-ket	672	27	61.4	438	5	AAU91454	Aau91454 Haemophil
600	27	61.4	311	6	ABU49855	Abu49855 Protein e	673	27	61.4	445	8	ADJ37218	Adj37218 Human nuc
601	27	61.4	312	7	ADE48124	Ade48124 Human tum	674	27	61.4	446	5	ABP74035	Abp74035 Candida a
602	27	61.4	312	9	ADY85567	Ady85567 Catalytic	675	27	61.4	449	6	ABU39381	Abu39381 Protein e
603	27	61.4	313	3	AAZ36395	Aaz36395 Arabidops	676	27	61.4	452	8	ADN23448	Adn23448 Bacterial
604	27	61.4	313	3	AAZ37925	Aaz37925 Arabidops	677	27	61.4	453	7	ABO82522	Abog82522 Pseudomon
605	27	61.4	315	4	AAZ10324	Aaz10324 Human tra	678	27	61.4	453	8	ADY09341	Ady09341 Plant ful
606	27	61.4	315	4	AAZ94269	Aaz94269 Human pro	679	27	61.4	454	7	ADC33425	Adc33425 Mouse MLT
607	27	61.4	315	4	AAZ94664	Aaz94664 Human pro	680	27	61.4	455	3	AAZ18657	Aaz18657 A human r
608	27	61.4	315	5	ABG76619	Abg76619 Human SOU	681	27	61.4	455	3	AAZ83278	Aaz83278 Human sur

682	27	61.4	455	3	AAY84321	A human c	755	27	61.4	623	7	ABM86336	Abm86336	Rice abio
683	27	61.4	455	6	ADA54909	Human pro	756	27	61.4	629	8	ADS21815	Bacterial	Abd21815
684	27	61.4	455	7	ADC33423	Human Mtr	757	27	61.4	630	5	ABB80766	Truncated	Abb80766
685	27	61.4	455	9	ADY18428	PRO polyp	758	27	61.4	630	5	ABB80765	Geneswite	Abb80765
686	27	61.4	455	9	ADY18426	PRO polyp	759	27	61.4	630	6	AAE35248	Geneswite	Aae35248
687	27	61.4	457	5	ABP63095	FLO11 gen	760	27	61.4	630	6	AAE35246	PGS1633 v	Aae35246
688	27	61.4	460	7	ABO71892	Pseudomon	761	27	61.4	636	5	AAO21857	Isofrenol	Aao21857
689	27	61.4	466	3	AAY87880	M. tuberc	762	27	61.4	641	6	ABU61961	Human Tol	Abu61961
690	27	61.4	466	5	ABU04691	Mycobacte	763	27	61.4	641	8	ADS26559	Bacterial	Ad26559
691	27	61.4	468	4	ABG25295	Novel hum	764	27	61.4	642	5	AAM50928	Arbidops	Aam50928
692	27	61.4	473	4	AAM25322	Human pro	765	27	61.4	642	5	ADC84501	GenPept a	Adc84501
693	27	61.4	480	8	ABM83859	Human dia	766	27	61.4	642	9	AEA25903	A. thalia	Aea25903
694	27	61.4	482	7	ABO79622	Pseudomon	767	27	61.4	648	6	AAE35247	Geneswite	Aae35247
695	27	61.4	485	8	ADS42127	Bacterial	768	27	61.4	654	5	ABE80764	Geneswite	Abe80764
696	27	61.4	492	6	ABU29998	Protein e	769	27	61.4	654	5	ABE80765	Geneswite	Abe80765
697	27	61.4	509	6	ABU30306	Protein e	770	27	61.4	675	5	ABG30875	Human pol	Abg30875
698	27	61.4	512	8	ADN25694	Bacterial	771	27	61.4	685	5	ABP63124	lovf gene	Abp63124
699	27	61.4	515	8	ADX91343	Plant ful	772	27	61.4	688	7	ADG47829	Mouse n-c	Adg47829
700	27	61.4	524	4	AAM93469	Human pol	773	27	61.4	690	6	ABU66304	Human CAN	Abu66304
701	27	61.4	524	6	ABP80864	N. gonorr	774	27	61.4	690	7	ADF70231	Human Cal	Adf70231
702	27	61.4	524	8	ADU18025	Human can	775	27	61.4	699	2	AAR32549	Tomato ha	Aar32549
703	27	61.4	527	8	ADU18025	Human can	776	27	61.4	699	4	AG707070	S cerevis	Ag707070
704	27	61.4	528	6	ABU29517	Protein e	777	27	61.4	699	4	ABM90164	Rice abio	Abm90164
705	27	61.4	528	8	ADX95068	Plant ful	778	27	61.4	700	7	ADJ11630	Rice abio	Adj11630
706	27	61.4	529	2	AAM19001	Reline he	779	27	61.4	700	7	ABM86544	Rice abio	Abm86544
707	27	61.4	532	8	ADT55588	Plant pol	780	27	61.4	705	3	ABO80732	Amino aci	Abu80732
708	27	61.4	537	2	AAY03839	Chimeric	781	27	61.4	711	4	ABU53080	Intracell	Abu53080
709	27	61.4	537	6	ADA17081	Nuclear f	782	27	61.4	713	6	ABU28888	Protein e	Abu28888
710	27	61.4	537	6	ADA17082	Nuclear f	783	27	61.4	713	7	ADC00959	Enterohae	Adc00959
711	27	61.4	537	8	ADS88220	Human pro	784	27	61.4	722	7	ADC39094	Novel hum	Adc39094
712	27	61.4	537	8	ADS30942	Bacterial	785	27	61.4	727	6	ABM83677	Human dia	Abm83677
713	27	61.4	537	8	ADU18025	Human can	786	27	61.4	729	6	ABU25232	Protein e	Abu25232
714	27	61.4	537	8	ADX68537	Plant ful	787	27	61.4	729	7	ADJ71151	Human hea	Adj71151
715	27	61.4	537	9	ADG05480	Cyclin-de	788	27	61.4	731	7	ADC99081	Human Kpp	Adc99081
716	27	61.4	543	4	AAE67295	Amino aci	789	27	61.4	732	8	ABM83676	Human dia	Abm83676
717	27	61.4	549	9	ABM95188	M. xanthu	790	27	61.4	734	4	AAM39297	Rice abio	Aam39297
718	27	61.4	550	2	AAR42085	NP-KappaB	791	27	61.4	734	4	AAM39297	Novel hum	Aam39297
719	27	61.4	550	2	AAR42255	Human p65	792	27	61.4	738	4	AU28031	Human bre	Au28031
720	27	61.4	550	2	AAR42254	Human p65	793	27	61.4	738	9	ADZ09749	Human bre	Adz09749
721	27	61.4	550	6	ADA17083	Nuclear f	794	27	61.4	740	3	ABU18330	Plasmodiu	Abu18330
722	27	61.4	550	6	ADA17084	Nuclear f	795	27	61.4	750	8	ABM83675	Human dia	Abm83675
723	27	61.4	551	3	AAY94383	Human NF-	796	27	61.4	758	4	AAE30812	Amino aci	Aae30812
724	27	61.4	551	6	ADA17076	Nuclear f	797	27	61.4	766	4	ABU53068	Transport	Abu53068
725	27	61.4	551	6	ADA17077	Nuclear f	798	27	61.4	771	6	ABU61962	Human Tol	Abu61962
726	27	61.4	551	6	ADA17080	Nuclear f	799	27	61.4	771	8	ADS21365	Bacterial	Ad21365
727	27	61.4	551	8	ADF90217	Human NF-	800	27	61.4	773	6	ABU24441	Protein e	Abu24441
728	27	61.4	551	8	ADM83059	Human NF-	801	27	61.4	778	6	ABU23609	Protein e	Abu23609
729	27	61.4	551	9	ADN02411	Human nuc	802	27	61.4	779	3	AAE18787	Protein e	Aae18787
730	27	61.4	551	9	ADV50588	Human nuc	803	27	61.4	780	7	ABM88746	Rice abio	Abm88746
731	27	61.4	558	6	ADA17078	Nuclear f	804	27	61.4	781	4	ABG24696	Novel hum	Abg24696
732	27	61.4	558	6	ADA17079	Nuclear f	805	27	61.4	783	5	ABP69432	Human pol	Abp69432
733	27	61.4	559	6	ADB09366	Alloioococ	806	27	61.4	783	8	ADRO1085	Human old	Adro1085
734	27	61.4	569	6	ADB09368	Alloioococ	807	27	61.4	783	8	ABM80302	PRO polyp	Abm80302
735	27	61.4	574	4	AAM78955	Human pro	808	27	61.4	783	9	ADY18358	Human DNA	Ady18358
736	27	61.4	574	9	ADX98559	Human 5'-	809	27	61.4	784	2	AAW48245	Human pro	Aaw48245
737	27	61.4	574	9	ADY15212	PRO polyp	810	27	61.4	784	2	AAW86350	Human DNA	Aaw86350
738	27	61.4	574	9	ADY19695	PRO polyp	811	27	61.4	784	2	AAW86350	Human DNA	Aaw86350
739	27	61.4	576	4	ABB62943	Drosophil	812	27	61.4	784	2	AAW90069	Human TNF	Aaw90069
740	27	61.4	581	7	ADC97208	E. faeciu	813	27	61.4	784	5	ABG73879	Human TNF	Abg73879
741	27	61.4	583	4	AAU37865	Streptoco	814	27	61.4	784	5	AAE16091	Human tum	Aae16091
742	27	61.4	583	6	ABU02324	S. pneumo	815	27	61.4	784	5	AAE16091	Human DNA	Aae16091
743	27	61.4	583	6	ABP81636	Streptoco	816	27	61.4	784	6	ABU61956	Human Tol	Abu61956
744	27	61.4	583	6	ABU46225	Protein e	817	27	61.4	784	7	ADC28305	Human pro	Adc28305
745	27	61.4	584	6	ABU53081	Intracell	818	27	61.4	784	7	ADU15005	Human Tol	Adu15005
746	27	61.4	588	8	ADS27297	Bacterial	819	27	61.4	784	8	ADN02005	Human inf	Adn02005
747	27	61.4	588	8	ADS26935	Bacterial	820	27	61.4	784	8	ADP56652	Human Tol	Adp56652
748	27	61.4	592	4	AAM79939	Human pro	821	27	61.4	784	8	ADP48593	Human Tol	Adp48593
749	27	61.4	595	8	ADP81120	Protein o	822	27	61.4	784	8	ADP48593	Novel hum	Adp48593
750	27	61.4	612	5	ABB91863	Herbicida	823	27	61.4	784	8	ADQ66397	PRO polyp	Adq66397
751	27	61.4	617	8	ABR41950	Mouse ATP	824	27	61.4	784	8	ADP23787	PRO polyp	Adp23787
752	27	61.4	617	8	ADP23322	PRO polyp	825	27	61.4	784	8	ADQ39727	Human myo	Adq39727
753	27	61.4	617	9	ADM08730	Human pro	826	27	61.4	784	8	ADQ39728	Human myo	Adq39728
754	27	61.4	620	2	AAR32548	Tomato hs	827	27	61.4	784	8	ADU23112	Human Tol	Adu23112

828	27	61.4	784	9	ABE11660	Aeb11660 Human tol	901	27	61.4	1289	2	AAW94674	Aaw94674 Bacteriop
829	27	61.4	787	3	AAE69362	Aay69362 Amino aci	902	27	61.4	1289	7	ADC89665	Adc89665 Bacteriop
830	27	61.4	790	5	ABB90599	Abb90599 Chlamydia	903	27	61.4	1289	8	ADJ12069	Adj12069 Bacteriop
831	27	61.4	793	8	ABM84550	Abm84550 Human dia	904	27	61.4	1289	8	ADJ72082	Adj72082 T4 Gene 3
832	27	61.4	795	2	AAK34896	Aay34896 Chlamydia	905	27	61.4	1297	4	ABB66143	Abb66143 Drosophil
833	27	61.4	797	2	AAW85043	Aaw85043 NFKappaB	906	27	61.4	1341	2	AAAY31945	Aay31945 Plasmodiu
834	27	61.4	797	2	AAW85042	Aaw85042 PKB-green	907	27	61.4	1366	7	ADCS1488	Adc51488 Bacterial
835	27	61.4	797	3	AAAY70782	Aay70782 EGFP-NFka	908	27	61.4	1397	4	ABGI5812	Abg15812 Novel hum
836	27	61.4	797	3	AAAY70783	Aay70783 NFKappaB-	909	27	61.4	1411	2	AAAY31948	Aay31948 Plasmodiu
837	27	61.4	800	4	AAAB65673	Aab65673 Novel pro	910	27	61.4	1417	2	AAAY31947	Aay31947 Plasmodiu
838	27	61.4	800	4	AAAB71957	Aab71957 Human TGF	911	27	61.4	1425	7	AEA90310	Aea90310 Human NOV
839	27	61.4	800	5	ABP43736	Abp43736 Morif zip	912	27	61.4	1430	2	AAAY31949	Aay31949 Plasmodiu
840	27	61.4	800	7	ADC33422	Adc33422 Human MLT	913	27	61.4	1437	7	ADJ69204	Adj69204 Human hea
841	27	61.4	800	7	ADJ69295	Adj69295 Human hea	914	27	61.4	1457	7	ADJ69205	Adj69205 Human hea
842	27	61.4	800	8	ADI29281	Adi29281 Human MAR	915	27	61.4	1457	8	ADJ58460	Adj58460 BAB13458
843	27	61.4	800	8	ADQ96318	Adq96318 T cell ac	916	27	61.4	1458	4	AAU07132	Aau07132 Porcine r
844	27	61.4	800	8	ADQ96320	Adq96320 T cell ac	917	27	61.4	1463	2	AAU29940	Aar29940 Deduced f
845	27	61.4	800	8	ADQ15108	Adq15108 Human can	918	27	61.4	1463	5	ABG86497	ABG86497 PRRS viru
846	27	61.4	802	7	ADC33424	Adc33424 Mouse MLT	919	27	61.4	1799	7	ADH87293	Adh87293 Enterococ
847	27	61.4	805	3	AAAB22940	Aab22940 GFP-NF-ka	920	27	61.4	1922	4	ABB63631	Abb63631 Drosophil
848	27	61.4	805	5	ABG94503	Abg94503 Protease	921	27	61.4	1936	8	ADQ89658	Adq89658 Antagonis
849	27	61.4	809	3	AAAY84881	Aay84881 Amino aci	922	27	61.4	2056	4	ABBS59344	Abbs59344 Drosophil
850	27	61.4	821	8	ADS29598	Ads29598 Bacterial	923	27	61.4	2074	6	ABU20226	Abu20226 Protein e
851	27	61.4	844	9	ADZ80965	Adz80965 Amino aci	924	27	61.4	2228	7	ABR61599	AbR61599 Human gol
852	27	61.4	858	4	AAAY71998	Aay71998 Rat autot	925	27	61.4	2230	6	ABU07445	Abu07445 Protein d
853	27	61.4	858	4	AAAY71986	Aay71986 Rat autot	926	27	61.4	2230	7	ABR61600	AbR61600 Human gol
854	27	61.4	858	4	AAAY71995	Aay71995 Rat autot	927	27	61.4	2250	7	ABR61601	AbR61601 Human gol
855	27	61.4	858	4	AAAY71996	Aay71996 Rat autot	928	27	61.4	2252	7	ABR61602	AbR61602 Human gol
856	27	61.4	858	4	AAAY71999	Aay71999 Rat autot	929	27	61.4	2538	7	ABM88489	Abm88489 Rice abio
857	27	61.4	858	4	AAAY71997	Aay71997 Rat autot	930	27	61.4	2548	7	ADC31246	Adc31246 Human nov
858	27	61.4	858	8	ADY09346	Ady09346 Plant ful	931	27	61.4	2548	7	ABM90354	Abm90354 Rice abio
859	27	61.4	862	5	ABG32516	Abg32516 Rat lysop	932	27	61.4	3427	7	ADJ69818	Adj69818 Human hea
860	27	61.4	864	6	ABRS3354	AbR53354 Protein s	933	27	61.4	3460	5	ABBO5007	Abbo5007 Human ree
861	27	61.4	864	7	ADK63402	Adk63402 Disease t	934	27	61.4	3460	7	ADBE60143	Adbe60143 Human pro
862	27	61.4	864	8	ADT87099	Adt87099 Yeast Str	935	27	61.4	3460	7	ADN95182	Adn95182 Human BEC
863	27	61.4	872	6	ABP72580	Abp72580 Caenorhab	936	27	61.4	3460	8	ADQ20919	Adq20919 Human sof
864	27	61.4	872	6	ABP97917	Abp97917 Amino aci	937	27	61.4	3460	8	ADQ88204	Adq88204 Human 353
865	27	61.4	885	5	AAAY1989	Aay1989 Rat brain	938	27	61.4	3460	9	ADY70357	Ady70357 Human bet
866	27	61.4	885	5	AAU10538	Aau10538 Rat phosp	939	27	61.4	3460	9	ADY70664	Ady70664 Human PTK
867	27	61.4	885	6	ABR41948	AbR41948 Rat phosp	940	27	61.4	3460	9	AEA81155	Aea81155 Human ree
868	27	61.4	895	7	ADM04396	Adm04396 Human pro	941	27	61.4	3461	5	ABBO5008	Abbo5008 Mouse ree
869	27	61.4	901	7	ADG39839	Adg39839 Protein s	942	27	61.4	3461	5	ABBS7065	Abbs7065 Mouse isc
870	27	61.4	907	4	ABUS3073	Abu53073 Intracell	943	27	61.4	3461	7	ADBE60142	Adbe60142 Rat Prote
871	27	61.4	941	4	ABUS3072	Abu53072 Intracell	944	27	61.4	3470	4	ABG25297	Abg25297 Novel hum
872	27	61.4	951	7	ADC46880	Adc46880 Human TA-	945	27	61.4	3859	8	ADH74482	Adh74482 Lelystad
873	27	61.4	957	5	AAE23375	Aae23375 Human int	946	27	61.4	4134	2	AAAY31946	Aay31946 Plasmodiu
874	27	61.4	1002	7	ABO70916	AbO70916 Pseudomon	947	27	61.4	4345	4	ABBS66417	Abbs66417 Drosophil
875	27	61.4	1006	7	ADC31479	Adc31479 Human nov	948	27	61.4	4437	6	ABU11384	Abu11384 Protein e
876	27	61.4	1010	8	ADO84842	Ado84842 E faecali	949	27	61.4	4547	4	ABBS9051	Abbs9051 Drosophil
877	27	61.4	1029	5	ABB91099	Abb91099 Herbicida	950	27	61.4	4889	8	ADN96835	Adn96835 Bugula br
878	27	61.4	1029	6	ADA68655	Ada68655 Arabidops	951	27	61.4	4899	4	ABBS5885	Abbs5885 Drosophil
879	27	61.4	1068	9	ADU06422	Adu06422 Novel bro	952	27	61.4	7201	4	ABB71136	Abb71136 Drosophil
880	27	61.4	1068	2	AAAR43341	Aar43341 p110, 3/2	953	26	61.4	245	7	ADC94821	Adc94821 E. faeciu
881	27	61.4	1068	2	AAAR43342	Aar43342 Human p11	954	26	59.1	9	5	ABJ01523	Abj01523 158P1D7 r
882	27	61.4	1068	5	AAAU0687	Aau0687 Human p11	955	26	59.1	10	5	ABJ01407	Abj01407 158P1D7 r
883	27	61.4	1068	8	ADH68169	Adh68169 PI3K-alpha	956	26	59.1	10	5	ABJ01667	Abj01667 158P1D7 r
884	27	61.4	1068	9	ADU06422	Adu06422 Novel bro	957	26	59.1	10	5	ABJ01703	Abj01703 158P1D7 r
885	27	61.4	1068	8	ADZ00491	Adz00491 p110-beta	958	26	59.1	11	6	ABP71515	Abp71515 Human NF-
886	27	61.4	1163	7	ADG39838	Adg39838 Protein s	959	26	59.1	12	7	ADD24027	Add24027 Breast ca
887	27	61.4	1171	9	AEBA0845	Aeb40845 L. pneumo	960	26	59.1	13	5	AAEI5337	Aae15337 Human chi
888	27	61.4	1183	3	AAAY9699	Aay9699 S. cerevi	961	26	59.1	13	6	ADP71517	Adp71517 Human NF-
889	27	61.4	1207	6	ADA35479	Ada35479 Acinetoba	962	26	59.1	13	7	ADI00457	Adi00457 Chimeric
890	27	61.4	1218	3	AAAB07563	Aab07563 Protein e	963	26	59.1	13	7	ADV52851	Adv52851 Hedgehog
891	27	61.4	1223	8	ADJ48692	Adj48692 Oil-aasoc	964	26	59.1	17	9	ADV52851	Adv52851 Hedgehog
892	27	61.4	1233	3	ABG30304	Abg30304 Novel hum	965	26	59.1	19	7	ADFI4659	Adfi4659 Rheumatoi
893	27	61.4	1237	3	AAAY9699	Aay9699 S. cerevi	966	26	59.1	21	9	ADV52856	Adv52856 Hedgehog
894	27	61.4	1237	6	ABRS2715	AbR52715 Protein s	967	26	59.1	22	2	AAAR61249	Aar61249 Specif
895	27	61.4	1237	7	ADK61936	Adk61936 Disease t	968	26	59.1	22	2	AAAR90209	Aar90209 Anticoupl
896	27	61.4	1269	4	AAAB35150	Aab35150 Bacteriop	969	26	59.1	25	5	ABG62695	Abg62695 Eubacteri
897	27	61.4	1272	7	ADF05447	Adf05447 Bacterial	970	26	59.1	27	9	ADV52855	Adv52855 Hedgehog
898	27	61.4	1273	6	ABU40858	Abu40858 Protein e	971	26	59.1	34	4	ABBI6517	Abbi6517 Human ner
899	27	61.4	1289	2	AAAY97370	Aay97370 Phage T4	972	26	59.1	39	6	ABP71521	Abp71521 Human NF-
900	27	61.4	1289	2	AAAW92354	Aaw92354 Bacteriop	973	26	59.1	40	4	AAOI0453	Aao10453 Human pol

974 26 59.1 43 2 AAW59193 Human Str  
975 26 59.1 43 6 ABP54175 Human lun  
976 26 59.1 53 4 ABB10595 Human pan  
977 26 59.1 53 4 AAM92348 Human dig  
978 26 59.1 53 5 ABB79267 Human pro  
979 26 59.1 53 8 ADS05992 Staphyloc  
980 26 59.1 54 8 ADM01105 Legume le  
981 26 59.1 54 8 ADL95706 Legume le  
982 26 59.1 56 4 AAU14425 Human nov  
983 26 59.1 56 8 ADH80743 Human pol  
984 26 59.1 59 5 ABP32956 Human ORP  
985 26 59.1 60 5 ABG69324 Human CYP  
986 26 59.1 60 5 ABP29151 Streptoco  
987 26 59.1 62 4 ABB17478 Human ner  
988 26 59.1 62 8 AEB86962 Polyketid  
989 26 59.1 62 8 AEB86977 Polyketid  
990 26 59.1 62 8 AEB86774 Polyketid  
991 26 59.1 62 8 AEB86759 Polyketid  
992 26 59.1 64 3 AAB16630 Bacteriop  
993 26 59.1 65 2 AAY12665 Human 5'  
994 26 59.1 65 6 ABU18474 Protein e  
995 26 59.1 67 4 ABB14964 Human ner  
996 26 59.1 67 6 ABU18067 Protein e  
997 26 59.1 76 7 ABO65370 Klebsiell  
998 26 59.1 79 4 AAG75402 Human col  
999 26 59.1 80 7 ABO66333 Klebsiell  
1000 26 59.1 81 4 AAU32132 Novel hum

## ALIGNMENTS

RESULT 1  
ID ABB08362 standard; protein; 9 AA.  
AC ABB08362;  
XX  
XX 07-MAY-2002 (first entry)  
DE Synthetic epitope 2 of human cancer antigen eIF3.  
KW Human; melanoma antigen eukaryotic initiation factor 3; eIF3;  
KW ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;  
KW anti-cancer; vaccine.  
XX Homo sapiens.  
FH Location/Qualifiers  
FT Domain 1 /note= "HLA-2 binding residue"  
FT Domain 2 /note= "HLA-2 binding residue"  
FT Domain 3 .8 /note= "HLA-2 binding residue"  
FT Domain 9 /note= "T-cell receptor (TCR) binding domain"  
FT Domain /note= "HLA-2 binding residue"  
XX WO200192307-A2.  
PN  
XX  
XX 06-DEC-2001.  
XX  
XX 30-MAY-2001; 2001WO-US017456.  
XX  
XX 31-MAY-2000; 2000US-0209391P.  
PR 17-AUG-2000; 2000US-0226258P.  
PR 20-DEC-2000; 2000US-0257008P.  
XX  
XX (GENZ ) GENZYME CORP.  
PA Nicolette CA;  
XX WPI; 2002-139606/18.  
XX  
XX

DR N-PSDB; ABA97213.  
XX New therapeutic compounds useful against human ovarian cancer, for  
PT modulating immune response in a subject, and for generating antibodies  
PT that specifically recognize and bind to these molecules.  
XX Claim 29; Page 59; 68pp; English.  
XX The invention relates to novel therapeutic compounds, that are designed  
CC to enhance binding to MHC molecules and to enhance immunoregulatory  
CC properties relative to their natural counterparts. The activity of the  
CC compounds of the invention may be described as cytostatic and  
CC immunomodulatory. The compounds are useful against human ovarian cancer,  
CC for modulating immune response in a subject, and for generating  
CC antibodies that specifically recognize and bind to these molecules.  
CC Compositions comprising the compounds are useful as components of anti-  
CC cancer vaccines and to expand immune effector cells that are specific for  
CC cells characterized by expression of antigen eIF3 (melanoma antigen  
CC eukaryotic initiation factor). The peptides or polypeptides conjugated to  
CC a detectable agent may be used in diagnostic procedures, such as in the  
CC detection and purification of antibodies, and as immunogens for  
CC production of antibodies. The polynucleotides can be used as primers for  
CC detecting genes or gene transcripts expressed in APC to confirm  
CC transduction of the polynucleotides into host cells. The current sequence  
CC represents synthetic epitope 2 of human cancer antigen eIF3  
XX Sequence 9 AA;  
SQ  
Query Match 100.0%; Score 44; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLQLEFDV 9  
DB 1 FLQLEFDV 9  
RESULT 2  
ABR82214  
ID ABR82214 standard; peptide; 9 AA.  
XX  
XX ABR82214;  
XX 13-OCT-2003 (first entry)  
XX  
XX Human antigen eIF3 derived compound 2.  
XX  
XX Eukaryotic translation initiation factor 3; eIF3; neoplasia; cancer;  
KW cytostatic; gene therapy; human; antigen.  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX WO2003050543-A1.  
XX  
XX 19-JUN-2003.  
XX  
XX 05-DEC-2001; 2001WO-US047997.  
XX  
XX 05-DEC-2001; 2001WO-US047997.  
XX (GENZ ) GENZYME CORP.  
XX Nicolette CA;  
XX  
XX WPI; 2003-532936/50.  
DR N-PSDB; ACC85031.  
XX  
XX Aiding in the diagnosis of a neoplastic condition, useful for treating  
PT cancer and related malignancies comprises determining the amount of  
PT expression of an eIF3 protein in a test sample isolated from the cell or  
PT tissue.  
XX

```

PS Claim 12; Page 30; 77pp; English.
XX
CC The invention relates to aiding in the diagnosis of a neoplastic
CC condition or susceptibility to a neoplastic condition of an animal cell
CC or tissue. The method involves determining the amount of expression of an
CC eukaryotic translation initiation factor 3 (eIF3) protein in a test
CC sample isolated from the cell or tissue, and diagnosing a neoplastic
CC condition or susceptibility to a neoplastic condition based on the amount
CC of expression of the eIF3 protein. The methods, compounds and kits are
CC useful in therapeutics, diagnostic and screening methods for human cancer
CC and related malignancies, e.g. ovarian, breast, lung, colon, prostate,
CC pancreatic or gastrointestinal cancer, or melanoma. Sequences ABR82213-16
CC represent compounds derived from the human antigen eIF3
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FLQLEFDVAV 9
Db 1 FLQLEFDVAV 9
|||||
RESULT 3
ABB08367
ID ABB08367 standard; protein; 352 AA.
XX
AC ABB08367;
XX
XX 07-MAY-2002 (first entry)
XX
XX Human cancer antigen eIF3 variant 2 amino acid sequence.
XX
XX Human; melanoma antigen eukaryotic initiation factor 3; eIF3;
XX ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;
XX anti-cancer; vaccine.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 242 /note= "wild-type Asn is replaced by Phe"
FT Domain 242 /note= "HLA-2 binding residue"
FT Domain 243 /note= "HLA-2 binding residue"
FT Domain 244..249 /note= "T-cell receptor (TCR) binding domain"
FT Misc-difference 246 /note= "wild-type Leu is replaced by Glu"
FT Misc-difference 247 /note= "wild-type Met is replaced by Phe"
FT Misc-difference 249 /note= "wild-type Arg is replaced by Ala"
FT Domain 250 /note= "HLA-2 binding residue"
XX
XX WO200192307-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US017456.
XX
XX 31-MAY-2000; 2000US-0209391P.
XX 17-AUG-2000; 2000US-0226258P.
XX 20-DEC-2000; 2000US-0257008P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Nicolette CA;
XX

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DR WPI; 2002-139606/18.
XX
XX New therapeutic compounds useful against human ovarian cancer, for
XX modulating immune response in a subject, and for generating antibodies
XX that specifically recognize and bind to these molecules.
XX
XX Claim 7; Page; 68pp; English.
XX
XX The invention relates to novel therapeutic compounds, that are designed
XX to enhance binding to MHC molecules and to enhance immunoregulatory
XX properties relative to their natural counterparts. The activity of the
XX compounds of the invention may be described as cytostatic and
XX immunomodulatory. The compounds are useful against human ovarian
XX cancer, for modulating immune response in a subject, and for generating
XX antibodies that specifically recognize and bind to these molecules.
XX Compositions comprising the compounds are useful as components of anti-
XX cancer vaccines and to expand immune effector cells that are specific for
XX cells characterised by expression of antigen eIF3 (melanoma antigen
XX eukaryotic initiation factor). The peptides or polypeptides conjugated to
XX a detectable agent may be used in diagnostic procedures, such as in the
XX detection and purification of antibodies, and as immunogens for
XX detection of antibodies. The polynucleotides can be used as primers for
XX detecting genes or gene transcripts expressed in APC to confirm
XX transduction of the polynucleotides into host cells. The current sequence
XX represents the human cancer antigen eIF3 variant 2 amino acid sequence.
XX Note: This sequence is not present in the specification, but may be
XX created from the sequence of the wild-type human cancer antigen eIF3
XX sequence given in ABB08360
XX
XX Sequence 352 AA;
Query Match 100.0%; Score 44; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FLQLEFDVAV 9
Db 242 FLQLEFDVAV 250
|||||
RESULT 4
AAB62030
ID AAB62030 standard; protein; 1278 AA.
XX
XX AAB62030;
XX
XX 14-MAY-2001 (first entry)
XX
XX Recombinant P. furiosus helicase 7.
XX
XX MCM; minichromosome maintenance protein; archaeal polypeptide; PCNA;
XX RFC-P38; RFC-P55; RPA; CDC6; FEN-1; DUTPase; ligase; helicase dna2; PCR;
XX helicase 7; nucleic acid amplification; polymerase chain reaction.
XX
XX Pyrococcus furiosus.
XX
XX WO200109347-A2.
XX
XX 08-FEB-2001.
XX
XX 28-JUL-2000; 2000WO-US020532.
XX
XX 30-JUL-1999; 99US-0146580P.
XX
XX (STRA-) STRATAGENE.
XX
XX Hogrefe HH, Cline JM, Hansen CJ, Borns MC;
XX
XX WPI; 2001-182959/18.
XX N-PSDB; AAF57034.
XX
XX Composition for improving nucleic acid polymerase reactions, useful e.g.
XX in synthesis or amplification, contains at least one archaeal accessory
XX

```

PT protein.  
 XX Claim 182; Fig 34; 147pp; English.  
 XX  
 CC The invention provides a composition (A) for enhancing nucleic acid  
 CC polymerase reactions that comprises an archaeal MCM (minichromosome  
 CC maintenance protein) and at least one of the archaeal polypeptides (PCNA,  
 CC RFC-P38 or -P55, RFA, CDC6, PEN-1, dUTPase, ligase, helicase dna2, or  
 CC helicases 2-8). (A) And similar compositions containing different  
 CC combinations of accessory proteins, are used to improve performance of  
 CC synthesis, amplification, mutagenizing, labeling and detecting reactions,  
 CC e.g. for gene characterization, cloning, detection of allelic variants,  
 CC diagnosis and screening for disease, particularly where done by  
 CC polymerase chain reaction (PCR). Some of the proteins also stabilize  
 CC duplexes during polymerase reactions or improve exonuclease reactions,  
 CC for example RFA also improves specificity of nucleic acid/protein  
 CC interaction and PCNA improves polymerase-mediated repair processes and  
 CC hybridization and PCNA improves polymerase-mediated repair processes and  
 CC are used for recombinant production of proteins, and fragments of the  
 CC nucleic acid as probes and primers for screening related sequences. The  
 CC accessory proteins increase accuracy and efficiency of polymerase  
 CC reactions, allow use of lower denaturation and extension temperatures  
 CC (possibly isothermal processing), and improve synthesis of long targets.  
 CC The present sequence represents a P. furiosus recombinant helicase 7  
 XX  
 SQ Sequence 1278 AA;

Query Match 84.1%; Score 37; DB 4; Length 1278;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8  
 :|||||  
 DB 650 YLQLEFDA 657

RESULT 5  
 ADB06652  
 ID ADB06652 standard; protein; 282 AA.  
 XX  
 AC ADB06652;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Alloiococcus otitis antigenic protein SEQ ID NO:592.  
 XX  
 KW Alloiococcus otitis; antigenic protein; immunogenic; immunisation;  
 KW gene therapy; Gram-positive bacterium; infection.  
 XX  
 OS Alloiococcus otitis.  
 XX  
 PN WO2003048304-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 25-NOV-2002; 2002WO-US036123.  
 XX  
 XX 29-NOV-2001; 2001US-0333777P.  
 PR 18-NOV-2002; 2002US-0426742P.  
 XX  
 XX (AMHP ) WYETH HOLDINGS CORP.  
 PA  
 XX Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;  
 PI WPI; 2003-505284/47.  
 XX N-PSDB; ADB06651.  
 DR  
 XX New Alloiococcus otitis polynucleotides and polypeptides, useful for  
 PT treating and diagnosing diseases, drug screening assays and monitoring of  
 PT effects during drug clinical trials.  
 XX  
 PS Claim 33; SEQ ID NO 592; 1019pp; English.  
 XX

CC The present invention describes an isolated polynucleotide (I) of  
 CC Alloiococcus otitis genomic DNA, which encodes an antigenic protein.  
 CC Alloiococcus otitis is a Gram-positive bacterium. Also described: (1)  
 CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an  
 CC expression vector comprising the novel isolated polynucleotide (1), its  
 CC complement, degenerate variant or fragment; (3) a genetically engineered  
 CC host cell, transfected, transformed or infected with the vector of (2);  
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
 CC composition comprising the polypeptide, its complement, biological  
 CC equivalent or fragment, or the polynucleotide that is comprised in the  
 CC expression vector; (6) a pharmaceutical composition comprising the  
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
 CC immunizing against Alloiococcus otitis by administering to a host the  
 CC immunogenic composition; (9) detecting and/or identifying Alloiococcus  
 CC otitis in the biological sample; (10) a kit comprising a container  
 CC containing the novel polynucleotide, its degenerate variant or fragment,  
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
 CC genetically engineered host cell under conditions suitable to produce the  
 CC polypeptide from the culture. (I) can be used in gene therapy. The  
 CC polynucleotides, polypeptides, antibodies and compositions of the present  
 CC invention can be used for treating and diagnosing diseases, drug  
 CC screening assays and monitoring of effects during drug clinical trials.  
 CC The polynucleotides are useful for expressing and detecting Alloiococcus  
 CC otitis. The present sequence represents an Alloiococcus otitis  
 CC antigen protein from the present invention.  
 XX  
 SQ Sequence 282 AA;

Query Match 79.5%; Score 35; DB 6; Length 282;  
 Best Local Similarity 77.8%; Pred. No. 87;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDAV 9  
 :|||||  
 DB 184 FLQLEIDSV 192

RESULT 6  
 ADB06654  
 ID ADB06654 standard; protein; 285 AA.  
 XX  
 AC ADB06654;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Alloiococcus otitis antigenic protein SEQ ID NO:594.  
 XX  
 KW Alloiococcus otitis; antigenic protein; immunogenic; immunisation;  
 KW gene therapy; Gram-positive bacterium; infection.  
 XX  
 OS Alloiococcus otitis.  
 XX  
 PN WO2003048304-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 25-NOV-2002; 2002WO-US036123.  
 XX  
 XX 29-NOV-2001; 2001US-0333777P.  
 PR 18-NOV-2002; 2002US-0426742P.  
 XX  
 XX (AMHP ) WYETH HOLDINGS CORP.  
 PA  
 XX Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;  
 PI WPI; 2003-505284/47.  
 XX N-PSDB; ADB06653.  
 DR  
 XX New Alloiococcus otitis polynucleotides and polypeptides, useful for  
 PT treating and diagnosing diseases, drug screening assays and monitoring of  
 PT effects during drug clinical trials.  
 XX

PS Claim 33; SEQ ID NO 594; 1019pp; English.

XX The present invention describes an isolated polynucleotide (I) of  
 CC Alloicoccus otitidis genomic DNA, which encodes an antigenic protein.  
 CC Alloicoccus otitidis is a Gram-positive bacterium. Also described: (1)  
 CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
 CC expression vector comprising the novel isolated polynucleotide (I), its  
 CC complement, degenerate variant or fragment; (3) a genetically engineered  
 CC host cell, transfected, transformed or infected with the vector of (2);  
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
 CC composition comprising the polypeptide, its complement, biological  
 CC equivalent or fragment, or the polynucleotide that is comprised in the  
 CC expression vector; (6) a pharmaceutical composition comprising the  
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
 CC immunising against Alloicoccus otitidis by administering to a host the  
 CC immunogenic composition; (9) detecting and/or identifying Alloicoccus  
 CC otitidis in the biological sample; (10) a kit comprising a container  
 CC containing the novel polynucleotide, its degenerate variant or fragment,  
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
 CC genetically engineered host cell under conditions suitable to produce the  
 CC polypeptide from the culture. (I) can be used in gene therapy. The  
 CC polynucleotides, polypeptides, antibodies and compositions of the present  
 CC invention can be used for treating and diagnosing diseases, drug  
 CC screening assays and monitoring for effects during drug clinical trials.  
 CC The polynucleotides are useful for expressing and detecting Alloicoccus  
 CC otitidis. The present sequence represents an Alloicoccus otitidis  
 CC antigen protein from the present invention.

XX SQ Sequence 285 AA;

Query Match 79.5%; Score 35; DB 6; Length 285;  
 Best Local Similarity 77.8%; Pred. No. 88;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLEFDVAV 9  
 |||||:|  
 Db 187 FLQLEIDSV 195

RESULT 7  
 ADN26780  
 ID ADN26780 standard; protein; 654 AA.  
 XX  
 AC ADN26780;  
 DT 02-DEC-2004 (first entry)  
 XX Bacterial polypeptide #9433.  
 DE  
 KW Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2002; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX WPI; 2004-061375/06.  
 XX  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 XX for expression of a polynucleotide encoding a polypeptide from a  
 XX microbial source, useful for producing plants with improved properties.  
 XX  
 XX Claim 1; SEQ ID NO 9433; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 654 AA;

Query Match 79.5%; Score 35; DB 8; Length 654;  
 Best Local Similarity 77.8%; Pred. No. 2.1e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLEFDVAV 9  
 |||||:|  
 Db 89 FLQLEHDAV 97

RESULT 8  
 ADS28720  
 ID ADS28720 standard; protein; 680 AA.

XX

AC ADS28720;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #17753.

XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX

PR 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 17753; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
XX Sequence 680 AA;  
SQ  
Query Match 79.5%; Score 35; DB 8; Length 680;  
Best Local Similarity 77.8%; Pred. NO. 2.2e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLQLEPDAV 9  
DB 114 FLQIEHDAV 122  
RESULT 9  
ABB59769  
ID ABB59769 standard; protein; 1612 AA.  
AC  
XX ABB59769;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Drosophila melanogaster polypeptide SEQ ID NO 6099.  
DE  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
KW  
XX Drosophila melanogaster.  
OS  
XX WO200171042-A2.  
FN  
XX 27-SEP-2001.  
PD  
XX

PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
DR N-PSDB; ABL03872.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX  
PS Disclosure; SEQ ID NO 6099; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1612 AA;  
Query Match 79.5%; Score 35; DB 4; Length 1612;  
Best Local Similarity 66.7%; Pred. No. 5.6e+02;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLQLEPDAV 9  
DB 254 YLELEFDAL 262  
RESULT 10  
ADR09173  
ID ADR09173 standard; protein; 254 AA.  
XX  
XX ADR09173;  
XX  
XX 04-NOV-2004 (first entry)  
XX  
XX Human protein useful for treating neurological disease Seq 2679.  
XX  
XX human; oligo-capping method; diagnostic marker; gene therapy;  
KW osteoporosis; neurological disease; Alzheimer's disease;  
KW Parkinson's disease; dementia; short memory; cancer;  
KW sense or motor function; emotional reaction; fear response; panic;  
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
KW tranquiliser.  
XX  
XX Homo sapiens.  
OS  
XX EP1447413-A2.  
PN  
XX 18-AUG-2004.  
PD  
XX 12-FEB-2004; 2004EP-00003145.  
PF  
XX 14-FEB-2003; 2003JP-00102207.  
PR 09-MAY-2003; 2003JP-00131452.  
XX  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
PA  
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
XX



DR WPI; 2004-583265/57.  
 XX N-PSDB; ADR07217.  
 PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,  
 PT Alzheimer's disease, Parkinson's disease, dementia and various cancers.  
 XX  
 PS Claim 1; SEQ ID NO 2679; 2686pp; English.  
 XX  
 CC This invention relates to novel, isolated full length human cDNA  
 CC molecules and the encoded proteins thereof. Specifically, it refers to  
 CC cDNA clones obtained by an oligo-capping method, where none of these  
 CC clones are identical to any known human mRNAs. The present invention  
 CC describes an immunoassay to identify agonists and antagonists, as well as  
 CC antibodies, antisense molecules and siRNAs that can all be used to bind  
 CC to and modulate expression of the cDNA molecules. As such, these  
 CC molecules are useful for diagnostic markers or therapeutic targets for  
 CC the various diseases or morbid states. In particular, they are useful in  
 CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
 CC disease, Parkinson's disease, dementia, short memory and various cancers,  
 CC as well as for maintaining equilibrium of sense or motor function, and  
 CC for treating emotional reaction, fear response and panic. Accordingly,  
 CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,  
 CC cytotatic and tranquiliser activities. This polypeptide is a protein  
 CC encoded by a full length human cDNA sequence of the invention. NOTE: This  
 CC sequence is not given in the sequence listing of the specification but  
 CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-  
 CC office.  
 XX  
 SQ Sequence 254 AA;  
 Query Match 77.3%; Score 34; DB 8; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LQLEFDA 8  
 DB 183 LQLEFDA 189  
 RESULT 11  
 AEW74402  
 ID AEW74402 standard; protein; 217 AA.  
 AC AEW74402;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE DNA clone originating in barley containing SNP sequence #812.  
 XX  
 KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.  
 XX  
 OS Hordeum vulgare.  
 XX  
 FN WO2003057877-A1.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 16-DEC-2002; 2002WO-IB005403.  
 XX  
 PR 20-DEC-2001; 2001JP-00387059.  
 PR 20-DEC-2001; 2001JP-00387131.  
 PR 20-DEC-2001; 2001JP-00403299.  
 PR 20-DEC-2001; 2001JP-00403300.  
 PR 27-SEP-2002; 2002JP-00327515.  
 XX  
 PA (UYNI-) UNIV JAPAN OKAYAMA.  
 XX  
 PI Sato K, Takeda K, Kohara Y;  
 XX  
 DR WPI; 2003-587127/55.  
 XX  
 PT Single nucleotide polymorphism sites in barley varieties and DNA  
 PT sequences containing them for analysis and identification of barley

PT varieties and production of barley transformants with desired  
 XX characteristics.  
 PT  
 PS Disclosure; SEQ ID XX; 284pp; Japanese.  
 XX  
 CC The present invention relates to oligonucleotide clones originating in  
 CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms  
 CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley  
 CC varieties, identification of particular varieties and genotype-phenotype  
 CC analysis, isolation of specific genes and creation of new varieties by  
 CC transformation of barley varieties with them and production of new barley  
 CC varieties with desired properties. The present sequence represents an  
 CC oligonucleotide clone sequence featured in the specification. The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published-pct-sequences  
 XX  
 SQ Sequence 217 AA;  
 Query Match 75.0%; Score 33; DB 7; Length 217;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLEFDV 9  
 DB 44 FLQLEFNAV 52  
 RESULT 12  
 ADP98863  
 ID ADP98863 standard; protein; 374 AA.  
 XX  
 AC ADP98863;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE C. albicans specific gene, orf6.4105, protein sequence.  
 XX  
 KW Diploid fungal cell; allele; Gene disruption cassette;  
 KW promoter replacement fragment; antifungal; fungicide; gene therapy;  
 KW infection; Candida albicans.  
 XX  
 OS Candida albicans.  
 XX  
 PN WO2004056965-A2.  
 XX  
 PD 08-JUL-2004.  
 XX  
 PF 19-DEC-2003; 2003WO-US040618.  
 XX  
 PR 19-DEC-2002; 2002US-0434832P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 PA (ELIT-) ELITRA CANADA LTD.  
 XX  
 PI Roemer T, Jiang B, Boone C, Bussey H;  
 XX  
 DR WPI; 2004-500296/47.  
 DR N-PSDB; ADP988553.  
 XX  
 CC Constructing a strain of diploid fungal cells in which both alleles of a  
 CC gene are modified comprises modifying the alleles of a gene in the fungal  
 CC cells by recombination using a gene disruption cassette and a promoter  
 CC replacement fragment.  
 PT  
 PS Claim 44; SEQ ID NO 7038; 163pp; English.  
 XX  
 CC The invention relates to a novel method for constructing a strain of  
 CC diploid fungal cells in which both alleles of a gene are modified. The  
 CC method comprises modifying the alleles of a gene in diploid fungal cells  
 CC by recombination using a gene disruption cassette and a promoter  
 CC replacement fragment. The invention further comprises: assembling a  
 CC collection of diploid fungal cells each of which comprises modified

alleles of a different gene; a strain of diploid fungal cells comprising modified alleles of a gene, where the first allele of the gene is inactivated by a gene disruption cassette comprising a nucleotide sequence encoding an expressible selectable marker; and the expression of the second allele of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second allele of the gene, and where the gene encodes the polypeptide mentioned above; a collection of diploid fungal strains comprising the diploid strains cited above, where substantially all the different genes that encode the above amino acid sequences are modified and are present in different diploid strains in the collection; a nucleic acid molecule microarray comprising nucleic acid molecules, where each nucleic acid molecule comprises a nucleotide sequence that is hybridizable to a target nucleotide sequence comprising any of the 310 nucleotide sequences listed in the specification (ADP98516-ADP98825); identifying a gene that is essential to the survival or growth of a fungus, that contributes to the virulence and/or pathogenicity of a fungus, or that contributes to the resistance of a diploid fungus to an antifungal agent; identifying an antifungal agent that inhibits the growth of a diploid fungus, or a therapeutic agent for treatment of a mammalian disease; correlating changes in the levels of proteins or gene transcripts with the inhibition of growth or proliferation of a diploid fungal cell; a purified or isolated nucleic acid molecule comprising a nucleotide sequence encoding a gene product required for proliferation of *Candida albicans*, where the gene product consists of any of the above-mentioned amino acid sequences; a vector comprising a promoter operably linked to the nucleic acid molecule cited above; a host cell containing the vector; a purified or isolated polypeptide comprising any of the 61 amino acid sequences given in the specification (ADP96718-ADP96778); a fusion protein comprising a fragment of a first polypeptide fused to a second polypeptide, the fragment consisting of at least 6 consecutive residues of any of ADP98826-ADP99135; producing a polypeptide; identifying a compound which modulates the activity of a gene product encoded by a nucleic acid comprising any of ADP98516-ADP98825; eliciting an immune response in an animal; a strain of *Candida albicans*, where a first allele of a gene comprising any of ADP98516-ADP98825 is inactive and a second allele of the gene is under the control of a heterologous promoter; identifying a compound or binding partner that binds to the polypeptide comprising any of ADP98826-ADP99135, or its fragment; identifying a compound having the ability to inhibit growth or proliferation of *Candida albicans*; inhibiting growth or proliferation of *Candida albicans* cells; manufacturing an antimycotic compound; treating an infection of a subject by *Candida albicans*; preventing or containing contamination of an object by *Candida albicans*, or for preventing or inhibiting formation of a biofilm on a surface of a biofilm comprising *Candida albicans*; a pharmaceutical composition comprising a therapeutic amount of an agent which reduces the activity or level of a gene product encoded by a nucleic acid comprising any of ADP98516-ADP98825 in a pharmaceutical carrier; an antibody preparation which binds the polypeptide; methods for evaluating a compound against a target gene product encoded by any of ADP98516-ADP98825; identifying an antimycotic compound; a computer or a computer readable medium that comprises at least one of the nucleotide sequences mentioned in the specification or at least one amino acid sequence selected from ADP98826-ADP99135; a method assisted by a computer for identifying a putatively essential gene of a fungus; and a protein array comprising proteins, where at least one protein comprises an amino acid sequence or a portion of an amino acid sequence selected from ADP98516-ADP98825. The novel methods and compositions have fungicidal activity. The compositions may be used in gene therapy. The composition and methods are useful for drug screening purposes or for diagnosing, preventing or treating infections associated with *Candida albicans*. These may also be used for constructing strains useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This sequence represents the protein of a *Candida albicans* fungal specific gene of the invention. CC NOTE: This sequence was downloaded from an electronic sequence listing provided on the WIPO website.

XX Sequence 374 AA;

Query Match 75.0%; Score 33; DB 8; Length 374;  
Best Local Similarity 85.7%; Pred. No. 3e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 3 QLEFDAY 9  
| | | | |  
DB 293 QLEFDAY 299  
RESULT 13  
ADS23723  
ID ADS23723 standard; protein; 388 AA.  
XX AC ADS23723;  
XX DT 02-DEC-2004 (first entry)  
XX DE Bacterial polypeptide #12756.  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX OS Bacteria.  
XX FN US2003233675-A1.  
XX PD 18-DEC-2003.  
XX PF 20-FEB-2003; 2003US-00369493.  
XX PR 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX Claim 1; SEQ ID NO 12756; 122pp; English.  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 388 AA;

Query Match 75.0%; Score 33; DB 8; Length 388;

Best Local Similarity 87.5%; Pred. No. 3.1e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLNFDVAV 9

|||||

Db 54 LQLNFDVAV 61

RESULT 14

ABP06827

ID ABP06827 standard; protein; 72 AA.

XX AC ABP06827;

XX DT 24-JUN-2002 (first entry)

XX DE Human ORFX protein sequence SEQ ID NO:13636.

XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis.

XX OS Homo sapiens.

XX WO200192523-A2.

XX PD 06-DEC-2001.

XX PF 29-MAY-2001; 2001WO-US010836.

XX PR 30-MAY-2000; 2000US-0206132P.

XX PR 29-AUG-2000; 2000US-0228716P.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach MD;

XX DR WPI; 2002-106308/14.

XX DR N-PSDB; ABN22579.

XX PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders.

XX PS Disclosure; SEQ ID NO 13636; 1037pp; English.

XX CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host

CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage. N.B. The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 72 AA;

Query Match 72.7%; Score 32; DB 5; Length 72;

Best Local Similarity 66.7%; Pred. No. 83;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLDFDAV 9

|||||

Db 54 FLQLDWDVV 62

RESULT 15

ABU70578

ID ABU70578 standard; protein; 173 AA.

XX AC ABU70578;

XX DT 10-JUN-2003 (first entry)

XX DE Human adipocyte Selected Interacting domain, SID, #209.

XX KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;  
 KW antidiabetic; protein-protein interaction; diabetes;  
 KW yeast 2-hybrid assay; metabolic disorder; obesity.

XX OS Homo sapiens.

XX WO200286122-A2.

XX PD 31-OCT-2002.

XX PF 14-MAR-2002; 2002WO-EP003768.

XX PR 14-MAR-2001; 2001US-0275734P.

XX PA (HYBR-) HYBRIGENICS.

XX PI Legrain P, Daviet L;

XX DR WPI; 2003-103412/09.

XX DR N-PSDB; ACA57122.

XX PT New complex between two interacting proteins in adipocyte cells, useful  
 PT for identifying selected interacting domains that modulate protein  
 PT interactions, or for preventing or treating metabolic disorders such as  
 PT obesity or diabetes.

XX PS Claim 6; Page 175; 382pp; English.

XX CC The invention relates to a complex between two interacting proteins in  
 CC adipocyte cells, given in the specification. The proteins are identified  
 CC by selecting a bait protein from a known adipocyte marker and then  
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by  
 CC members of an adipocyte cDNA library. The proteins are designated SID  
 CC (RTM) (selected interacting domains) proteins. Also included are a  
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a  
 CC recombinant host cell expressing at least one of the interacting  
 CC polypeptides of the complex, selecting a modulating compound in adipocyte  
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid  
 CC sequences given in the specification (including its fragment or variant),  
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences  
 CC given in the specification (including its fragment or variant), a vector  
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell  
 CC comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.  
CC The complex, polypeptides, polynucleotides and compounds are useful for  
CC preventing or treating metabolic disorders such as obesity or diabetes.  
CC The polynucleotides are useful as probes or primers. the complex is  
CC particularly useful for identifying selected interacting domains (SID  
CC (RTM)) for screening drugs that modulate the protein interaction, thus  
CC exhibiting the therapeutic effect. The present sequence represents a SID  
CC (prey) protein of the invention  
XX  
SQ Sequence 173 AA;  
  
Query Match 72.7%; Score 32; DB 6; Length 173;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FLQLKPD 7  
|||:|  
Db 141 FLQLKPD 147  
  
RESULT 16  
ABU21843  
ID ABU21843 standard; protein; 225 AA.  
XX AC ABU21843;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #7370.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Burkholderia fungorum.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR N-PSDB; ACA25713.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
XX PT for homologous nucleic acids required for cellular proliferation to  
XX PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 49767; 1766pp; English.  
XX CC The invention relates to an isolated nucleic acid comprising any one of  
XX CC the 6213 antisense sequences given in the specification where expression  
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid  
XX CC encoding a polypeptide whose expression is inhibited by the antisense  
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX CC polypeptide or its fragment whose expression is inhibited by the  
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding  
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX CC proliferation or the activity of a gene in an operon required for  
XX CC proliferation; (7) identifying a compound that influences the activity of  
XX CC the gene product or that has an activity against a biological pathway  
XX CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 225 AA;  
  
Query Match 72.7%; Score 32; DB 6; Length 225;  
Best Local Similarity 66.7%; Pred. No. 2.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 FLQLEFPAV 9  
:|:|:|:|  
Db 111 YLKLEFDPV 119  
  
RESULT 17  
ABU24075  
ID ABU24075 standard; protein; 274 AA.  
XX AC ABU24075;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #9602.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Clostridium acetobutylicum.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR N-PSDB; ACA27945.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
XX PT for homologous nucleic acids required for cellular proliferation to  
XX PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 51999; 1766pp; English.  
XX CC The invention relates to an isolated nucleic acid comprising any one of  
XX CC the 6213 antisense sequences given in the specification where expression  
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 274 AA;

Query Match 72.7%; Score 32; DB 6; Length 274;  
 Best Local Similarity 55.6%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLEFPAV 9  
 Db 205 FLKLDPDGI 213  
 |||:|:|:

RESULT 18  
 ADD27919  
 ID ADD27919 standard; protein; 415 AA.

AC ADD27919;

DT 15-JAN-2004 (first entry)

XX Human PCOX-1a protein SEQ ID NO:5.

KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
 KW COX-1 variant protein; genetic disease; tissue typing;  
 KW forensic identification; human; PCOX-1a.

XX Homo sapiens.

XX WO2003029411-A2.

XX 10-APR-2003.

XX 28-SEP-2002; 2002WO-US030947.

XX 28-SEP-2001; 2001US-0326133P.

PR 15-APR-2002; 2002US-0373225P.

PR 16-APR-2002; 2002US-0373661P.

XX 16-SEP-2002; 2002US-0411575P.

XX (UYUO ) UNIV BRIGHAM YOUNG.

XX Simmons D, Chandrasekharan VN;

XX WPI; 2003-421222/39.

DR N-PSDB; ADD27918.

XX

PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
 PT encoding the polypeptide, useful for identifying a compound that binds to  
 PT and modulates the activity of COX-1 variant polypeptide.

XX Claim 18; SEQ ID NO 5; 150pp; English.

XX The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
 CC variant polypeptide (I). (I) is useful for identifying a compound which  
 CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
 CC used for mapping their respective genes on a chromosome, and so locating  
 CC gene regions associated with genetic disease, identifying an individual  
 CC from a minute biological sample (tissue typing), and to aid in forensic  
 CC identification of a biological sample. The present sequence represents  
 CC PCOX-1a, which is used in the exemplification of the present invention.

SQ Sequence 415 AA;

Query Match 72.7%; Score 32; DB 7; Length 415;  
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEED 7  
 Db 170 FLQLKFD 176  
 |||:|:|:

RESULT 19

ABO78318

ID ABO78318 standard; protein; 419 AA.

XX ABO78318;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #10493.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD11889.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 27064; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
 CC production of *P. aeruginosa*-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of *P. aeruginosa*-caused

CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences AB067826-  
 CC AB04396 represent P. aeruginosa polypeptides of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html

XX Sequence 419 AA;

SQ Query Match 72.7%; Score 32; DB 7; Length 419;  
 Best Local Similarity 75.0%; Pred. No. 5.4e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLERDAV 9

Db 226 LQVEFDAL 233

RESULT 20

ID ADZ59939 standard; protein; 440 AA.

AC ADZ59939;

XX 30-JUN-2005 (first entry)

XX Human COX-1 variant ALT-2 SEQ ID NO 4.

XX analgesic; antipyretic; cardiovascular-gen.; anticoagulant;  
 KW antiarteriosclerotic; thrombolytic; vasotropic; antiinflammatory;  
 KW ophthalmological; antirheumatic; antiarthritic; osteopathic; antigout;  
 KW protein purification; pain; neurological disease; fever;  
 KW temperature disorder; cardiovascular disease; atherosclerosis;  
 KW metabolic disorder; thrombosis; hematological disease; restenosis;  
 KW vasculitis; inflammation; ocular disease; glaucoma; hypotensive;  
 KW ocular hypertension; uveitis; antiallergic; allergic conjunctivitis;  
 KW musculoskeletal disease; rheumatoid arthritis; ankylosing spondylitis;  
 KW osteoarthritis; bursitis; gout; splice variant; cyclooxygenase 1; COX-1;  
 KW ALT-2; enzyme; splice variant.

XX Homo sapiens.

XX WO2005035713-A2.

XX 21-APR-2005.

XX 20-AUG-2004; 2004WO-US027105.

XX 15-SEP-2003; 2003US-00663377.

XX (ALLR ) ALLERGAN INC.

XX Liang Y, Woodward DF;

XX WPI; 2005-296270/30.

XX N-PSDB; ADZ59938.

XX New isolated cyclooxygenase-1 (COX-1) polypeptide or variants, useful for  
 PT treating or preventing, e.g. pain, fever, atherosclerosis, thrombosis,  
 PT restenosis, glaucoma, allergic conjunctivitis, rheumatoid arthritis, or  
 PT osteoarthritis.

XX Claim 3; SEQ ID NO 4; 129pp; English.

XX The invention describes an isolated COX-1 polypeptide. Also described  
 CC are: a COX-1 variant binding, agent, which binds an amino acid sequence  
 CC selected from SEQ ID NO. 14, 16, or 18, or its epitope; a cell comprising  
 CC the exogenously expressed polypeptide above; a method for identifying a  
 CC compound that modulates a COX-1 variant; a method for identifying a  
 CC compound that specifically binds to a COX-1 variant; a method for  
 CC identifying a compound that differentially modulates a COX-1 variant; a  
 CC method for identifying a compound that differentially binds to a COX-1  
 CC variant; an isolated nucleic acid molecule comprising: a nucleotide

CC sequence that encodes a polypeptide comprising an amino acid sequence  
 CC having at least 50% amino acid identity with SEQ ID NO. 10, or an amino  
 CC acid sequence selected from SEQ ID NO. 20, 22, or 24, or its conservative  
 CC variant; a nucleotide sequence that encodes an amino acid sequence  
 CC selected from SEQ ID NO. 2, 4, 6, or 8; or a nucleotide sequence selected  
 CC from 4 fully defined 1818-2280 bp sequences (SEQ ID NO. 1, 3, 5, or 7)  
 CC given in the specification; a vector comprising the isolated nucleic acid  
 CC molecule above; and a host cell comprising the vector above. The  
 CC polypeptides are useful for treating or preventing diseases or conditions  
 CC associated with COX-1 or COX-1 variant, including pain, fever,  
 CC cardiovascular disorder (e.g. atherosclerosis, thrombosis, restenosis, or  
 CC vasculitis), ocular disorder (e.g. glaucoma, ocular hypertension,  
 CC uveitis, allergic conjunctivitis, or related disorders), or inflammatory  
 CC disorders (e.g. rheumatoid arthritis, ankylosing spondylitis,  
 CC osteoarthritis, bursitis, tendinitis, or gout). The methods are useful  
 CC for designing drugs that bind to or modulate a wild-type COX-1. Compounds  
 CC identified can be used for preventing or reducing the severity of any of  
 CC a variety of conditions where modulation of the COX-1 enzyme or a COX-1  
 CC variant is beneficial. This is the amino acid sequence of human COX-1  
 CC variant ALT-2.

XX SQ Sequence 440 AA;

Query Match 72.7%; Score 32; DB 9; Length 440;

Best Local Similarity 85.7%; Pred. No. 5.7e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLRFD 7

Db 196 FLQLRFD 202

RESULT 21

ADW72143

ID ADW72143 standard; protein; 489 AA.

XX AC ADW72143;

XX 07-APR-2005 (first entry)

XX Human COX1 protein as biomarker for colorectal cancer.

XX genetic marker; tumor marker; diagnosis; prognosis; colorectal tumor.

XX Homo sapiens.

XX US2005014165-A1.

XX 20-JAN-2005.

XX 22-OCT-2003; 2003US-00690880.

XX 18-JUL-2003; 2003US-0488660P.

XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.

XX Lee NM, Chen LC;

XX WPI; 2005-080950/09.

XX N-PSDB; ADW72121.

XX REFSEQ; XP\_044882.

XX New biomarker panel for colorectal cancer and colorectal polyps, useful  
 PT for managing patient care and in discovering therapeutic interventions of  
 PT colorectal cancer and colorectal polyps.

XX Claim 42; SEQ ID NO 41; 80pp; English.

XX The invention relates to a panel of biomarkers, comprising fully defined  
 CC nucleotide and amino acid sequences, for colorectal cancer and colorectal  
 CC polyps. The specification also claims a method of measuring expression  
 CC levels of the polynucleotides or polypeptides from the biomarkers for  
 CC colorectal cancer and colorectal polyps; and a kit for the measurement.

CC The panel is useful for managing patient care in colorectal cancer and  
 CC colorectal polyps, where management of patient care includes one or more  
 CC of risk assessment, early diagnosis, establishing prognosis, monitoring  
 CC patient treatment, and detecting relapse, and is useful in discovering  
 CC therapeutic intervention of colorectal cancer and colorectal polyps. This  
 CC sequence corresponds to a protein biomarker used in the method of the  
 CC invention.

XX SQ Sequence 489 AA;

Query Match 72.7%; Score 32; DB 9; Length 489;  
 Best Local Similarity 85.7%; Pred. No. 6.4e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
 ||||:|  
 Db 246 FLQLKPD 252

RESULT 22  
 ADD12559  
 ID ADD12559 standard; protein; 514 AA.

XX AC ADD12559;

XX DT 01-JAN-2004 (first entry)

XX DE Human ENZM-19 protein SEQ ID NO:19.

XX KW human; enzyme; ENZM; cytostatic; antiarteriosclerotic; anti-HIV;  
 KW anti-allergic; cerebroprotective; antiparkinsonian; anticonvulsant;  
 KW nootropic; neuroprotective; antiinflammatory; ophthalmological;  
 KW antithyroid; antiarthritic; antibacterial; virucide; protozoacide;  
 KW antiparasitic; fungicide; anorectic; cardiant; hypotensive;  
 KW antiinfertility; hepatotropic; gene therapy; autoimmune disorder;  
 KW inflammatory disorder; AIDS; allergy; atopic dermatitis; arthritis;  
 KW thyroiditis; infection; metabolic disorder; obesity;  
 KW reproductive disorder; infertility; neurological disorder;  
 KW Parkinson's disease; Alzheimer's disease; stroke; epilepsy;  
 KW cardiovascular disorder; myocardial infarction; hypertension;  
 KW eye disorder; cell proliferative disease; cancer; atherosclerosis;  
 KW hepatitis.

XX OS Homo sapiens.

XX PN WO2003072729-A2.

XX PD 04-SEP-2003.

XX PF 21-FEB-2003; 2003WO-US0005478.

XX PR 22-FEB-2002; 2002US-0359513P.

XX PR 19-MAR-2002; 2002US-0365795P.

XX XX (INCY-) INCYTE GENOMICS INC.

XX PI Sprague WW, Kable AE, Lee S, Griffin JA, Becha SD, Lee EA;

PI Hafalia AJA, Khare R, Emerling BM, Marquis JP, Ramkumar J;

PI Elliott VS, Richardson TW, Baughn MR, Jin P, Chien D, Hawkins PR;

PI Wilson AD, Chawla NK, Tran UK, Lee SY, Zebbarjadian Y, Jiang X;

PI Jackson AA, Bhatia UK, Burrill JD, Blake JJ, Ho A, Zheng W;

XX WPI; 2003-731608/69.

XX DR N-PSDB; ADD12616.

XX XX New human enzymes and polynucleotides, useful for diagnosing, preventing  
 PT or treating diseases or conditions associated with aberrant enzyme  
 PT expression, e.g. cancer, hepatitis, AIDS, atherosclerosis, obesity,  
 PT infection or stroke.

XX PS Claim 1; SEQ ID NO 19; 426pp; English.

XX XX The present sequence represents a human enzyme designated ENZM-19. Human

CC enzymes of the present invention have cytostatic, antiarteriosclerotic,  
 CC anti-HIV, anti-allergic, cerebroprotective, antiparkinsonian,  
 CC anticonvulsant, nootropic, neuroprotective, antiinflammatory,  
 CC ophthalmological, antithyroid, antiarthritic, antibacterial, virucide,  
 CC protozoacide, antiparasitic, fungicide, anorectic, cardiant, hypotensive,  
 CC antiinfertility and hepatotropic activities, and can be used in gene  
 CC therapy. The human enzymes and polynucleotides encoding them can be used  
 CC in diagnosing, preventing or treating diseases or conditions associated  
 CC with the decreased expression or overexpression of the enzymes, such as  
 CC autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis,  
 CC arthritis or thyroiditis), infections (e.g. bacterial, viral, parasitic,  
 CC protozoal or fungal), metabolic disorders (e.g. obesity), reproductive  
 CC disorders (e.g. infertility), neurological disorders (Parkinson's  
 CC disease, Alzheimer's disease, stroke, epilepsy), cardiovascular disorders  
 CC (e.g. myocardial infarction or hypertension), eye disorders, or cell  
 CC proliferative diseases (e.g. cancer, atherosclerosis, hepatitis). They  
 CC are also useful in assessing the effects of exogenous compounds on the  
 CC expression of nucleic acid and amino acid sequences of the enzymes.

XX SQ Sequence 514 AA;

Query Match 72.7%; Score 32; DB 7; Length 514;  
 Best Local Similarity 85.7%; Pred. No. 6.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
 ||||:|

Db 307 FLQLKPD 313

RESULT 23  
 ADZ59941  
 ID ADZ59941 standard; protein; 537 AA.

XX AC ADZ59941;

XX DT 30-JUN-2005 (first entry)

XX DE Human COX-1 variant ALT-3 SEQ ID NO 6.

XX KW analgesic; antipyretic; cardiovascular-gen.; anticoagulant;  
 KW antiarteriosclerotic; thrombolytic; vasotropic; antiinflammatory;  
 KW ophthalmological; antirheumatic; antiarthritic; osteopathic; antigout;  
 KW protein purification; pain; neurological disease; fever;  
 KW temperature disorder; cardiovascular disease; atherosclerosis;  
 KW metabolic disorder; thrombosis; hematological disease; restenosis;  
 KW vasculitis; inflammation; ocular disease; glaucoma; hypotensive;  
 KW ocular hypertension; uveitis; anti-allergic; allergic conjunctivitis;  
 KW musculoskeletal disease; rheumatoid arthritis; ankylosing spondylitis;  
 KW osteoarthritis; bursitis; gout; splice variant; cyclooxygenase 1; COX-1;  
 KW ALT-3; enzyme; splice variant.

XX OS Homo sapiens.

XX PN WO2005035713-A2.

XX PD 21-APR-2005.

XX PF 20-AUG-2004; 2004WO-US027105.

XX PR 15-SEP-2003; 2003US-00663377.

XX XX (ALLR ) ALLERGAN INC.

XX PI Liang Y, Woodward DF;

XX WPI; 2005-296270/30.

XX DR N-PSDB; ADZ59940.

XX XX New isolated cyclooxygenase-1 (COX-1) polypeptide or variants, useful for  
 PT treating or preventing, e.g. pain, fever, atherosclerosis, thrombosis,  
 PT restenosis, glaucoma, allergic conjunctivitis, rheumatoid arthritis, or  
 PT osteoarthritis.

XX PS Claim 3; SEQ ID NO 6; 129pp; English.

XX CC The invention describes an isolated COX-1 polypeptide. Also described

CC are: a COX-1 variant binding, agent, which binds an amino acid sequence

CC selected from SEQ ID NO. 14, 16, or 18, or its epitope; a cell comprising

CC the exogenously expressed polypeptide above; a method for identifying a

CC compound that modulates a COX-1 variant; a method for identifying a

CC compound that specifically binds to a COX-1 variant; a method for

CC identifying a compound that differentially modulates a COX-1 variant; a

CC method for identifying a compound that differentially binds to a COX-1

CC variant; an isolated nucleic acid molecule comprising: a nucleotide

CC sequence that encodes a polypeptide comprising an amino acid sequence

CC having at least 50% amino acid identity with SEQ ID NO. 10, or an amino

CC acid sequence selected from SEQ ID NO. 20, 22, or 24, or its conservative

CC variant; a nucleotide sequence that encodes an amino acid sequence

CC selected from SEQ ID NO. 2, 4, 6, or 8; or a nucleotide sequence selected

CC from 4 fully defined 1818-2280 bp sequences (SEQ ID NO. 1, 3, 5, or 7)

CC given in the specification; a vector comprising the isolated nucleic acid

CC molecule above; and a host cell comprising the vector above. The

CC polypeptides are useful for treating or preventing diseases or conditions

CC associated with COX-1 or COX-1 variant, including pain, fever,

CC cardiovascular disorder (e.g. atherosclerosis, thrombosis, restenosis, or

CC vasculitis), ocular disorder (e.g. glaucoma, ocular hypertension,

CC uveitis, allergic conjunctivitis, or related disorders), or inflammatory

CC disorders (e.g. rheumatoid arthritis, ankylosing spondylitis,

CC osteoarthritis, bursitis, tendinitis, or gout). The methods are useful

CC for designing drugs that bind to or modulate a wild-type COX-1. Compounds

CC identified can be used for preventing or reducing the severity of any of

CC a variety of conditions where modulation of the COX-1 enzyme or a COX-1

CC variant is beneficial. This is the amino acid sequence of human COX-1

CC variant ALR-3.

XX SQ Sequence 537 AA;

Query Match 72.7%; Score 32; DB 9; Length 537;

Best Local Similarity 85.7%; Pred. No. 7.1e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKFD 7

Db 330 FLQLKFD 336

RESULT 24

ID ADC24201 standard; protein; 551 AA.

XX AC ADC24201;

XX 18-DEC-2003 (first entry)

XX DE Human NOV2b protein SEQ ID NO:8.

XX human; NOVX; cardiant; antiarteriosclerotic; hypotensive; vasotropic;

KW dermatological; anorectic; immunosuppressive; cytostatic;

KW antinfertility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory;

KW neuroprotective; anabolic; nootropic; antiparkinsonian; gene therapy;

KW cardiomyopathy; atherosclerosis; hypertension; congenital heart defect;

KW pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity;

KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;

KW prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma;

KW fertility; haemophilia; graft versus host disease; AIDS;

KW bronchial asthma; Crohn's disease; multiple sclerosis;

KW infectious disease; anorexia; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorder; dyslipidaemia; wasting disorder.

XX OS Homo sapiens.

XX WO2003076584-A2.

XX 18-SEP-2003.

XX PF 06-MAR-2003; 2003WO-US006951.

XX PR 06-MAR-2002; 2002US-0361974P.

XX PR 19-MAR-2002; 2002US-0365477P.

XX PR 22-MAR-2002; 2002US-0366928P.

XX PR 06-AUG-2002; 2002US-0401661P.

XX PR 05-MAR-2003; 2003US-00401661.

XX (CURA-) CURAGEN CORP.

XX Alsbrook JP, Burgess CE, Edinger SR, Gerlach VL, Ji W, Kekuda R;

PI Li L, MacDougall JR, Miller CE, Millet I, Patturajan M, Pena CRA;

PI Rieger DK, Sciore P, Shenoy SG, Smithson G, Spytek KA, Stone DJ;

PI Voss EZ, Zhong M;

XX WPI; 2003-722330/68.

DR N-PSDB; ADC24200.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing or

PT treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,

PT obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or

PT multiple sclerosis.

XX Claim 1; SEQ ID NO 8; 229pp; English.

XX The present invention describes novel human proteins, designated NOVX

CC proteins. The NOVX sequences have cardiant, antiarteriosclerotic,

CC hypotensive, vasotropic, dermatological, anorectic, immunosuppressive,

CC cytostatic, antinfertility, haemostatic, anti-HIV, antiasthmatic,

CC antiinflammatory, neuroprotective, anabolic, nootropic and

CC antiparkinsonian activities, and can be used in gene therapy. The NOVX

CC sequences can be used as a therapeutic in the manufacture of a medicament

CC for treating a syndrome associated with a human disease, such as a

CC pathology associated with NOVX. The NOVX proteins and nucleic acids

CC encoding them are useful for diagnosing or treating pathologies, diseases

CC or conditions associated with NOVX sequences, including cardiomyopathy,

CC atherosclerosis, hypertension, congenital heart defects, pulmonary

CC stenosis, scleroderma, obesity, metabolic disturbances associated with

CC obesity, transplantation, adrenoleukodystrophy, congenital adrenal

CC hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,

CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,

CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious

CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,

CC or Parkinson's disease), immune disorders, haematopoietic disorders,

CC dyslipidaemias, and wasting disorders associated with chronic diseases.

CC The proteins can also be used as immunogens to produce antibodies and as

CC vaccines. The sequences may further be used in chromosome mapping,

CC identifying individual from minute biological samples (tissue typing),

CC and in forensic identification of a biological sample. The present

CC sequence represents human NOV2b from the present invention.

XX SQ Sequence 551 AA;

Query Match 72.7%; Score 32; DB 7; Length 551;

Best Local Similarity 85.7%; Pred. No. 7.3e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKFD 7

Db 307 FLQLKFD 313

RESULT 25

ID ADD12554

ID ADD12554 standard; protein; 551 AA.

XX AC ADD12554;

XX 01-JAN-2004 (first entry)

XX Human ENZM-14 protein SEQ ID NO:14.

XX DE



KW human; enzyme; ENZM; cytostatic; antiarteriosclerotic; anti-HIV;  
KW anti-allergic; cerebroprotective; antiparkinsonian; anticonvulsant;  
KW nootropic; neuroprotective; anti-inflammatory; ophthalmological;  
KW antithyroid; antiarthritic; antibacterial; virucide; protozoacide;  
KW antiparasitic; fungicide; anorectic; cardiant; hypotensive;  
KW anti-infertility; hepatotropic; gene therapy; autoimmune disorder;  
KW inflammatory disorder; AIDS; allergy; atopic dermatitis; arthritis;  
KW thyroiditis; infection; metabolic disorder; obesity;  
KW reproductive disorder; infertility; neurological disorder;  
KW Parkinson's disease; Alzheimer's disease; stroke; epilepsy;  
KW cardiovascular disorder; myocardial infarction; hypertension;  
KW eye disorder; cell proliferative disease; cancer; atherosclerosis;  
KW hepatitis.  
XX OS Homo sapiens.  
XX PN WO2003072729-A2.  
XX PD 04-SEP-2003.  
XX XX 21-FEB-2003; 2003WO-US005478.  
XX XX 22-FEB-2002; 2002US-0359513P.  
XX PR 19-MAR-2002; 2002US-0365795P.  
XX XX (INCY-) INCYTE GENOMICS INC.  
XX PI Sprague WW, Kable AE, Lee S, Griffin JA, Becha SD, Lee EA;  
PI Hafalia AJA, Khare R, Emerling BM, Marquis JP, Ramkumar J;  
PI Elliott VS, Richardson TW, Baughn MR, Jin P, Chien D, Hawkins PR;  
PI Wilson AD, Chawla NK, Tran UK, Lee SY, Zebarradian Y, Jiang X;  
PI Jackson AA, Bhatia UG, Burrill JD, Blake JJ, Ho A, Zheng W;  
XX WPI; 2003-731608/69.  
XX DR N-PSDB; ADD12611.  
XX XX New human enzymes and polynucleotides, useful for diagnosing, preventing  
PT or treating diseases or conditions associated with aberrant enzyme  
PT expression, e.g. cancer, hepatitis, AIDS, atherosclerosis, obesity,  
PT infection or stroke.  
XX XX Claim 1; SEQ ID NO 14; 426pp; English.  
XX XX The present sequence represents a human enzyme designated ENZM-14. Human  
CC enzymes of the present invention have cytostatic, antiarteriosclerotic,  
CC anti-HIV, anti-allergic, cerebroprotective, antiparkinsonian,  
CC anticonvulsant, nootropic, neuroprotective, anti-inflammatory, virucide,  
CC ophthalmological, antithyroid, antiarthritic, antibacterial, anorectic,  
CC protozoacide, antiparasitic, fungicide, anorectic, cardiant, hypotensive,  
CC anti-infertility and hepatotropic activities, and can be used in gene  
CC therapy. The human enzymes and polynucleotides encoding them can be used  
CC in diagnosing, preventing or treating diseases or conditions associated  
CC with the decreased expression or overexpression of the enzymes, such as  
CC autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis,  
CC arthritis or thyroiditis), infections (e.g. bacterial, viral, parasitic,  
CC protozoal or fungal), metabolic disorders (e.g. obesity), reproductive  
CC disorders (e.g. infertility), neurological disorders (Parkinson's  
CC disease, Alzheimer's disease, stroke, epilepsy), cardiovascular disorders  
CC (e.g. myocardial infarction or hypertension), eye disorders, or cell  
CC proliferative diseases (e.g. cancer, atherosclerosis, hepatitis). They  
CC are also useful in assessing the effects of exogenous compounds on the  
CC expression of nucleic acid and amino acid sequences of the enzymes.  
XX XX Sequence 551 AA;  
SQ Query Match 72.7%; Score 32; DB 7; Length 551;  
Best Local Similarity 85.7%; Pred. No. 7.3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FLOLEPD 7  
| | | | |  
Db 307 FLOLQKFD 313

RESULT 26  
ADSS85251  
ID ADS85251 standard; protein; 551 AA.  
XX AC ADS85251;  
XX DT 30-DEC-2004 (first entry)  
XX XX Human cyclooxygenase splice variant COX1sv1.  
XX DE cardiant; cerebroprotective; vasotropic; anticoagulant; cyclooxygenase;  
KW COX1; COX1 isoform; COX2 isoform; COX1sv1; cyclooxygenase inhibitor;  
KW myocardial infarction; stroke; peripheral vascular thrombosis;  
KW splice variant; human.  
XX XX Homo sapiens.  
XX OS Homo sapiens.  
XX PN US2004203030-A1.  
XX PD 14-OCT-2004.  
XX XX 18-DEC-2003; 2003US-00741853.  
XX PR 19-DEC-2002; 2002US-0435478P.  
XX XX (GARR/) GARRETT-ENGELE P W.  
XX PI Garrett-Englele PW;  
XX XX WPI; 2004-746971/73.  
XX DR N-PSDB; ADS85250.  
XX XX Novel purified cyclooxygenases (COX)1sv1 polypeptide, alternatively  
PT spliced isoform of COX1, useful for screening compound capable to bind to  
PT or interact with COX1sv1 polypeptide.  
XX PS Claim 4; SEQ ID NO 2; 19pp; English.  
XX CC The invention describes a purified cyclooxygenases (COX)1sv1 polypeptide  
CC (I), comprising a fully defined COX1sv1 (an alternatively spliced isoform  
CC of COX1) polypeptide sequence (S1) of 551 amino acids as given in the  
CC specification. Also described are: a purified human nucleic acid (II)  
CC comprising a fully defined COX1sv1 polynucleotide sequence (S2) of 1653  
CC base pairs as given in the specification, or its complement; expression  
CC vector (III) comprising a nucleotide sequence encoding (S1); antibodies  
CC specific to (I), useful for distillation cells that express (I) from  
CC human or non-human cells (including bacteria) that do not express (I);  
CC and producing (I). (I) is useful for screening for compounds able to bind  
CC selectively to (I), which involves providing (I), providing one or more  
CC COX1 or COX2 isoform polypeptide that are not (I), contacting (I) and the  
CC COX1 or COX2 isoform polypeptide that is not (I) with a test preparation  
CC comprising one or more compounds, and determining the binding of the test  
CC preparation to (I) and to the COX1 or COX2 isoform polypeptide that is  
CC not (I), where a test preparation that binds to (I) but does not bind to  
CC the COX1 or COX2 polypeptide that is not (I) contains a compound that  
CC selectively binds (I). In the above method, (I) is obtained by expressing  
CC (I) from (III). (I) is also useful for screening for a compound able to  
CC bind to or interact with (I) or its fragment, which involves expressing  
CC (I) or its fragment from a recombinant nucleic acid, providing to (I) a  
CC labeled COX1 ligand that binds to (I) and a test preparation comprising  
CC one or more compounds, and measuring the effect of the test preparation  
CC on binding of the labeled COX1 ligand to (I), where a test preparation  
CC that alters the binding of the labeled COX1 ligand to (I) contains a  
CC compound that binds to or interacts with (I). The providing and measuring  
CC steps are performed in vitro. (I) is expressed from (III). The COX1sv1  
CC ligand is a cyclooxygenase inhibitor. The expression vector comprises  
CC (II). The test preparation contains one compound. The compound identified  
CC using (I), is useful for modulating activity of (I) to achieve  
CC therapeutic effect upon diseases e.g. risk of myocardial infarction,  
CC stroke and peripheral vascular thromboses. (I) is useful as a marker for  
CC identifying the presence of COX1sv1, and as an immunogen for producing  
CC antibodies binding to (I). This is the amino acid sequence of a novel

```
CC splice variant of human cyclooxygenase COX1slv1.
XX Sequence 551 AA;
SQ

Query Match          72.7%; Score 32; DB 8; Length 551;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLKPD 7
Db      307 FLQLKPD 313

RESULT 27
AAY29648
ID AAY29648 standard; protein; 552 AA.
XX
AC AAY29648;
XX
DT 19-OCT-1999 (first entry)
XX
DE Sheep prostaglandin H1 synthase query protein.
XX
KW H-rae; HIV-1; reverse transcriptase; prostaglandin H2 synthase; PGHS-2;
KW protein folding inhibitor; PFI; growth; proliferation; drug.
XX
OS Ovis sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 143 /note= "unspecified"
FT Misc-difference 144 /note= "unspecified"
FT Misc-difference 145 /note= "unspecified"
FT Misc-difference 146 /note= "unspecified"
FT Misc-difference 147 /note= "unspecified"
FT Misc-difference 148 /note= "unspecified"
FT Misc-difference 149 /note= "unspecified"
FT Misc-difference 150 /note= "unspecified"
FT Misc-difference 151 /note= "unspecified"
FT Misc-difference 152 /note= "unspecified"
FT Misc-difference 153 /note= "unspecified"
FT Misc-difference 154 /note= "unspecified"
FT Misc-difference 165 /note= "unspecified"
FT Misc-difference 166 /note= "unspecified"
FT Misc-difference 167 /note= "unspecified"
FT Misc-difference 168 /note= "unspecified"
FT Misc-difference 169 /note= "unspecified"
FT Misc-difference 170 /note= "unspecified"
FT Misc-difference 171 /note= "unspecified"
FT Misc-difference 172 /note= "unspecified"
FT Misc-difference 173 /note= "unspecified"
FT Misc-difference 174 /note= "unspecified"
FT

FT Misc-difference 175 /note= "unspecified"
FT Misc-difference 176 /note= "unspecified"
FT Misc-difference 177 /note= "unspecified"
FT Misc-difference 178 /note= "unspecified"
FT Misc-difference 179 /note= "unspecified"
FT
XX WO9940435-A1.
XX
XX 12-AUG-1999.
XX
XX 06-FEB-1999; 99WO-US002612.
XX
XX 09-FEB-1998; 98US-0074070P.
XX (NETZ/) NETZER W J.
XX Netzer WJ;
XX
XX WPI; 1999-508524/42.
XX
XX Methods for discovery, development and use of drugs and drug lead
XX molecules that inhibit protein folding.
XX
XX Example; Page 37-38; 116pp; English.
XX
XX The present invention describes the identification of protein folding
XX inhibitors (PFI) by determining the ratio of unfolded to folded protein
XX in the presence and absence of a test compound under protein biosynthetic
XX conditions after stress. Identifying PFI comprises: (i) contacting a
XX protein biosynthetic system under protein synthesis conditions with at
XX least one test compound; and (ii) determining whether the test compound
XX increases the ratio of unfolded protein to folded protein, where an
XX increase in the ratio is indicative that the test compound is a PFI. The
XX method can be used for the discovery, development and use of drugs and
XX drug lead molecules that inhibit protein folding. The inhibitors
XX identified can be used in methods to inhibit cellular action of a protein
XX by inhibiting de novo folding in vivo, and optionally in conjunction with
XX heat shock treatment. The inhibitors can be used to modulate cellular
XX processes, e.g. enhancing the immunogenicity of a peptide or protein. The
XX inhibitors can modulate growth or proliferation of a cell by inhibiting
XX irreversible folding of the protein target. The tests can be carried out
XX using a wide range of procedures therefore making the detection more
XX simple and flexible for the operator. The present sequence represents
XX sheep prostaglandin H1 synthase (PGHS-1) used in the exemplification of
XX the present invention
XX
SQ Sequence 552 AA;

Query Match          72.7%; Score 32; DB 2; Length 552;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLKPD 7
Db      323 FLQLKPD 329

RESULT 28
ADD12555
ID ADD12555 standard; protein; 552 AA.
XX
AC ADD12555;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human ENZM-15 protein SEQ ID NO:15.
XX
XX human; enzyme; ENZM; cytostatic; antiarteriosclerotic; anti-HIV;
KW
```

KW antiallergic; cerebroprotective; antiparkinsonian; anticonvulsant;  
 KW neurotropic; neuroprotective; antiinflammatory; ophthalmological;  
 KW antithyroid; antiarthritic; antibacterial; virucide; protozoacide;  
 KW antiparasitic; fungicide; anorectic; cardiant; hypotensive;  
 KW antinfertility; hepatotropic; gene therapy; autoimmune disorder;  
 KW inflammatory disorder; AIDS; allergy; atopic dermatitis; arthritis;  
 KW thyroiditis; infection; metabolic disorder; obesity;  
 KW reproductive disorder; infertility; neurological disorder;  
 KW Parkinson's disease; Alzheimer's disease; stroke; epilepsy;  
 KW cardiovascular disorder; myocardial infarction; hypertension;  
 KW eye disorder; cell proliferative disease; cancer; atherosclerosis;  
 KW hepatitis.  
 XX Homo sapiens.  
 XX WO2003072729-A2.  
 XX  
 XX 04-SEP-2003.  
 XX  
 PF 21-FEB-2003; 2003WO-US0005478.  
 XX  
 XX 22-FEB-2002; 2002US-0359513P.  
 PR 19-MAR-2002; 2002US-0365795P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Sprague WW, Kable AE, Lee S, Griffin JA, Becha SD, Lee EA;  
 PI Hafalia AJA, Khare R, Emwling BM, Marquis JP, Ramkumar J;  
 PI Elliott VS, Richardson TW, Baughn MR, Jin P, Chien D, Hawkins PR;  
 PI Wilson AD, Chawla NK, Tran UK, Lee SY, Zebardjian Y, Jiang X;  
 PI Jackson AA, Bhatia UG, Burrill JD, Blake JJ, Ho A, Zheng W;  
 XX  
 XX WPI: 2003-731608/69.  
 DR N-PSDB; ADD12612.  
 XX  
 XX New human enzymes and polynucleotides, useful for diagnosing, preventing  
 PT or treating diseases or conditions associated with aberrant enzyme  
 PT expression, e.g. cancer, hepatitis, AIDS, atherosclerosis, obesity,  
 PT infection or stroke.  
 XX  
 XX Claim 1; SEQ ID NO 15; 426pp; English.  
 XX  
 CC The present sequence represents a human enzyme designated ENZM-15. Human  
 CC enzymes of the present invention have cytostatic, antiarteriosclerotic,  
 CC anti-HIV, antiallergic, cerebroprotective, antiparkinsonian,  
 CC anticonvulsant, neurotropic, neuroprotective, antiinflammatory,  
 CC ophthalmological, antithyroid, antiarthritic, antibacterial, virucide,  
 CC protozoacide, antiparasitic, fungicide, anorectic, cardiant, hypotensive,  
 CC antinfertility and hepatotropic activities, and can be used in gene  
 CC therapy. The human enzymes and polynucleotides encoding them can be used  
 CC in diagnosing, preventing or treating diseases or conditions associated  
 CC with the decreased expression or overexpression of the enzymes, such as  
 CC autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis,  
 CC arthritis or thyroiditis), infections (e.g. bacterial, viral, parasitic,  
 CC protozoal or fungal), metabolic disorders (e.g. obesity), reproductive  
 CC disorders (e.g. infertility), neurological disorders (Parkinson's  
 CC disease, Alzheimer's disease, stroke, epilepsy), cardiovascular disorders  
 CC (e.g. myocardial infarction or hypertension), eye disorders, or cell  
 CC proliferative diseases (e.g. cancer, atherosclerosis, hepatitis). They  
 CC are also useful in assessing the effects of exogenous compounds on the  
 CC expression of nucleic acid and amino acid sequences of the enzymes.  
 XX

SQ Sequence 552 AA;

Query Match 72.7%; Score 32; DB 7; Length 552;  
 Best Local Similarity 85.7%; Pred. No. 7.3e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLEPD 7  
 |||||:  
 Db 345 FLOLEKFD 351

# RESULT 29

ABB09701  
 ID ABB09701 standard; protein; 562 AA.  
 XX  
 AC ABB09701;  
 XX  
 DT 11-JUN-2002 (first entry)  
 XX  
 XX Amino acid sequence of human COX-1b polypeptide.  
 XX  
 KW COX-1b; prostaglandin synthase-1; COX-1; prostaglandin; D2;  
 KW 15-deoxy-Delta(12-14) J2; arachidonic acid; inflammation;  
 KW rheumatoid arthritis; vascular disorder; skin disorder;  
 KW venous insufficiency; atherosclerosis; skin ulcer; cancer;  
 KW Alzheimer's disease; pain; migraine; cyclooxygenase; COX-2.  
 XX  
 XX Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 67  
 FT /note= "N-glycosylation site"  
 FT Modified-site 103  
 FT /note= "N-glycosylation site"  
 FT Modified-site 143  
 FT /note= "N-glycosylation site"  
 FT  
 XX  
 XX FR2811677-A1.  
 PN  
 XX  
 XX 18-JAN-2002.  
 PD  
 XX  
 XX 12-JUL-2000; 2000FR-00009139.  
 PF  
 XX  
 XX 12-JUL-2000; 2000FR-00009139.  
 PR  
 XX  
 XX (INNO-) LAB INNOTHERA SA.  
 PA  
 XX  
 XX Anger LM, Hanf R;  
 PI  
 XX WPI: 2002-149748/20.  
 XX  
 DR N-PSDB; ABL41898.  
 DR  
 XX  
 XX Cell line that expresses isoform of prostaglandin synthase-1, useful for  
 PT treating e.g. inflammation, converts arachidonic acid to antiinflammatory  
 PT prostaglandins.  
 PT  
 XX Claim 4; Fig 6; 63pp; French.  
 PS  
 XX  
 CC The present sequence represents a human COX-1b polypeptide. COX-1b  
 CC represents an alternative splicing of the 3'-region of exon 9 of the  
 CC mammalian gene for prostaglandin synthase-1 (COX-1). COX-1b  
 CC preferentially produces the antiinflammatory prostaglandins D2 or 15-  
 CC deoxy-Delta(12-14) J2 from arachidonic acid. COX-1b is used to treat  
 CC inflammation (particularly rheumatoid arthritis); vascular and skin  
 CC disorders (e.g. venous insufficiency, atherosclerosis or skin ulcers);  
 CC cancer (especially of the colon); Alzheimer's disease; pain and/or  
 CC migraine. Cells that express COX-1b are useful for screening compounds  
 CC for inhibition of cyclooxygenase activity, particularly for selective  
 CC action against COX-1, COX-1b or COX-2. Inhibitors are potentially useful  
 CC for treating the specified conditions  
 XX  
 XX Sequence 562 AA;  
 SQ  
 Query Match 72.7%; Score 32; DB 5; Length 562;  
 Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLOLEPD 7  
 |||||:  
 Db 355 FLOLEKFD 361  
 RESULT 30  
 ADZ51367

ID ADZ51367 standard; protein; 562 AA.  
XX  
AC ADZ51367;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Amino acid sequence of ovarian cancer marker M713.  
XX  
KW cytostatic; gene therapy; ovarian cancer; ovarian cancer marker; M713;  
KW prostaglandin-endoperoxide synthase 1.  
XX  
OS Homo sapiens.  
XX  
PN WO2005034732-A2.  
XX  
PD 21-APR-2005.  
XX  
PF 07-OCT-2004; 2004WO-US033166.  
XX  
PR 07-OCT-2003; 2003US-0509171P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Endege WO, Ford D, Gannavarapu M, Glatt K, Hoersch S, Kamatkar S;  
PI Monahan JE, Schlegel R, Xu YV, Zhao X;  
XX  
XX WPI; 2005-306219/31.  
DR N-PSDB; ADZ51366.  
XX  
XX Assessing whether a patient is afflicted with ovarian cancer comprises  
PT determining a significant difference between the levels of expression of  
PT an ovarian cancer marker in the patient sample and the sample from a  
PT control subject.  
XX  
PS Example 1; SEQ ID NO 24; 164pp; English.  
XX  
CC The specification describes a method of assessing whether a patient is  
CC afflicted with ovarian cancer. The method comprises determining the  
CC presence of a significant difference between the levels of expression of  
CC an ovarian cancer marker in the patient sample and the sample from a  
CC control subject. The method of the invention is useful for assessing,  
CC diagnosing, preventing or treating ovarian cancer. The markers may also  
CC be used in screening for agents that may treat or prevent ovarian cancer.  
CC The present sequence represents the marker M713, which is prostaglandin-  
CC endoperoxide synthase 1 transcript variant 2.  
XX  
SQ Sequence 562 AA;  
XX  
Query Match 72.7%; Score 32; DB 9; Length 562;  
Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 FLQLEFD 7  
Db 355 FLQLKFD 361  
XX  
RESULT 31  
ADZ59937  
ID ADZ59937 standard; protein; 574 AA.  
XX  
AC ADZ59937;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Human COX-1 variant ALT-1 SEQ ID NO 2.  
XX  
XX analgesic; antipyretic; cardiovascular-gen.; anticoagulant;  
KW antiarteriosclerotic; thrombolytic; vasotropic; antiinflammatory;  
KW ophthalmological; antiirheumatic; antiarthritic; osteopathic; antigout;  
KW protein purification; pain; neurological disease; fever;  
KW temperature disorder; cardiovascular disease; atherosclerosis;  
KW metabolic disorder; thrombosis; hematological disease; restenosis;  
XX

KW vasculitis; inflammation; ocular disease; glaucoma; hypotensive;  
KW ocular hypertension; uveitis; antiallergic; allergic conjunctivitis;  
KW musculoskeletal disease; rheumatoid arthritis; ankylosing spondylitis;  
KW osteoarthritis; bursitis; gout; splice variant; cyclooxygenase 1; COX-1;  
KW ALT-1; enzyme; splice variant.  
XX  
OS Homo sapiens.  
XX  
PN WO2005035713-A2.  
XX  
PD 21-APR-2005.  
XX  
PF 20-AUG-2004; 2004WO-US027105.  
XX  
PR 15-SEP-2003; 2003US-00663377.  
XX  
PA (ALLR ) ALLERGAN INC.  
XX  
PI Liang Y, Woodward DF;  
XX  
DR WPI; 2005-296270/30.  
DR N-PSDB; ADZ59936.  
XX  
XX New isolated cyclooxygenase-1 (COX-1) polypeptide or variants, useful for  
PT treating or preventing, e.g. pain, fever, atherosclerosis, thrombosis,  
PT restenosis, glaucoma, allergic conjunctivitis, rheumatoid arthritis, or  
PT osteoarthritis.  
XX  
PS Claim 3; SEQ ID NO 2; 129pp; English.  
XX  
CC The invention describes an isolated COX-1 polypeptide. Also described  
CC are: a COX-1 variant binding, agent, which binds an amino acid sequence  
CC selected from SEQ ID NO. 14, 16, or 18, or its epitope; a cell comprising  
CC the exogenously expressed polypeptide above; a method for identifying a  
CC compound that modulates a COX-1 variant; a method for identifying a  
CC compound that specifically binds to a COX-1 variant; a method for  
CC identifying a compound that differentially modulates a COX-1 variant; a  
CC method for identifying a compound that differentially binds to a COX-1  
CC variant; an isolated nucleic acid molecule comprising: a nucleotide  
CC sequence that encodes a polypeptide comprising an amino acid sequence  
CC having at least 50% amino acid identity with SEQ ID NO. 10, or an amino  
CC acid sequence selected from SEQ ID NO. 20, 22, or 24, or its conservative  
CC variant; a nucleotide sequence that encodes an amino acid sequence  
CC selected from SEQ ID NO. 2, 4, 6, or 8; or a nucleotide sequence selected  
CC from 4 fully defined 1818-2280 bp sequences (SEQ ID NO. 1, 3, 5, or 7)  
CC given in the specification; a vector comprising the isolated nucleic acid  
CC molecule above; and a host cell comprising the vector above. The  
CC polypeptides are useful for treating or preventing diseases or conditions  
CC associated with COX-1 or COX-1 variant, including pain, fever,  
CC cardiovascular disorder (e.g. atherosclerosis, thrombosis, or  
CC vasculitis), ocular disorder (e.g. glaucoma, ocular hypertension,  
CC uveitis, allergic conjunctivitis, or related disorders), or inflammatory  
CC disorders (e.g. rheumatoid arthritis, ankylosing spondylitis,  
CC osteoarthritis, bursitis, tendinitis, or gout). The methods are useful  
CC for designing drugs that bind to or modulate a wild-type COX-1. Compounds  
CC identified can be used for preventing or reducing the severity of any of  
CC a variety of conditions where modulation of the COX-1 enzyme or a COX-1  
CC variant is beneficial. This is the amino acid sequence of human COX-1  
CC variant ALT-1.  
XX  
SQ Sequence 574 AA;  
XX  
Query Match 72.7%; Score 32; DB 9; Length 574;  
Best Local Similarity 85.7%; Pred. No. 7.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 FLQLEFD 7  
Db 330 FLQLKFD 336  
XX  
RESULT 32  
ADD27944

ID ADD27944 standard; protein; 580 AA.  
 XX AC ADD27944;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE COX-1 amino acid sequence SEQ ID NO:34.  
 XX KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
 KW COX-1 variant protein; genetic disease; tissue typing;  
 KW forensic identification.  
 XX OS Unidentified.  
 XX PN WO2003029411-A2.  
 XX PD 10-APR-2003.  
 XX PF 28-SEP-2002; 2002WO-US030947.  
 XX PR 28-SEP-2001; 2001US-0326133P.  
 PR 15-APR-2002; 2002US-0373225P.  
 PR 16-APR-2002; 2002US-0373661P.  
 PR 16-SEP-2002; 2002US-0411575P.  
 XX PA (UYYO ) UNIV BRIGHAM YOUNG.  
 XX PI Simmons D, Chandrasekharan VN;  
 XX DR WPI; 2003-421222/39.  
 XX PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
 PT encoding the polypeptide, useful for identifying a compound that binds to  
 PT and modulates the activity of COX-1 variant polypeptide.  
 XX PS Disclosure; SEQ ID NO 34; 150pp; English.  
 XX CC The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
 CC variant polypeptide (I). (I) is useful for identifying a compound which  
 CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
 CC used for mapping their respective genes on a chromosome, and so locating  
 CC gene regions associated with genetic disease, identifying an individual  
 CC from a minute biological sample (tissue typing), and to aid in forensic  
 CC identification of a biological sample. The present sequence represents a  
 CC sequence which is used in the exemplification of the present invention.  
 XX SQ Sequence 580 AA;  
 Query Match 72.7%; Score 32; DB 7; Length 580;  
 Best Local Similarity 85.7%; Pred. No. 7.7e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 DB 344 FLQLKFD 350  
 RESULT 33  
 ADD27968  
 ID ADD27968 standard; protein; 580 AA.  
 XX AC ADD27968;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE COX-1 amino acid sequence.  
 XX KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
 KW COX-1 variant protein; genetic disease; tissue typing;  
 KW forensic identification.  
 XX OS Unidentified.

PN WO2003029411-A2.  
 XX PD 10-APR-2003.  
 XX PF 28-SEP-2002; 2002WO-US030947.  
 XX PR 28-SEP-2001; 2001US-0326133P.  
 PR 15-APR-2002; 2002US-0373225P.  
 PR 16-APR-2002; 2002US-0373661P.  
 PR 16-SEP-2002; 2002US-0411575P.  
 XX PA (UYYO ) UNIV BRIGHAM YOUNG.  
 XX PI Simmons D, Chandrasekharan VN;  
 XX DR WPI; 2003-421222/39.  
 XX PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
 PT encoding the polypeptide, useful for identifying a compound that binds to  
 PT and modulates the activity of COX-1 variant polypeptide.  
 XX PS Disclosure; Fig 2; 150pp; English.  
 XX CC The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
 CC variant polypeptide (I). (I) is useful for identifying a compound which  
 CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
 CC used for mapping their respective genes on a chromosome, and so locating  
 CC gene regions associated with genetic disease, identifying an individual  
 CC from a minute biological sample (tissue typing), and to aid in forensic  
 CC identification of a biological sample. The present sequence represents a  
 CC sequence which is used in the exemplification of the present invention.  
 XX SQ Sequence 580 AA;  
 Query Match 72.7%; Score 32; DB 7; Length 580;  
 Best Local Similarity 85.7%; Pred. No. 7.7e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 DB 344 FLQLKFD 350  
 RESULT 34  
 ADZ5943  
 ID ADZ5943 standard; protein; 594 AA.  
 XX AC ADZ5943;  
 XX DT 30-JUN-2005 (first entry)  
 XX DE Human COX-1 variant ALT-4 SEQ ID NO 8.  
 XX KW analgesic; antipyretic; cardiovascular-gen.; anticoagulant;  
 KW antiarteriosclerotic; thrombolytic; vasotropic; antiinflammatory;  
 KW ophthalmological; antirheumatic; antiarthritic; osteopathic; antigout;  
 KW protein purification; pain; neurological disease; fever;  
 KW temperature disorder; cardiovascular disease; atherosclerosis;  
 KW metabolic disorder; thrombosis; hematological disease; restenosis;  
 KW vasculitis; inflammation; ocular disease; glaucoma; hypotensive;  
 KW ocular hypertension; uveitis; allergic; allergic conjunctivitis;  
 KW musculoskeletal disease; rheumatoid arthritis; ankylosing spondylitis;  
 KW osteoarthritis; bursitis; gout; splice variant; cyclooxygenase 1; COX-1;  
 KW ALT-4; enzyme; splice variant.  
 XX OS Homo sapiens.  
 XX PN WO2005035713-A2.  
 XX PD 21-APR-2005.  
 XX PF 20-AUG-2004; 2004WO-US027105.  
 XX

PR 15-SEP-2003; 2003US-00663377.  
 XX (ALLR ) ALLERGAN INC.  
 XX Liang Y, Woodward DF;  
 XX WPI; 2005-296270/30.  
 DR N-PSDB; AD259942.  
 XX  
 PT New isolated cyclooxygenase-1 (COX-1) polypeptide or variants, useful for  
 PT treating or preventing, e.g. pain, fever, atherosclerosis, thrombosis,  
 PT stenosis, glaucoma, allergic conjunctivitis, rheumatoid arthritis, or  
 PT osteoarthritis.  
 XX  
 XX Claim 3; SEQ ID NO 8; 139pp; English.  
 XX  
 CC The invention describes an isolated COX-1 polypeptide. Also described  
 CC are: a COX-1 variant binding, agent, which binds an amino acid sequence  
 CC selected from SEQ ID NO. 14, 16, or 18, or its epitope; a cell comprising  
 CC the exogenously expressed polypeptide above; a method for identifying a  
 CC compound that modulates a COX-1 variant; a method for identifying a  
 CC compound that specifically binds to a COX-1 variant; a method for  
 CC identifying a compound that differentially modulates a COX-1 variant; a  
 CC method for identifying a compound that differentially binds to a COX-1  
 CC variant; an isolated nucleic acid molecule comprising: a nucleotide  
 CC sequence that encodes a polypeptide comprising an amino acid sequence  
 CC having at least 50% amino acid identity with SEQ ID NO. 10, or an amino  
 CC acid sequence selected from SEQ ID NO. 20, 22, or 24, or its conservative  
 CC variant; a nucleotide sequence that encodes an amino acid sequence  
 CC selected from SEQ ID NO. 2, 4, 6, or 8; or a nucleotide sequence selected  
 CC from 4 fully defined 1818-2280 bp sequences (SEQ ID NO. 1, 3, 5, or 7)  
 CC given in the specification; a vector comprising the isolated nucleic acid  
 CC molecule above; and a host cell comprising the vector above. The  
 CC polypeptides are useful for treating or preventing diseases or conditions  
 CC associated with COX-1 or COX-1 variant, including pain, fever,  
 CC cardiovascular disorder (e.g. atherosclerosis, thrombosis, restenosis, or  
 CC vasculitis), ocular disorder (e.g. glaucoma, ocular hypertension,  
 CC uveitis, allergic conjunctivitis, or related disorders), or inflammatory  
 CC disorders (e.g. rheumatoid arthritis, ankylosing spondylitis,  
 CC osteoarthritis, bursitis, tendinitis, or gout). The methods are useful  
 CC for designing drugs that bind to or modulate a wild-type COX-1. Compounds  
 CC identified can be used for preventing or reducing the severity of any of  
 CC a variety of conditions where modulation of the COX-1 enzyme or a COX-1  
 CC variant is beneficial. This is the amino acid sequence of human COX-1  
 CC variant A17-4.  
 XX  
 XX Sequence 594 AA;  
 SQ  
 Query Match 72.7%; Score 32; DB 9; Length 594;  
 Best Local Similarity 85.7%; Pred. No. 7.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 |||||  
 Db 350 FLQLKFD 356  
 RESULT 35  
 AAR21690  
 ID AAR21690 standard; protein; 599 AA.  
 XX  
 AC AAR21690;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 23-JUL-1992 (first entry)  
 DT  
 DE Prostaglandin endoperoxide synthase.  
 XX Human; hPES; screening; anti-inflammatory; antibody.  
 KW  
 OS Homo sapiens.  
 XX  
 XX JP04045786-A.  
 PN

XX 14-FEB-1992.  
 PD  
 XX 13-JUN-1990; 90JJP-00152784.  
 PF  
 XX 13-JUN-1990; 90JJP-00152784.  
 PR  
 XX (MEIP ) MEIJI MILK PROD CO LTD.  
 PA  
 XX WPI; 1992-101937/13.  
 DR N-PSDB; AAQ23001.  
 DR  
 PT Human prostaglandin endo-peroxide synthase - for screening  
 PT antiinflammatory agents.  
 PT  
 XX Claim 1; Page 1; 10pp; Japanese.  
 PS  
 XX The protein sequence of hPES was deduced from the cDNA sequence obtd. by  
 CC screening a human genomic library in EMBL3. hPES can be used to screen  
 CC anti-inflammatory agents. An anti-body against a peptide specific to hPES  
 CC can be made, and used for the determin- ation of the protein. (Updated on  
 CC 25-MAR-2003 to correct PA field.)  
 XX  
 XX Sequence 599 AA;  
 SQ  
 Query Match 72.7%; Score 32; DB 2; Length 599;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 |||||  
 Db 355 FLQLKFD 361  
 RESULT 36  
 ABG96403  
 ID ABG96403 standard; protein; 599 AA.  
 XX  
 AC ABG96403;  
 XX  
 XX 11-DEC-2002 (first entry)  
 DT  
 DE Human ovarian cancer marker OV51.  
 XX  
 KW Human; ovarian cancer; marker; cancer; familial history; brain disorder;  
 KW central nervous system disorder; bacterial meningitis; viral meningitis;  
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;  
 KW brain herniation; inflammation; encephalitis; testicular disorder;  
 KW non-tuberculous granulomatous orchitis; connective tissue disorder;  
 KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;  
 KW histological type; carcinogenic; ovarian cancer marker.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200271928-A2.  
 PN  
 XX 19-SEP-2002.  
 PD  
 XX 14-MAR-2002; 2002WO-US007826.  
 PF  
 XX 14-MAR-2001; 2001US-0276025P.  
 PR  
 PR 14-MAR-2001; 2001US-0276026P.  
 PR 10-AUG-2001; 2001US-0311732P.  
 PR 19-SEP-2001; 2001US-0323580P.  
 PR 26-SEP-2001; 2001US-0324967P.  
 PR 26-SEP-2001; 2001US-0325102P.  
 PR 26-SEP-2001; 2001US-0325149P.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;  
 PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;  
 PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;

XX WPI; 2002-723277/78.  
 DR N-PSDB; ABS76502.  
 XX  
 PT Assessing whether a patient is afflicted with ovarian cancer, useful in  
 PT assessing the stage or progression of the disease, comprises comparing  
 PT the expression level of a cancer marker in a sample from a patient and  
 PT from a non cancer patient.  
 XX  
 XX Disclosure; Page 386-388; 481pp; English.  
 XX  
 CC The present invention relates to a new method for assessing whether a  
 CC patient is afflicted with ovarian cancer. The method involves comparing  
 CC the expression level of a marker in a patient sample and the normal level  
 CC of expression of the marker in a control non-ovarian cancer sample, where  
 CC the marker is selected from 363 cancer markers described in the  
 CC specification. The method of the invention is useful in diagnosing or  
 CC characterising cancer, in detecting the presence of cancer as early as  
 CC possible, and the recurrence of ovarian cancer. The method may also be of  
 CC particular use with patients having an enhanced risk of developing  
 CC ovarian cancer (e.g. patients having a familial history of ovarian  
 CC cancer). The cancer markers may be used in the management and treatment  
 CC of e.g. brain and central nervous system disorders (e.g. bacterial and  
 CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain  
 CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),  
 CC inflammations (e.g. bacterial or viral meningitis or encephalitis),  
 CC testicular disorders (e.g. nontuberculous granulomatous orchitis),  
 CC connective tissue disorders, or heart disorders (e.g. ischaemic heart  
 CC disease or atherosclerosis). The compositions and methods may also be  
 CC used in assessing the histological type of neoplasm associated with  
 CC ovarian cancer, monitoring the progression of ovarian cancer, determining  
 CC whether ovarian cancer has metastasized or is likely to metastasize,  
 CC selecting a composition for inhibiting ovarian cancer, assessing the  
 CC ovarian carcinogenic potential of a compound, or inhibiting ovarian  
 CC cancer or at risk of developing ovarian cancer. The present amino acid  
 CC sequence represents one of the ovarian cancer markers described in the  
 CC invention  
 XX  
 XX Sequence 599 AA;  
 SQ  
 Query Match 72.7%; Score 32; DB 5; Length 599;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 Db 355 FLQLKFD 361  
 RESULT 37  
 ABR42249  
 ID ABR42249 standard; protein; 599 AA.  
 AC ABR42249;  
 XX  
 XX 28-JUL-2003 (first entry)  
 DT  
 DE Human cyclooxygenase 1 (COX-1).  
 XX  
 KW Cyclooxygenase 1; COX-1; human; enzyme; vulnery; osteopathic;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003022224-A2.  
 PN  
 XX 20-MAR-2003.  
 PD  
 XX 11-SEP-2002; 2002WO-US028930.  
 PP  
 XX 11-SEP-2001; 2001US-00953067.  
 PR  
 XX (UYN-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 PA

XX O'Connor PJ;  
 PI  
 XX WPI; 2003-313185/30.  
 DR N-PSDB; ACC57773.  
 XX  
 XX Novel vector useful for enhancing wound healing or treating osteoporosis,  
 PT osteogenesis imperfecta, and brittle bone conditions, comprises a  
 PT promoter linked to a cyclooxygenase expression cassette.  
 XX  
 XX Disclosure; Page 69-72; 88pp; English.  
 XX  
 CC The present sequence is the protein sequence of human cyclooxygenase 1  
 CC (COX-1). A claimed vector for use in enhancing wound healing comprises a  
 CC promoter linked to a COX expression cassette. A claimed method for  
 CC enhanced wound healing involves delivering the vector to the location of  
 CC the wound. The wound may be a bone fracture or a skin wound. A claimed  
 CC method for treating osteoporosis, osteogenesis imperfecta and brittle  
 CC bone conditions comprises administering the vector. A claimed composition  
 CC for use in wound healing comprises a COX protein, especially COX-1, COX-2  
 CC or both  
 XX  
 XX Sequence 599 AA;  
 SQ  
 Query Match 72.7%; Score 32; DB 6; Length 599;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 Db 355 FLQLKFD 361  
 RESULT 38  
 ADC24199  
 ID ADC24199 standard; protein; 599 AA.  
 XX  
 AC ADC24199;  
 XX  
 XX 18-DEC-2003 (first entry)  
 DT  
 DE Human NOV2a protein SEQ ID NO:6.  
 XX  
 KW human; NOVX; cardiant; antiarteriosclerotic; hypotensive; vasotropic;  
 KW dermatological; anorectic; immunosuppressive; cytostatic;  
 KW antiinfertility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory;  
 KW neuroprotective; anabolic; nootropic; antiparkinsonian; gene therapy;  
 KW cardiomyopathy; atherosclerosis; hypertension; congenital heart defect;  
 KW pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity;  
 KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;  
 KW prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma;  
 KW fertility; haemophilia; graft versus host disease; AIDS;  
 KW bronchial asthma; Crohn's disease; multiple sclerosis;  
 KW infectious disease; anorexia; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; immune disorder;  
 KW haematopoietic disorder; dyslipidaemia; wasting disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003076584-A2.  
 PN  
 XX 18-SEP-2003.  
 PD  
 XX 06-MAR-2003; 2003WO-US006951.  
 PP  
 XX 06-MAR-2002; 2002US-0361974P.  
 PR  
 XX 19-MAR-2002; 2002US-0365477P.  
 PR  
 XX 22-MAR-2002; 2002US-0366928P.  
 PR  
 XX 06-AUG-2002; 2002US-0401661P.  
 PR  
 XX 05-MAR-2003; 2003US-00401661.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA

PI Alsobrook JP, Burgess CE, Edinger SR, Gerlach VL, Ji W, Kekuda R;  
 PI Li L, Macdougall JR, Miller CE, Millet I, Patturajan M, Pena CEa;  
 PI Rieger DK, Sciore P, Shenoy SG, Smithson G, Spytek KA, Stone DU;  
 PI Voss EZ, Zhong M;  
 XX  
 DR WPI; 2003-722330/68.  
 DR N-PSDB; ADC24198.  
 XX  
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing or  
 PT treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,  
 PT obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or  
 PT multiple sclerosis.  
 XX  
 PS Claim 1; SEQ ID NO 6; 229pp; English.  
 XX  
 CC The present invention describes novel human proteins, designated NOVX  
 CC proteins. The NOVX sequences have cardiac, antiarteriosclerotic,  
 CC hypotensive, vasotropic, dermatological, anorectic, immunosuppressive,  
 CC cytotatic, antiinfertility, haemostatic, anti-HIV, antiasthmatic,  
 CC antiinflammatory, neuroprotective, anabolic, nootropic and  
 CC antiparkinsonian activities, and can be used in gene therapy. The NOVX  
 CC sequences can be used as a therapeutic in the manufacture of a medicament  
 CC for treating a syndrome associated with a human disease, such as a  
 CC pathology associated with NOVX. The NOVX proteins and nucleic acids  
 CC encoding them are useful for diagnosing or treating pathologies, diseases  
 CC or conditions associated with NOVX sequences, including cardiomyopathy,  
 CC atherosclerosis, hypertension, congenital heart defects, pulmonary  
 CC stenosis, scleroderma, obesity, metabolic disturbances associated with  
 CC obesity, transplantation, adrenoleukodystrophy, congenital adrenal  
 CC hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,  
 CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,  
 CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious  
 CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,  
 CC or Parkinson's disease), immune disorders, haematopoietic disorders,  
 CC dyslipidaemias, and wasting disorders associated with chronic diseases.  
 CC The proteins can also be used as immunogens to produce antibodies and as  
 CC vaccines. The sequences may further be used in chromosome mapping,  
 CC identifying individual from minute biological samples (tissue typing),  
 CC and in forensic identification of a biological sample. The present  
 CC sequence represents human NOV2a from the present invention.  
 XX  
 SQ Sequence 599 AA;  
 Query Match 72.7%; Score 32; DB 7; Length 599;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 Db 355 FLQLKFD 361  
 RESULT 39  
 ADD27936  
 ID ADD27936 standard; protein; 599 AA.  
 XX  
 AC ADD27936;  
 XX  
 XX 15-JAN-2004 (first entry)  
 DT  
 DE Human COX-1 amino acid sequence SEQ ID NO:22.  
 XX  
 KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
 KW COX-1 variant protein; genetic disease; tissue typing;  
 KW forensic identification.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003029411-A2.  
 FN  
 XX 10-APR-2003.  
 PD  
 XX 28-SEP-2002; 2002WO-US030947.  
 PF

XX 28-SEP-2001; 2001US-0326133P.  
 PR 15-APR-2002; 2002US-0373225P.  
 PR 16-APR-2002; 2002US-0373661P.  
 PR 16-SEP-2002; 2002US-0411575P.  
 XX  
 PA (UYVO ) UNIV BRIGHAM YOUNG.  
 XX  
 PI Simons D, Chandrasekharan VN;  
 XX  
 DR WPI; 2003-421222/39.  
 XX  
 PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
 PT encoding the polypeptide, useful for identifying a compound that binds to  
 PT and modulates the activity of COX-1 variant polypeptide.  
 XX  
 XX Disclosure; SEQ ID NO 22; 150pp; English.  
 XX  
 CC The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
 CC variant polypeptide (I). (I) is useful for identifying a compound which  
 CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
 CC used for mapping their respective genes on a chromosome, and so locating  
 CC gene regions associated with genetic disease, identifying an individual  
 CC from a minute biological sample (tissue typing), and to aid in forensic  
 CC identification of a biological sample. The present sequence represents a  
 CC sequence which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 599 AA;  
 Query Match 72.7%; Score 32; DB 7; Length 599;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 Db 355 FLQLKFD 361  
 RESULT 40  
 ADN05626  
 ID ADN05626 standard; protein; 599 AA.  
 XX  
 AC ADN05626;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Antipsoriatic protein sequence #978.  
 XX  
 KW antipsoriatic; gene therapy; psoriasis; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004028479-A2.  
 FN  
 XX 08-APR-2004.  
 PD  
 XX 25-SEP-2003; 2003WO-US030907.  
 PF  
 XX 25-SEP-2002; 2002US-0414006P.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
 PI Wu TD;  
 XX  
 XX WPI; 2004-305105/28.  
 DR N-PSDB; ADN05625.  
 DR  
 XX New PRO nucleic acid or polypeptide, useful for preparing a  
 PT pharmaceutical composition for diagnosing or treating psoriasis in a  
 PT mammal.  
 XX  
 PS Claim 9; SEQ ID NO 2020; 3069pp; English.



XX The invention relates to novel polynucleotide and polypeptides for  
 CC treating psoriasis or a sequence having at least 80% identity to the  
 CC above sequences. The nucleic acid is useful for preparing a composition  
 CC for diagnosing or treating psoriasis in a mammal. This sequence  
 CC corresponds to one of the polypeptides of the invention.  
 XX  
 SQ Sequence 599 AA;  
 Query Match 72.7%; Score 32; DB 8; Length 599;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 Db 355 FLQLKFD 361  
 ||||:|  
 355 FLQLKFD 361  
 RESULT 41  
 ADZ59945  
 ID ADZ59945 standard; protein; 599 AA.  
 AC ADZ59945;  
 XX  
 XX 30-JUN-2005 (first entry)  
 DT  
 DE Wild type human COX-1 SEQ ID NO 10.  
 KW analgesic; antipyretic; cardiovascular-gen.; anticoagulant;  
 KW antiarteriosclerotic; thrombolytic; vasotropic; antiinflammatory;  
 KW ophthalmological; antirheumatic; antiarthritic; osteopathic; antigout;  
 KW protein purification; pain; neurological disease; fever;  
 KW temperature disorder; cardiovascular disease; atherosclerosis;  
 KW metabolic disorder; thrombosis; hematological disease; restenosis;  
 KW vasculitis; inflammation; ocular disease; glaucoma; hypotensive;  
 KW ocular hypertension; uveitis; antiallergic; allergic conjunctivitis;  
 KW musculoskeletal disease; rheumatoid arthritis; ankylosing spondylitis;  
 KW osteoarthritis; bursitis; gout; splice variant; cyclooxygenase 1; COX-1;  
 KW enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2005035713-A2.  
 PN  
 XX  
 XX 21-APR-2005.  
 PD  
 XX  
 XX 20-AUG-2004; 2004WO-US027105.  
 PF  
 XX  
 XX 15-SEP-2003; 2003US-00663377.  
 PR  
 XX  
 XX (ALLR ) ALLERGAN INC.  
 PA  
 XX  
 XX Liang Y, Woodward DF;  
 PI  
 XX  
 XX WPI; 2005-296270/30.  
 DR  
 DR N-PSDB; ADZ59944.  
 XX  
 XX New isolated cyclooxygenase-1 (COX-1) polypeptide or variants, useful for  
 PT treating or preventing, e.g. pain, fever, atherosclerosis, thrombosis,  
 PT restenosis, glaucoma, allergic conjunctivitis, rheumatoid arthritis, or  
 PT osteoarthritis.  
 PT  
 XX  
 PS Claim 2; SEQ ID NO 10; 129pp; English.  
 XX  
 XX The invention describes an isolated COX-1 polypeptide. Also described  
 CC are: a COX-1 variant binding, agent, which binds an amino acid sequence  
 CC selected from SEQ ID NO. 14, 16, or 18, or its epitope; a cell comprising  
 CC the exogenously expressed polypeptide above; a method for identifying a  
 CC compound that modulates a COX-1 variant; a method for identifying a  
 CC compound that specifically binds to a COX-1 variant; a method for  
 CC identifying a compound that differentially modulates a COX-1 variant; a  
 CC method for identifying a compound that differentially binds to a COX-1  
 CC variant; an isolated nucleic acid molecule comprising: a nucleotide

CC sequence that encodes a polypeptide comprising an amino acid sequence  
 CC having at least 50% amino acid identity with SEQ ID NO. 10, or an amino  
 CC acid sequence selected from SEQ ID NO. 20, 22, or 24, or its conservative  
 CC variant; a nucleotide sequence that encodes an amino acid sequence  
 CC selected from SEQ ID NO. 2, 4, 6, or 8; or a nucleotide sequence selected  
 CC from 4 fully defined 1818-2280 bp sequences (SEQ ID NO. 1, 3, 5, or 7)  
 CC given in the specification; a vector comprising the isolated nucleic acid  
 CC molecule above; and a host cell comprising the vector above. The  
 CC polypeptides are useful for treating or preventing diseases or conditions  
 CC associated with COX-1 or COX-1 variant, including pain, fever,  
 CC cardiovascular disorder (e.g. atherosclerosis, thrombosis, restenosis, or  
 CC vasculitis), ocular disorder (e.g. glaucoma, ocular hypertension,  
 CC uveitis, allergic conjunctivitis, or related disorders), or inflammatory  
 CC disorders (e.g. rheumatoid arthritis, ankylosing spondylitis,  
 CC osteoarthritis, bursitis, tendinitis, or gout). The methods are useful  
 CC for designing drugs that bind to or modulate a wild-type COX-1. Compounds  
 CC identified can be used for preventing or reducing the severity of any of  
 CC a variety of conditions where modulation of the COX-1 enzyme or a COX-1  
 CC variant is beneficial. This is the amino acid sequence of wild type human  
 CC COX-1.  
 CC  
 XX  
 SQ Sequence 599 AA;

Query Match 72.7%; Score 32; DB 9; Length 599;

Best Local Similarity 85.7%; Pred. No. 8e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKFD 7

Db 355 FLQLKFD 361  
 ||||:|

RESULT 42

ADZ51365

ID ADZ51365 standard; protein; 599 AA.

AC ADZ51365;

XX

XX 30-JUN-2005 (first entry)

DT

XX

DE Amino acid sequence of ovarian cancer marker OV51A.

XX

XX cytotatic; gene therapy; ovarian cancer; ovarian cancer marker; OV51A;

KW prostaglandin-endoperoxide synthase 1.

XX

XX Homo sapiens.

OS

XX

PN WO2005034732-A2.

XX

XX 21-APR-2005.

PD

XX

XX 07-OCT-2004; 2004WO-US033166.

PF

XX

XX 07-OCT-2003; 2003US-0509171P.

PR

XX

XX (MILL-) MILLENNIUM PHARM INC.

PA

XX

XX Endege WO, Ford D, Gannavarapu M, Glatt K, Hoersch S, Kamatkar S;

PI Monahan JE, Schlegel R, Xu Y, Zhao X;

PI

XX WPI; 2005-306219/31.

XX

XX N-PSDB; ADZ51364.

DR

XX

XX Assessing whether a patient is afflicted with ovarian cancer comprises

PT determining a significant difference between the levels of expression of

PT an ovarian cancer marker in the patient sample and the sample from a

PT control subject.

XX

XX Example 1; SEQ ID NO 22; 164pp; English.

PS

XX The specification describes a method of assessing whether a patient is

CC afflicted with ovarian cancer. The method comprises determining the

CC presence of a significant difference between the levels of expression of

CC

CC an ovarian cancer marker in the patient sample and the sample from a  
 CC control subject. The method of the invention is useful for assessing,  
 CC diagnosing, preventing or treating ovarian cancer. The markers may also  
 CC be used in screening for agents that may treat or prevent ovarian cancer.  
 CC The present sequence represents the marker OV51A, which is prostaglandin-  
 CC endoperoxide synthase 1 transcript variant 1.  
 XX  
 XX Sequence 599 AA;

SQ  
 Query Match 72.7%; Score 32; DB 9; Length 599;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKPD 7  
 ||||:|  
 DB 355 FLQLKPD 361

RESULT 43  
 ID AAP91008 standard; protein; 600 AA.  
 XX

AC AAP91008;

XX 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 13-MAR-1990 (first entry)

XX Prostaglandin endoperoxide synthetase.

XX Recombinant.

XX Ovis aries.

XX JP01228479-A.

XX 12-SEP-1989.

PF 10-MAR-1988; 88JP-00054941.

PR 10-MAR-1988; 88JP-00054941.

XX (MEIP ) MEIJI MILK PROD CO LTD.

XX WPI; 1989-312224/43.

DR N-PSDB; AAN91622.

XX Prostaglandin endo-peroxide synthetase coding DNA - useful as starting  
 PT material for recombinant, and for synthesis of various prostaglandin(s)  
 PT and laboratory reagent.

XX Claim 1; Fig 1; 11pp; Japanese.

XX (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003  
 CC to correct PA field.)

XX Sequence 600 AA;

Query Match 72.7%; Score 32; DB 1; Length 600;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKPD 7  
 ||||:|  
 DB 356 FLQLKPD 362

RESULT 44  
 ID ADD27937 standard; protein; 600 AA.  
 XX

XX ADD27937;

DT 15-JAN-2004 (first entry)  
 XX  
 XX Ovine COX-1 amino acid sequence SEQ ID NO:23.  
 DE  
 XX cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
 KW COX-1 variant protein; genetic disease; tissue typing;  
 KW forensic identification.  
 XX

OS Ovis sp.

XX WO2003029411-A2.

XX 10-APR-2003.

XX 28-SEP-2002; 2002WO-US030947.

XX 28-SEP-2001; 2001US-0326133P.

PR 15-APR-2002; 2002US-0373225P.

PR 16-APR-2002; 2002US-0373661P.

PR 16-SEP-2002; 2002US-0411575P.

XX (UYYO ) UNIV BRIGHAM YOUNG.

XX Simmons D, Chandrasekharan VN;

WPI; 2003-421222/39.

XX Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
 PT encoding the polypeptide, useful for identifying a compound that binds to  
 PT and modulates the activity of COX-1 variant polypeptide.

XX Disclosure; SEQ ID NO 23; 150pp; English.

XX The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
 CC variant polypeptide (I). (I) is useful for identifying a compound which  
 CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
 CC used for mapping their respective genes on a chromosome, and so locating  
 CC gene regions associated with genetic disease, identifying an individual  
 CC from a minute biological sample (tissue typing), and to aid in forensic  
 CC identification of a biological sample. The present sequence represents a  
 CC sequence which is used in the exemplification of the present invention.

XX Sequence 600 AA;

Query Match 72.7%; Score 32; DB 7; Length 600;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKPD 7  
 ||||:|  
 DB 356 FLQLKPD 362

RESULT 45

ABB57303

ID ABB57303 standard; protein; 602 AA.

XX ABB57303;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related protein sequence SEQ ID NO:849.

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX Mus musculus.

XX WO200189188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP004192.

XX PR 18-MAY-2000; 2000JP-00145977.  
 XX PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 XX PI Iehikawa K, Asai S, Takahaashi Y, Nagata T, Ishii Y;  
 XX DR WPI; 2002-034733/04.  
 XX DR N-PSDB; ABI99766.  
 XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 PT expression levels of particular genes defined in the specification or by  
 PT determining the expression profile of a gene group comprising these  
 PT genes.  
 XX PS Claim 2; Page 2109-2111; 2690pp; English.  
 XX CC The present invention describes a method for examining ischaemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischaemic condition (e.g. compressive  
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the  
 CC protein sequences in ABB57020 to ABB57374) or by determining the  
 CC expression profile of a gene group comprising these genes. The expression  
 CC levels or expression profiles produced by these genes are used as an  
 CC indicator when screening for ischaemic condition-improving drugs or  
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR  
 CC primers for a mouse ischaemic condition related sequence, which are used  
 CC in the exemplification of the present invention  
 XX SQ Sequence 602 AA;  
 Query Match 72.7%; Score 32; DB 5; Length 602;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 Db 358 FLQLKFD 364  
 |||||  
 RESULT 46  
 ABR42251  
 ID ABR42251 standard; protein; 602 AA.  
 XX AC ABR42251;  
 XX DT 28-JUL-2003 (first entry)  
 XX DE Mouse cyclooxygenase 1 (COX-1).  
 XX KW Cyclooxygenase 1; COX-1; mouse; enzyme; vulnarary; osteopathic;  
 XX KW gene therapy.  
 XX OS Mus sp.  
 XX PN WO2003022224-A2.  
 XX PD 20-MAR-2003.  
 XX PF 11-SEP-2002; 2002WO-US028930.  
 XX PR 11-SEP-2001; 2001US-00953067.  
 XX PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 XX PI O'connor PJ;  
 XX DR WPI; 2003-313185/30.  
 XX DR N-PSDB; ACC5775.  
 XX

PT Novel vector useful for enhancing wound healing or treating osteoporosis,  
 PT osteogenesis imperfecta, and brittle bone conditions, comprises a  
 PT promoter linked to a cyclooxygenase expression cassette.  
 XX PS Disclosure; Page 81-84; 88pp; English.  
 XX CC The present sequence is the protein sequence of mouse cyclooxygenase 1  
 CC (COX-1). A claimed vector for use in enhancing wound healing comprises a  
 CC promoter linked to a COX expression cassette. A claimed method for  
 CC enhanced wound healing involves delivering the vector to the location of  
 CC the wound. The wound may be a bone fracture or a skin wound. A claimed  
 CC method for treating osteoporosis, osteogenesis imperfecta and brittle  
 CC bone conditions comprises administering the vector. A claimed composition  
 CC for use in wound healing comprises a COX protein, especially COX-1, COX-2  
 CC or both  
 XX SQ Sequence 602 AA;  
 Query Match 72.7%; Score 32; DB 6; Length 602;  
 Best Local Similarity 85.7%; Pred. No. 8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLKFD 7  
 Db 358 FLQLKFD 364  
 |||||  
 RESULT 47  
 ADD27941  
 ID ADD27941 standard; protein; 602 AA.  
 XX AC ADD27941;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE Rat COX-1 amino acid sequence SEQ ID NO:30.  
 XX KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
 KW COX-1 variant protein; genetic disease; tissue typing;  
 KW forensic identification.  
 XX OS Rattus sp.  
 XX PN WO2003029411-A2.  
 XX PD 10-APR-2003.  
 XX PF 28-SEP-2002; 2002WO-US030947.  
 XX PR 28-SEP-2001; 2001US-0326133P.  
 XX PR 15-APR-2002; 2002US-0373225P.  
 XX PR 16-APR-2002; 2002US-0373661P.  
 XX PR 16-SEP-2002; 2002US-0411575P.  
 XX PA (UYYO ) UNIV BRIGHAM YOUNG.  
 XX PI Simmons D, Chandrasekharan VN;  
 XX DR WPI; 2003-421222/39.  
 XX PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
 PT encoding the polypeptide, useful for identifying a compound that binds to  
 PT and modulates the activity of COX-1 variant polypeptide.  
 XX PS Disclosure; SEQ ID NO 30; 150pp; English.  
 XX CC The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
 CC variant polypeptide (I). (I) is useful for identifying a compound which  
 CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
 CC used for mapping their respective genes on a chromosome, and so locating  
 CC gene regions associated with genetic disease, identifying an individual  
 CC from a minute biological sample (tissue typing), and to aid in forensic  
 CC identification of a biological sample. The present sequence represents a

CC sequence which is used in the exemplification of the present invention.

XX Sequence 602 AA;

Query Match 72.7%; Score 32; DB 7; Length 602;  
Best Local Similarity 85.7%; Pred. No. 8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||:|  
Db 358 FLQLKFD 364

RESULT 48  
ADD27940  
ID ADD27940 standard; protein; 602 AA.

XX AC ADD27940;

XX DT 15-JAN-2004 (first entry)

XX DE Murine COX-1 amino acid sequence SEQ ID NO:29.

XX KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
XX KW COX-1 variant protein; genetic disease; tissue typing;  
XX KW forensic identification.

XX OS Mus sp.

XX PN WO2003029411-A2.

XX PD 10-APR-2003.

XX PF 28-SEP-2002; 2002WO-US030947.

XX PR 28-SEP-2001; 2001US-0326133P.

XX PR 15-APR-2002; 2002US-0373225P.

XX PR 16-APR-2002; 2002US-0373661P.

XX PR 16-SEP-2002; 2002US-0411575P.

XX PA (UYYO ) UNIV BRIGHAM YOUNG.

XX PI Simmons D, Chandrasekharan VN;

XX PS WPI; 2003-421222/39.

XX PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
XX PT encoding the polypeptide, useful for identifying a compound that binds to  
XX PT and modulates the activity of COX-1 variant polypeptide.

XX PS Disclosure; SEQ ID NO 29; 150pp; English.

XX CC The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
XX CC variant polypeptide (I). (I) is useful for identifying a compound which  
XX CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
XX CC used for mapping their respective genes on a chromosome, and so locating  
XX CC gene regions associated with genetic disease, identifying an individual  
XX CC from a minute biological sample (tissue typing), and to aid in forensic  
XX CC identification of a biological sample. The present sequence represents a  
XX CC sequence which is used in the exemplification of the present invention.

XX SQ Sequence 602 AA;

Query Match 72.7%; Score 32; DB 7; Length 602;  
Best Local Similarity 85.7%; Pred. No. 8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||:|  
Db 358 FLQLKFD 364

RESULT 49

ADD27938

ID ADD27938 standard; protein; 603 AA.

XX AC ADD27938;

XX DT 15-JAN-2004 (first entry)

XX DE Canine COX-1 amino acid sequence SEQ ID NO:24.

XX KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
XX KW COX-1 variant protein; genetic disease; tissue typing;  
XX KW forensic identification.

XX OS Canis sp.

XX PN WO2003029411-A2.

XX PD 10-APR-2003.

XX PF 28-SEP-2002; 2002WO-US030947.

XX PR 28-SEP-2001; 2001US-0326133P.

XX PR 15-APR-2002; 2002US-0373225P.

XX PR 16-APR-2002; 2002US-0373661P.

XX PR 16-SEP-2002; 2002US-0411575P.

XX PA (UYYO ) UNIV BRIGHAM YOUNG.

XX PI Simmons D, Chandrasekharan VN;

XX DR WPI; 2003-421222/39.

XX PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide

XX PT encoding the polypeptide, useful for identifying a compound that binds to

XX PT and modulates the activity of COX-1 variant polypeptide.

XX PS Disclosure; SEQ ID NO 24; 150pp; English.

XX CC The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
XX CC variant polypeptide (I). (I) is useful for identifying a compound which  
XX CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
XX CC used for mapping their respective genes on a chromosome, and so locating  
XX CC gene regions associated with genetic disease, identifying an individual  
XX CC from a minute biological sample (tissue typing), and to aid in forensic  
XX CC identification of a biological sample. The present sequence represents a  
XX CC sequence which is used in the exemplification of the present invention.

XX SQ Sequence 603 AA;

Query Match 72.7%; Score 32; DB 7; Length 603;  
Best Local Similarity 85.7%; Pred. No. 8e+02; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||:|  
Db 359 FLQLKFD 365

RESULT 50

ADD27939

ID ADD27939 standard; protein; 606 AA.

XX AC ADD27939;

XX DT 15-JAN-2004 (first entry)

XX DE Rabbit COX-1 amino acid sequence SEQ ID NO:27.

XX KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;  
XX KW COX-1 variant protein; genetic disease; tissue typing;  
XX KW forensic identification.

XX OS Oryctolagus cuniculus.

XX WO2003029411-A2.  
XX 10-APR-2003.  
XX 28-SEP-2002; 2002WO-US030947.  
XX 28-SEP-2001; 2001US-0326133P.  
XX 15-APR-2002; 2002US-0373225P.  
XX 16-APR-2002; 2002US-0373661P.  
XX 16-SEP-2002; 2002US-0411575P.  
XX (UYYO ) UNIV BRIGHAM YOUNG.  
XX  
XX Simmons D, Chandrasekharan VN;  
XX WPI; 2003-421222/39.  
XX  
XX Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
PT encoding the polypeptide, useful for identifying a compound that binds to  
PT and modulates the activity of COX-1 variant polypeptide.  
XX  
XX Disclosure; SEQ ID NO 27; 150pp; English.  
XX  
XX The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
CC variant polypeptide (I). (I) is useful for identifying a compound which  
CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
CC used for mapping their respective genes on a chromosome, and so locating  
CC gene regions associated with genetic disease, identifying an individual  
CC from a minute biological sample (tissue typing), and to aid in forensic  
CC identification of a biological sample. The present sequence represents a  
CC sequence which is used in the exemplification of the present invention.  
XX  
XX Sequence 606 AA;  
XX  
XX Query Match 72.7%; Score 32; DB 7; Length 606;  
XX Best Local Similarity 85.7%; Pred. No. 8.1e+02;  
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLQLEPD 7  
Db 362 FLQLKFD 368

Search completed: May 9, 2006, 02:15:28  
Job time : 135.4 secs

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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:17:29 ; Search time 16.4 Seconds  
(without alignments)  
52.802 Million cell updates/sec

Title: US-09-870-216C-5  
Perfect score: 44  
Sequence: 1 FLQLEFDV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	79.5	680	2	G82526
2	33	75.0	129	2	G64232
3	33	75.0	430	2	B82096
4	32	72.7	154	2	G95328
5	32	72.7	228	2	T09802
6	32	72.7	228	2	T12000
7	32	72.7	229	2	S50328
8	32	72.7	274	2	G97034
9	32	72.7	599	2	JH0259
10	32	72.7	599	2	A29947
11	32	72.7	600	2	S00561
12	32	72.7	600	2	A28960
13	32	72.7	602	2	S39782
14	32	72.7	602	2	A35564
15	32	72.7	602	2	S69198
16	32	72.7	756	2	F83704
17	31	70.5	204	2	A32252
18	31	70.5	210	2	A40979
19	31	70.5	321	2	G70415
20	31	70.5	360	2	T06786
21	31	70.5	384	2	A86324
22	31	70.5	390	2	F81393
23	31	70.5	400	2	B90139
24	31	70.5	578	2	T44444
25	31	70.5	875	2	T19678
26	31	70.5	1042	2	G64514
27	31	70.5	1852	2	JCS546
28	30	68.2	100	2	AE2073
29	30	68.2	155	2	E84198

30	68.2	211	2	D69888	micrococcal nuclea
31	68.2	226	2	G45170	cytochrome-c oxida
32	68.2	229	2	G90730	antitermination pr
33	68.2	237	2	B81870	probable membrane
34	68.2	257	2	D85581	hypothetical prote
35	68.2	272	1	G82076	3',5'-cyclic-nucle
36	68.2	280	2	T38816	hypothetical prote
37	68.2	290	2	B97100	pyridoxal kinase r
38	68.2	296	2	T12770	probable endonucle
39	68.2	299	2	T23932	hypothetical prote
40	68.2	300	2	C69857	formyltetrahydrofo
41	68.2	301	2	C85574	probable LysR-like
42	68.2	301	2	C90723	probable transcrip
43	68.2	365	2	T04247	hypothetical prote
44	68.2	372	2	T01551	receptor kinase ho
45	68.2	420	2	T51874	hypothetical prote
46	68.2	429	2	T01550	receptor kinase ho
47	68.2	433	2	T31511	hypothetical prote
48	68.2	457	1	G70116	histidine-tRNA lig
49	68.2	700	2	D70917	probable tkt prote
50	68.2	770	2	T15742	hypothetical prote
51	68.2	908	2	AE2675	pyruvate, orthophos
52	68.2	933	2	C97457	pyruvate, phosphat
53	68.2	938	2	T45924	probable translati
54	68.2	976	2	B87291	2-oxoglutarate deh
55	68.2	980	2	AD1922	methyl-accepting c
56	68.2	1092	2	S77546	cobN protein - Syn
57	68.2	1373	2	E97722	hypothetical prote
58	68.2	1494	2	T13798	hypothetical prote
59	68.2	1634	1	JCS500	phosphoinositide 3
60	68.2	2559	2	T09144	probable guanine n
61	65.9	90	2	D69874	transcription regu
62	65.9	157	2	D84155	conserved hypoteth
63	65.9	169	2	S76351	hypothetical prote
64	65.9	179	2	D82718	50S ribosomal prot
65	65.9	182	2	T36540	probable orotate p
66	65.9	219	2	T18541	moB protein precu
67	65.9	234	2	C69519	conserved hypoteth
68	65.9	238	2	AH0106	hypothetical prote
69	65.9	242	2	H70980	probable rabW prot
70	65.9	276	2	T12971	hypothetical prote
71	65.9	280	2	H81356	probable fructose-
72	65.9	298	2	S12579	carbonate dehydrat
73	65.9	304	2	I59261	probable rhizopine
74	65.9	309	2	C96019	hypothetical prote
75	65.9	324	2	G95709	hypothetical prote
76	65.9	327	2	T13782	hypothetical prote
77	65.9	339	2	T21665	hypothetical prote
78	65.9	343	2	AB2451	soxR family transc
79	65.9	346	2	B97202	hypothetical prote
80	65.9	410	2	S69023	hypothetical prote
81	65.9	450	2	B71976	conserved hypoteth
82	65.9	450	2	F64530	hypothetical prote
83	65.9	472	2	T08860	hypothetical prote
84	65.9	473	2	B84556	hypothetical prote
85	65.9	513	2	B64431	modulation factor
86	65.9	577	2	D75406	aspartyl-tRNA synt
87	65.9	615	2	A93105	probable ANP-depen
88	65.9	638	2	AF3463	flagellar protein
89	65.9	654	2	T50198	probable transcrip
90	65.9	671	2	D86324	protein FlAD16.25
91	65.9	680	2	S26764	major coat protein
92	65.9	687	2	D96553	hypothetical prote
93	65.9	734	2	E72271	5-methyltetrahydro
94	65.9	1024	2	C64208	hypothetical prote
95	65.9	1088	2	T05731	DNA-directed DNA p
96	65.9	1244	2	T19615	hypothetical prote
97	65.9	1249	2	A56511	myosin I myoA - Em
98	65.9	1283	2	T49692	related to SCP160
99	65.9	1505	2	S26765	genome polyprotein
100	65.9	1596	2	A35927	190K DNA-binding p
101	65.9	1848	2	A44140	cellulose-binding
102	65.9	1866	1	GNWE2C	genome polyprotein

103	29	65.9	4910	2	S64942	probable membrane	176	28	63.6	1413	2	T26467	hypothetical prote
104	28.5	64.8	464	2	D71219	probable L-asparta	177	28	63.6	1751	2	T09394	gag-pro-pol polypr
105	28	63.6	62	2	A82269	hypothetical prote	178	28	63.6	1857	1	S01787	fatty-acid synthas
106	28	63.6	117	2	E83998	hypothetical prote	179	28	63.6	2111	2	T15390	hypothetical prote
107	28	63.6	140	2	C72218	conserved hypotnet	180	28	63.6	2459	2	AF2136	peptide synthetase
108	28	63.6	162	1	S07661	probable phosphotr	181	28	63.6	2712	2	T05113	hypothetical prote
109	28	63.6	163	2	A10905	protein-Npi-phosph	182	28	63.6	3144	2	S64791	VP813 protein - ye
110	28	63.6	163	2	F85984	phosphotransferase	183	28	63.6	6260	2	T30228	polyketide synthas
111	28	63.6	163	2	C91139	phosphotransferase	184	27	61.4	24	2	A45336	cystic fibrosis tr
112	28	63.6	163	2	I76720	phosphotransferase	185	27	61.4	63	2	S65918	homeotic protein e
113	28	63.6	180	2	H82109	probable glycine c	186	27	61.4	87	2	JC5852	polyketide synthas
114	28	63.6	190	2	E84355	DNA-directed RNA p	187	27	61.4	87	2	D86816	hypothetical prote
115	28	63.6	195	2	A75452	conserved hypotnet	188	27	61.4	105	2	AF1985	nitrogen fixation
116	28	63.6	203	2	T50421	hypothetical prote	189	27	61.4	112	2	D49846	spal3 protein - Sh
117	28	63.6	206	2	T25161	hypothetical prote	190	27	61.4	113	1	S57775	thioredoxin h, cyt
118	28	63.6	218	2	G82922	conserved hypotnet	191	27	61.4	129	2	S73744	MG296 homolog A05
119	28	63.6	228	2	C38941	cytochrome-c oxida	192	27	61.4	133	2	C71485	hypothetical prote
120	28	63.6	228	2	B82087	probable smp prote	193	27	61.4	135	2	S36197	hypothetical prote
121	28	63.6	239	2	T20515	hypothetical prote	194	27	61.4	146	2	E54403	hemoglobin C beta
122	28	63.6	244	2	H69594	6-carboxyhexanoate	195	27	61.4	146	2	S16371	hemoglobin beta-II
123	28	63.6	259	2	B82978	catabolite repress	196	27	61.4	146	2	D54403	hemoglobin C beta
124	28	63.6	282	2	S0454	hypothetical prote	197	27	61.4	157	2	D75022	6-pyruvoyl tetrahy
125	28	63.6	300	2	T00274	hypothetical prote	198	27	61.4	157	2	C71209	hypothetical prote
126	28	63.6	301	2	S75998	hypothetical prote	199	27	61.4	161	2	S67178	translation initia
127	28	63.6	317	1	XNSMUD	UDPGlucose-hexose-	200	27	61.4	168	2	D64604	methylated-DNA-lpr
128	28	63.6	319	2	AF0489	probable iron tran	201	27	61.4	168	2	C71910	methylated-DNA-lpr
129	28	63.6	335	2	G71867	hypothetical prote	202	27	61.4	172	2	S62761	hypothetical prote
130	28	63.6	335	2	B64572	hypothetical prote	203	27	61.4	177	2	D89082	imidazoleglycerol-
131	28	63.6	342	2	B83272	conserved hypotnet	204	27	61.4	177	2	T24500	hypothetical prote
132	28	63.6	352	2	T03845	probable sterol 24	205	27	61.4	178	2	S73409	hypothetical prote
133	28	63.6	361	2	S63686	sterol 24-C-methyl	206	27	61.4	182	2	PN0541	recombination prot
134	28	63.6	364	2	B85430	hypothetical prote	207	27	61.4	184	2	B95350	protein import
135	28	63.6	368	2	A27535	ubiquinol-cytochro	208	27	61.4	194	2	F64075	urease accessory p
136	28	63.6	368	2	AE1543	alanine racemase h	209	27	61.4	203	2	T60277	MADS box protein A
137	28	63.6	370	2	S54297	protein phosphatas	210	27	61.4	204	1	WZVZB3	24K HandIII-C prot
138	28	63.6	372	2	I64223	bifunctional endo-	211	27	61.4	204	2	I42503	C5L protein - vacc
139	28	63.6	384	2	D90547	oligopeptide ABC t	212	27	61.4	218	2	T25229	hypothetical prote
140	28	63.6	391	2	C84166	hypothetical prote	213	27	61.4	226	2	H70322	conserved hypotnet
141	28	63.6	399	2	S34681	hypothetical prote	214	27	61.4	227	2	T13783	cytochrome-c oxida
142	28	63.6	411	2	AE3052	two component sens	215	27	61.4	227	2	S12378	MADS box protein d
143	28	63.6	417	2	F98233	two-component sens	216	27	61.4	228	2	E45170	cytochrome-c oxida
144	28	63.6	426	2	B90410	hypothetical prote	217	27	61.4	228	2	T07066	MADS-box protein h
145	28	63.6	455	2	S78356	replicative DNA he	218	27	61.4	228	2	T07410	MADS box protein h
146	28	63.6	464	2	C72861	late expression fa	219	27	61.4	230	2	S34231	hypothetical prote
147	28	63.6	465	2	T41830	LEF-4 orf90 - Bomb	220	27	61.4	230	2	B95353	protein import
148	28	63.6	465	2	AC0438	conserved hypotnet	221	27	61.4	231	2	S31693	MADS box protein g
149	28	63.6	467	2	S52133	argininosuccinate	222	27	61.4	231	2	D69224	hypothetical prote
150	28	63.6	489	2	F82085	glutamate synthase	223	27	61.4	235	2	S60158	chlamyopsin - Chla
151	28	63.6	499	2	AH2413	alginatate o-acetyl	224	27	61.4	235	2	B86394	protein T24P13.12
152	28	63.6	511	1	S31308	aldehyde dehydroge	225	27	61.4	239	2	JC5736	H+-transporting tw
153	28	63.6	512	2	G75367	potassium uptake p	226	27	61.4	240	2	S32236	ribosomal protein
154	28	63.6	529	2	G86265	F3F19.17 protein -	227	27	61.4	240	2	D59261	sulfate ABC transp
155	28	63.6	538	2	A86157	probable importin	228	27	61.4	246	2	T50628	hypothetical prote
156	28	63.6	540	2	T20352	hypothetical prote	229	27	61.4	246	2	T46839	hypothetical prote
157	28	63.6	618	2	T05518	hypothetical prote	230	27	61.4	247	2	AD3649	transcription regu
158	28	63.6	654	2	G83213	hypothetical prote	231	27	61.4	248	2	D84269	DNA-directed RNA p
159	28	63.6	688	2	T05353	hypothetical prote	232	27	61.4	249	2	T43940	RNA-polymerase cha
160	28	63.6	690	2	T34149	hypothetical prote	233	27	61.4	258	2	S33535	myosin heavy chain
161	28	63.6	703	2	I64226	DNA helicase II (m	234	27	61.4	262	2	T01713	ribosomal protein
162	28	63.6	715	2	B84853	hypothetical prote	235	27	61.4	263	2	G72771	probable Prolifera
163	28	63.6	747	2	F86474	unknown protein [i	236	27	61.4	269	2	C86726	conserved hypotnet
164	28	63.6	766	2	T03218	armadillo-like pro	237	27	61.4	269	2	G86321	F6A14.11 protein -
165	28	63.6	807	2	A64575	VirB4 homolog - He	238	27	61.4	284	2	B25624	tropomyosin I, emb
166	28	63.6	845	2	T30090	probable zinc prot	239	27	61.4	284	2	A25624	formate hydratase
167	28	63.6	925	1	TVH048	transforming prote	240	27	61.4	285	1	B84461	hypothetical prote
168	28	63.6	954	2	T24748	hypothetical prote	241	27	61.4	287	2	T28367	formyltetrahydrofo
169	28	63.6	969	2	T33156	hypothetical prote	242	27	61.4	289	2	A84058	NADH2 dehydrogenas
170	28	63.6	1048	2	S57155	NMD5 protein - yea	243	27	61.4	290	2	S26016	transcription regu
171	28	63.6	1067	2	T31714	probable zinc prot	244	27	61.4	301	2	S57531	hypothetical prote
172	28	63.6	1230	2	S47466	cellulose 1,4-beta	245	27	61.4	302	2	T31542	cysteine synthase
173	28	63.6	1293	2	T01512	hypothetical prote	246	27	61.4	306	2	D95258	cysteine synthase
174	28	63.6	1378	2	AB2817	DNA-directed RNA p	247	27	61.4	306	2	D98123	acylttransferase (B
175	28	63.6	1411	2	C97595	RNA polymerase bet	248	27	61.4	306	2	A39853	



249	27	61.4	306	2	AD0637	lipid A biosynthes	322	27	61.4	617	2	IS0716	Al isoform of vacu	
250	27	61.4	309	2	S51573	nocB protein precu	323	27	61.4	618	2	A56807	H+-transporting tw	
251	27	61.4	311	2	AF0150	probable outer mem	324	27	61.4	639	2	E98281	cobT protein [impo	
252	27	61.4	328	2	C89871	hypothetical prote	325	27	61.4	639	2	AC3002	cobrynic acid syn	
253	27	61.4	334	2	S73554	MG413 homolog Cl2	326	27	61.4	642	2	C96586	hypothetical prote	
254	27	61.4	335	2	T03508	glyceraldehyde-3-P	327	27	61.4	656	2	H70365	hypothetical prote	
255	27	61.4	337	2	T28826	hypothetical prote	328	27	61.4	659	2	D81858	probable aminopept	
256	27	61.4	346	2	T21996	hypothetical prote	329	27	61.4	684	2	T47694	probable serine/th	
257	27	61.4	348	2	S16898	recombination prot	330	27	61.4	699	2	T07037	heat shock protein	
258	27	61.4	348	2	JN0639	recombination prot	331	27	61.4	699	2	S25541	heat shock protein	
259	27	61.4	351	2	S16896	recombination prot	332	27	61.4	699	2	S51454	EST1 protein - yea	
260	27	61.4	353	2	T33782	hypothetical prote	333	27	61.4	713	2	D90558	VgrG protein [impo	
261	27	61.4	357	1	P2WLB4	l2 protein - bovin	334	27	61.4	713	2	D85509	hypothetical prote	
262	27	61.4	358	2	S57176	hypothetical prote	335	27	61.4	730	2	T44313	hypothetical prote	
263	27	61.4	360	2	S17782	recombination prot	336	27	61.4	730	2	S70954	otnG protein - Vib	
264	27	61.4	360	2	I40347	recombination prot	337	27	61.4	738	2	S55519	chitin synthase (E	
265	27	61.4	361	1	IBRTE	hydroxymethylbilan	338	27	61.4	738	2	A53542	brefeldin A-sensit	
266	27	61.4	363	2	JC1377	recombination prot	339	27	61.4	740	2	D71602	hypothetical prote	
267	27	61.4	363	2	AH2806	RecA protein [impo	340	27	61.4	757	2	T24266	hypothetical prote	
268	27	61.4	365	2	H96647	hypothetical prote	341	27	61.4	758	2	S54522	hypothetical prote	
269	27	61.4	365	2	AF3218	chloromuconate cyc	342	27	61.4	762	2	D70407	DNA mismatch repai	
270	27	61.4	372	2	S42837	Tl6G12.3 protein -	343	27	61.4	774	2	H70040	hypothetical prote	
271	27	61.4	374	2	S18887	H+-exporting ATPas	344	27	61.4	778	2	E97224	ATP-dependent Ion	
272	27	61.4	375	2	T25089	hypothetical prote	345	27	61.4	790	2	D86528	omp85 analog [impo	
273	27	61.4	378	2	AE3350	recA protein [impo	346	27	61.4	790	2	D72094	omp85 analog - Chl	
274	27	61.4	392	2	T41820	VLF-1 orf77 - Bomb	347	27	61.4	821	2	C84304	DNA helicase [impo	
275	27	61.4	392	2	C96766	hypothetical prote	348	27	61.4	827	2	A90544	hypothetical prote	
276	27	61.4	396	1	JH0631	cellular tumor ant	349	27	61.4	838	2	P97768	hypothetical prote	
277	27	61.4	399	2	A69456	tungsten formylmet	350	27	61.4	848	2	T34823	probable turgor pr	
278	27	61.4	399	2	A69893	hypothetical prote	351	27	61.4	864	2	S60441	hypothetical prote	
279	27	61.4	404	2	H81983	pinlin glycosylatio	352	27	61.4	870	2	B71698	hypothetical prote	
280	27	61.4	406	2	B88573	protein Tl6G12.3 (	353	27	61.4	885	1	A55453	nucleotide diphosp	
281	27	61.4	411	2	H64239	UV protection prot	354	27	61.4	917	2	B85057	hypothetical prote	
282	27	61.4	412	2	A72473	probable Na+/H+ an	355	27	61.4	933	2	A75541	pyruvate dehydroge	
283	27	61.4	416	2	G97585	recA protein (reco	356	27	61.4	943	2	F70873	aconitate hydratase	
284	27	61.4	424	2	S57458	formylmethanofuran	357	27	61.4	963	2	T40290	hypothetical prote	
285	27	61.4	424	2	T12047	major outer membra	358	27	61.4	967	2	S58360	lanthibiotic pepS b	
286	27	61.4	431	2	A45142	cleavage stimulati	359	27	61.4	1017	2	T30195	DNA-directed DNA p	
287	27	61.4	434	2	H90131	regulator of epide	360	27	61.4	1029	2	F86359	hypothetical prote	
288	27	61.4	437	2	S15704	transforming prote	361	27	61.4	1068	1	A43322	1-phosphatidylinos	
289	27	61.4	437	2	A69075	formylmethanofuran	362	27	61.4	1068	1	T38110	1-phosphatidylinos	
290	27	61.4	438	2	C64143	hypothetical prote	363	27	61.4	1096	2	T21091	hypothetical prote	
291	27	61.4	439	2	H81414	probable heat shoc	364	27	61.4	1157	2	H69163	DNA helicase relat	
292	27	61.4	445	2	AF0483	metalloproteinase	365	27	61.4	1200	2	S68258	DNA polymerase gam	
293	27	61.4	452	2	T22948	hypothetical prote	366	27	61.4	1237	2	S64385	probable membrane	
294	27	61.4	461	2	E88134	probable aminotran	367	27	61.4	1242	2	T45976	myosin heavy chain	
295	27	61.4	462	2	A13282	prinosomal protein	368	27	61.4	1289	1	GUBPT4	proximal tail fibe	
296	27	61.4	466	2	E70865	trigger factor tig	369	27	61.4	1346	2	T14849	cytoadherence link	
297	27	61.4	475	1	RKXHLK	ribulose-bisphosph	370	27	61.4	1411	2	T18417	hypothetical prote	
298	27	61.4	479	2	T23643	hypothetical prote	371	27	61.4	1417	2	T18418	hypothetical prote	
299	27	61.4	491	2	S58330	probable membrane	372	27	61.4	1463	2	A36861	orf 1b protein - L	
300	27	61.4	497	2	AE2341	lignostilbene-alph	373	27	61.4	1509	1	A27224	myosin heavy chain	
301	27	61.4	508	2	S03551	hypothetical prote	374	27	61.4	1611	1	WTMPV	183K protein - pep	
302	27	61.4	509	2	E64010	hypothetical prote	375	27	61.4	2017	1	A36014	myosin heavy chain	
303	27	61.4	513	2	JCS965	cytochrome P450 Cy	376	27	61.4	2057	2	S61477	myosin II heavy ch	
304	27	61.4	515	2	S20493	endoglucanase - Cl	377	27	61.4	3461	2	S58870	reelin precursor -	
305	27	61.4	530	2	JC6030	3-oxo-salpa-stero	378	27	61.4	4717	2	T41581	hypothetical coile	
306	27	61.4	532	2	A45392	RNA-directed RNA p	379	26	5	60.2	288	2	S44630	f22b7.9 protein -
307	27	61.4	537	2	I53719	NF-kappa-B transcr	380	26	59.1	50	2	S77838	hypothetical prote	
308	27	61.4	547	2	T51761	cyclohex-1-ene-1-c	381	26	59.1	55	2	A32963	extracellular matr	
309	27	61.4	550	2	A42017	transcription fact	382	26	59.1	64	2	E81078	hypothetical prote	
310	27	61.4	551	2	A40851	transforming prote	383	26	59.1	76	2	F83563	hypothetical prote	
311	27	61.4	558	2	JC2004	nuclear factor-kap	384	26	59.1	85	2	AB3007	hypothetical prote	
312	27	61.4	574	1	S11032	5'-nucleotidase (E	385	26	59.1	94	2	T04289	hypothetical prote	
313	27	61.4	583	2	G95214	ABC transporter, A	386	26	59.1	97	1	AYKBL	citrate (pro-38)-l	
314	27	61.4	583	2	F98078	hypothetical prote	387	26	59.1	101	2	S71780	RNA-binding protei	
315	27	61.4	585	2	T18736	hypothetical prote	388	26	59.1	105	2	F84984	cytochrome o ubiqu	
316	27	61.4	598	2	E81084	aminopeptidase, pr	389	26	59.1	110	2	T17913	hypothetical prote	
317	27	61.4	611	2	I50715	A2 isoform of vacu	390	26	59.1	118	2	T01883	hypothetical prote	
318	27	61.4	612	2	T02414	probable protein k	391	26	59.1	125	2	AH2086	gas vesicle protei	
319	27	61.4	613	2	T21325	hypothetical prote	392	26	59.1	127	2	C83640	probable transcrip	
320	27	61.4	614	2	T29937	hypothetical prote	393	26	59.1	131	2	AF2034	hypothetical prote	
321	27	61.4	617	2	B46091	H+-exporting ATPas	394	26	59.1	133	2	AF1964	hypothetical prote	

395	26	59.1	142	2	D86348	F24J8.15 protein (	468	26	59.1	281	2	S75198	hypothetical prote
396	26	59.1	150	2	C86876	hypothetical prote	469	26	59.1	284	1	F64338	agmatinase (EC 3.5
397	26	59.1	152	2	AD1033	hypothetical prote	470	26	59.1	288	2	S18990	probable acyl-CoA
398	26	59.1	153	2	H82153	hypothetical prote	471	26	59.1	289	2	AD0694	probable HlyD-fam
399	26	59.1	162	2	H83575	conserved hypotet	472	26	59.1	289	2	AF2144	hypothetical prote
400	26	59.1	164	2	B88036	protein M01D1.3 [i	473	26	59.1	290	2	AG2309	hypothetical prote
401	26	59.1	165	2	AC0894	conserved hypotet	474	26	59.1	294	2	G84504	probable VSP-1-lik
402	26	59.1	169	2	AH0072	conserved hypotet	475	26	59.1	296	2	A13468	thiG protein [impo
403	26	59.1	171	2	A84382	hypothetical prote	476	26	59.1	297	2	T132390	hypothetical prote
404	26	59.1	173	2	E69183	hypothetical prote	477	26	59.1	298	2	S39150	clathrin assembly
405	26	59.1	175	2	F64250	hypoxanthine-guani	478	26	59.1	304	2	T32453	hypothetical prote
406	26	59.1	175	2	S73496	hypoxanthine-guani	479	26	59.1	306	2	G96674	beta-lactamase (EC
407	26	59.1	177	2	D83801	sporulation initia	480	26	59.1	306	2	S47330	penicillinase - Ba
408	26	59.1	177	2	S65159	hypothetical prote	481	26	59.1	311	2	T42088	hypothetical prote
409	26	59.1	179	2	B65097	hypothetical prote	482	26	59.1	313	2	AC3116	ABC transporter, s
410	26	59.1	179	2	F85969	hypothetical prote	483	26	59.1	313	2	E71698	cytochrome-c oxida
411	26	59.1	179	2	G91124	hypothetical prote	484	26	59.1	315	2	C97769	hypothetical prote
412	26	59.1	181	2	G90583	50S ribosomal prot	485	26	59.1	315	2	AC3522	high-affinity bran
413	26	59.1	184	2	B87506	hypothetical prote	486	26	59.1	316	2	T36027	hypothetical prote
414	26	59.1	185	2	AD1183	hypothetical prote	487	26	59.1	325	2	F81159	DNA polymerase III
415	26	59.1	185	2	AE1540	hypothetical prote	488	26	59.1	325	2	C81945	probable DNA-direc
416	26	59.1	187	2	JH0240	aspartic proteinas	489	26	59.1	327	2	AH0506	hypothetical prote
417	26	59.1	194	2	G64322	hypothetical prote	490	26	59.1	331	2	B98171	probable rhicopine
418	26	59.1	196	2	S54050	hypothetical prote	491	26	59.1	333	2	H82245	glyceralddehyde 3-p
419	26	59.1	197	2	AE1154	methyltransferase	492	26	59.1	333	2	F86367	protein F26F24.24
420	26	59.1	199	2	A11512	weakly methyltrans	493	26	59.1	339	2	A84496	probable replicati
421	26	59.1	203	2	AG2636	conserved hypotet	494	26	59.1	343	2	F81264	recA protein Cj167
422	26	59.1	203	2	AG2120	hypothetical prote	495	26	59.1	343	2	I40770	recombination prot
423	26	59.1	204	2	E65183	hypothetical prote	496	26	59.1	345	2	S19706	type II site-speci
424	26	59.1	217	2	G86686	deoxyguanosine kin	497	26	59.1	345	2	S77826	probable DNA-direc
425	26	59.1	217	2	E64236	cytidylate kinase	498	26	59.1	350	2	T01881	UDPglucose 4-epime
426	26	59.1	219	2	AH3308	outer membrane pro	499	26	59.1	350	2	T08911	UDPglucose 4-epime
427	26	59.1	222	2	F96759	probable tumor-rel	500	26	59.1	351	2	T04291	probable UDPglucos
428	26	59.1	224	2	B64000	hypothetical prote	501	26	59.1	351	2	RGHY01	GRP-binding regula
429	26	59.1	227	2	A38941	cytochrome-c oxida	502	26	59.1	354	1	RGBOO1	GRP-binding regula
430	26	59.1	227	2	T11479	cytochrome-c oxida	503	26	59.1	354	1	RGHU01	GRP-binding regula
431	26	59.1	227	2	T26623	hypothetical prote	504	26	59.1	354	1	RGMSO1	GRP-binding regula
432	26	59.1	228	2	T19619	hypothetical prote	505	26	59.1	354	1	RGTO1	GRP-binding regula
433	26	59.1	229	1	QBP82	antiterminator Q -	506	26	59.1	354	2	B81158	uroporphyrinogen d
434	26	59.1	230	2	F97418	hypothetical prote	507	26	59.1	354	2	F81946	probable uroporph
435	26	59.1	232	1	AS0175	orotate phosphorib	508	26	59.1	355	2	B82564	multidrug resistan
436	26	59.1	235	2	J83970	hypothetical prote	509	26	59.1	357	2	E82564	3-isopropylmalate
437	26	59.1	237	2	S40244	rab23 protein - mo	510	26	59.1	358	2	E70792	probable regulator
438	26	59.1	238	2	S23314	hypothetical prote	511	26	59.1	359	2	F91219	hypothetical prote
439	26	59.1	240	2	G84177	hypothetical prote	512	26	59.1	359	2	H86065	hypothetical prote
440	26	59.1	241	2	D84138	hypothetical prote	513	26	59.1	361	2	B96016	hypothetical prote
441	26	59.1	246	2	A56219	homeotic protein s	514	26	59.1	365	2	S66466	cathepsin B (EC 3.
442	26	59.1	248	2	T35233	hypothetical prote	515	26	59.1	367	1	D70395	conserved hypotet
443	26	59.1	253	2	C84177	proteasome, subuni	516	26	59.1	369	2	H88535	protein B0523.4 [i
444	26	59.1	253	2	S05491	uridine phosphoryl	517	26	59.1	371	2	S55490	hypothetical prote
445	26	59.1	253	2	G86070	uridine phosphoryl	518	26	59.1	372	2	T45628	glycero-phosphodie
446	26	59.1	253	2	A98224	uridine phosphoryl	519	26	59.1	376	2	G84404	hypothetical prote
447	26	59.1	259	2	T29569	hypothetical prote	520	26	59.1	380	2	T00683	hypothetical prote
448	26	59.1	259	2	E72224	ABC transporter, A	521	26	59.1	386	2	T38150	aminoalcoholphosph
449	26	59.1	262	2	AF0338	histidine-binding	522	26	59.1	387	2	H84209	phosphoesterase [i
450	26	59.1	262	2	B69533	conserved hypotet	523	26	59.1	387	2	S33039	hypothetical prote
451	26	59.1	265	2	S20988	lectin - garden pe	524	26	59.1	387	2	T19572	hypothetical prote
452	26	59.1	267	2	C75111	hypothetical prote	525	26	59.1	389	2	B44972	paramyosin - nemat
453	26	59.1	267	2	T08283	hypothetical prote	526	26	59.1	389	2	S36638	glycoprotein Epl -
454	26	59.1	267	2	E71022	hypothetical prote	527	26	59.1	389	2	F86268	aminoalcoholphosph
455	26	59.1	270	2	T06528	lectin - garden pe	528	26	59.1	389	2	T14412	ethanolaminophosph
456	26	59.1	272	2	T25608	hypothetical prote	529	26	59.1	389	2	T06384	probable ethanolam
457	26	59.1	273	2	E64316	hypothetical prote	530	26	59.1	390	2	AG2093	patatin-like prote
458	26	59.1	274	1	S11489	DNA-formamidopyrim	531	26	59.1	391	2	A43356	cathepsin B (EC 3.
459	26	59.1	275	2	A95215	exodeoxyribonuclea	532	26	59.1	394	2	T19571	hypothetical prote
460	26	59.1	275	2	A32301	exodeoxyribonuclea	533	26	59.1	396	2	A34401	cathepsin E (EC 3.
461	26	59.1	275	2	B98079	exodeoxyribonuclea	534	26	59.1	396	2	S36865	cathepsin E (EC 3.
462	26	59.1	275	2	T49288	hypothetical prote	535	26	59.1	396	2	T30584	transferase homolo
463	26	59.1	276	2	T52316	chlorophyll a/b-bi	536	26	59.1	398	2	S66465	cathepsin B (EC 3.
464	26	59.1	277	2	T35973	probable transport	537	26	59.1	398	2	S11800	pullulanase secret
465	26	59.1	279	2	A87235	hypothetical prote	538	26	59.1	400	2	C97727	hypothetical prote
466	26	59.1	279	2	T17656	hypothetical prote	539	26	59.1	401	2	E75213	nifs protein FAB01
467	26	59.1	280	2	T34276	hypothetical prote	540	26	59.1	405	2	T12805	hypothetical prote

541	26	59.1	406	1	REHUK	renin (EC 3.4.23.1	614	513	1	S50216	translation initia
542	26	59.1	408	2	T44859	glycosyltransferas	615	513	2	T38866	conserved hypother
543	26	59.1	409	1	A48559	nucleocapsid prote	616	515	1	A59309	interferon-inducib
544	26	59.1	409	1	VH1HAI	nucleocapsid prote	617	518	2	D71288	probable glutamate
545	26	59.1	409	1	VH1HAI	nucleocapsid prote	618	520	2	JS0291	intermediate filam
546	26	59.1	409	2	E72765	probable phosphoes	619	521	2	T06606	hypothetical prote
547	26	59.1	410	2	AE3092	hypothetical prote	620	523	2	D85538	hypothetical prote
548	26	59.1	410	2	E98194	hypothetical prote	621	523	2	H90687	hypothetical prote
549	26	59.1	412	2	H86708	isocitrate dehydro	622	524	2	D87440	2-isopropylmalate
550	26	59.1	417	2	F97789	ampG protein (impo	623	527	2	T38045	probable t-complex
551	26	59.1	418	2	T09969	UDP-N-acetylglucos	624	529	2	T18589	chaperonin beta ch
552	26	59.1	418	2	G70775	UDP-N-acetylglucos	625	529	2	A71899	hypothetical prote
553	26	59.1	419	2	B90084	hypothetical prote	626	534	2	S31300	regulatory protein
554	26	59.1	420	2	B87201	hypothetical prote	627	546	2	A84630	hypothetical prote
555	26	59.1	421	1	S05393	granaticin polyket	628	549	2	A37932	nuclear factor kap
556	26	59.1	422	2	T31804	hypothetical prote	629	550	2	H71952	ATP-dependent zinc
557	26	59.1	424	2	S76359	hypothetical prote	630	550	2	F64555	cell division prot
558	26	59.1	430	2	T21482	hypothetical prote	631	551	1	JC5225	derRNA-activated pr
559	26	59.1	432	2	F81320	transcription term	632	562	2	H70688	hypothetical prote
560	26	59.1	435	2	T00762	hypothetical prote	633	568	2	S73254	replication helica
561	26	59.1	435	2	B86362	hypothetical prote	634	574	1	JX2001	5'-nucleotidase (E
562	26	59.1	436	2	F81199	conserved hypother	635	574	1	JX0269	5'-nucleotidase (E
563	26	59.1	438	2	H72241	fixC protein - The	636	575	2	T38406	probable flavoprot
564	26	59.1	439	2	G96817	hypothetical prote	637	576	1	A35036	5'-nucleotidase (E
565	26	59.1	441	2	A40550	peroxisomal membra	638	577	2	T50116	probable mannosylt
566	26	59.1	442	2	H71298	histidine-tRNA lig	639	579	2	T22480	hypothetical prote
567	26	59.1	445	2	I50485	Warm temperature a	640	579	2	T22703	hypothetical prote
568	26	59.1	446	2	A42661	citrate carrier pr	641	581	2	AB3588	probable adenine d
569	26	59.1	446	2	AD0509	citrate-sodium sym	642	583	2	T12574	phosphoglucosutase
570	26	59.1	446	2	B42661	citrate carrier pr	643	585	2	B83218	hypothetical prote
571	26	59.1	446	2	A38244	citrate transport	644	585	2	F83913	hypothetical prote
572	26	59.1	448	2	G95038	IS1380-Spn1, trans	645	586	2	S59301	homothallic switch
573	26	59.1	448	2	D95040	IS1380-Spn1, trans	646	586	2	JC2407	homothallic switch
574	26	59.1	448	2	D95057	IS1380-Spn1, trans	647	587	2	E82431	methyl-accepting c
575	26	59.1	448	2	F95082	IS1380-Spn1, trans	648	588	2	AB0927	terminase, ATPase
576	26	59.1	448	2	B95155	IS1380-Spn1, trans	649	588	2	C96527	probable terminase
577	26	59.1	448	2	A95157	IS1380-Spn1, trans	650	608	2	C96527	protein F27015.26
578	26	59.1	448	2	B95165	IS1380-Spn1, trans	651	616	2	B33586	C4-dicarboxylate t
579	26	59.1	448	2	F95167	IS1380-Spn1, trans	652	618	2	S19659	H4-exporting ATPas
580	26	59.1	448	2	A95175	IS1380-Spn1, trans	653	621	2	D96032	C4-dicarboxylate t
581	26	59.1	448	2	F95185	IS1380-Spn1, trans	654	627	2	H84693	probable protein k
582	26	59.1	448	2	G95254	IS1380-Spn1, trans	655	633	2	B85555	probable Vgr prote
583	26	59.1	449	2	F88366	protein C04H5.5 [i	656	633	2	G90704	probable Vgr prote
584	26	59.1	459	2	H64024	hypothetical prote	657	636	2	AH2683	methyl-accepting c
585	26	59.1	461	2	D69814	metabolite transpo	658	668	2	H86729	exonuclease ABC s
586	26	59.1	461	2	S44733	b0523.4 protein -	659	675	2	T01234	probable anthranil
587	26	59.1	462	1	H64614	conserved hypother	660	699	2	S72772	transketolase (EC
588	26	59.1	463	2	B36936	nitrogenase (EC 1.	661	702	2	D90886	VgrE protein (impo
589	26	59.1	463	2	AB1155	amino acid transpo	662	704	2	AE2246	hypothetical prote
590	26	59.1	463	2	AH1513	amino acid transpo	663	705	2	A45508	heat shock protein
591	26	59.1	471	2	H70541	hypothetical prote	664	706	2	D90124	hypothetical prote
592	26	59.1	473	2	T33407	hypothetical prote	665	713	2	JW0088	3',5'-cyclic-nucle
593	26	59.1	474	2	E75069	glutamate synthase	666	714	2	B85732	Rhs element associ
594	26	59.1	475	1	KCR1IH	stromelysin 1 (EC	667	715	2	A48426	heat shock protein
595	26	59.1	476	2	T30781	kelch protein homo	668	716	2	S30687	hypothetical prote
596	26	59.1	477	1	KCHUS1	stromelysin 1 (EC	669	748	2	S66129	disintegrin (EC 3.
597	26	59.1	477	1	KCMS81	stromelysin 1 (EC	670	757	2	E82013	probable transcrip
598	26	59.1	477	2	S48045	toxin apxIII secrete	671	757	2	A81242	transcription acce
599	26	59.1	480	2	T04849	protein kinase hom	672	759	2	T42027	probable catalase
600	26	59.1	480	2	H42506	F3L protein - vacc	673	763	2	AG2764	nitrogen fixation
601	26	59.1	480	2	G36213	F3L protein - vacc	674	763	2	E97545	nitrogen fixation
602	26	59.1	487	2	T05117	hypothetical prote	675	767	2	E85079	hypothetical prote
603	26	59.1	488	2	G70655	probable small sub	676	779	2	AC2249	heterocyst differe
604	26	59.1	489	2	S50548	hypothetical prote	677	785	2	P97465	lyser type transcri
605	26	59.1	493	2	C64847	ymdC protein - Esc	678	792	2	T00082	hypothetical prote
606	26	59.1	493	2	H90806	probable synthase	679	801	2	H83737	glucosidase BH0704
607	26	59.1	493	2	D85666	probable synthase	680	804	2	C84245	DNA topoisomerase
608	26	59.1	499	2	S18865	heat shock protein	681	805	2	E97717	virB4 protein prec
609	26	59.1	499	2	AH0485	probable insulinase	682	805	2	E71719	DNA gyrase chain B
610	26	59.1	501	1	S46591	fumarate reductase	683	807	2	A71663	DNA-binding protei
611	26	59.1	502	1	A34101	cytochrome P450 3A	684	835	2	A40971	hypothetical prote
612	26	59.1	508	2	AH0280	NAD(P) transhydrog	685	843	2	F96537	hypothetical prote
613	26	59.1	509	2	S45631	DNA primase chain	686	847	2	T04772	hypothetical prote

687	26	59.1	848	2	A44972	paramyosin - nemat	760	25	56.8	50	2	G85604	hypothetical prote
688	26	59.1	866	2	S04027	paramyosin - Caeno	761	25	56.8	57	2	S29109	probable calcium-b
689	26	59.1	868	2	A82515	conserved hypothet	762	25	56.8	58	2	G97868	hypothetical prote
690	26	59.1	872	2	T19296	hypothetical prote	763	25	56.8	60	2	T40760	MHC class II histo
691	26	59.1	879	2	A48575	paramyosin - nemat	764	25	56.8	62	2	B34514	hypothetical prote
692	26	59.1	882	2	AH1697	probable sugar hyd	765	25	56.8	69	2	T17563	hypothetical prote
693	26	59.1	885	2	A84373	leucine-tRNA synth	766	25	56.8	69	2	E83982	hypothetical prote
694	26	59.1	901	2	F85833	phage infection pr	767	25	56.8	76	2	T40983	hypothetical prote
695	26	59.1	913	1	A41109	protein-tyrosine-p	768	25	56.8	76	2	F83566	hypothetical prote
696	26	59.1	918	2	S44769	C29E4.2 protein -	769	25	56.8	78	2	A81374	very hypothetical
697	26	59.1	922	2	T03854	hypothetical prote	770	25	56.8	96	2	S51928	homeotic protein C
698	26	59.1	927	2	A45039	TF4 protein - yea	771	25	56.8	98	1	W3WL84	E3 protein - bovin
699	26	59.1	981	2	G90601	DNA polymerase III	772	25	56.8	101	2	A97578	hypothetical prote
700	26	59.1	986	2	T52176	aldhyde oxidase I	773	25	56.8	101	2	A97625	hypothetical prote
701	26	59.1	1003	2	S33760	myosin IE heavy ch	774	25	56.8	101	2	A12798	conserved hypothet
702	26	59.1	1029	2	H96658	hypothetical prote	775	25	56.8	108	2	A04069	hemagglutinin prec
703	26	59.1	1036	2	H64245	hypothetical prote	776	25	56.8	122	2	AD0456	50S ribosomal prot
704	26	59.1	1040	1	A38306	alpha-mannosidase	777	25	56.8	123	2	T17552	hypothetical prote
705	26	59.1	1040	1	T46931	alpha-mannosidase	778	25	56.8	128	2	AF1122	hypothetical prote
706	26	59.1	1067	2	AB0260	probable phage hos	779	25	56.8	130	2	AG2468	50S ribosomal prot
707	26	59.1	1071	2	B84062	hypothetical prote	780	25	56.8	135	2	D84516	hypothetical prote
708	26	59.1	1083	2	H86921	probable arabinosy	781	25	56.8	137	2	A11176	E. coli PnMB prote
709	26	59.1	1084	2	S23319	hypothetical prote	782	25	56.8	137	2	AE1534	hypothetical prote
710	26	59.1	1100	2	S38043	pre-tRNA splicing	783	25	56.8	137	2	AB1119	hypothetical prote
711	26	59.1	1111	2	T00324	hypothetical prote	784	25	56.8	140	2	AI3155	hypothetical prote
712	26	59.1	1133	2	T01757	hypothetical prote	785	25	56.8	140	2	H98131	probable transcrip
713	26	59.1	1141	2	T20611	hypothetical prote	786	25	56.8	141	2	PC4298	cadherin FIB2 - hu
714	26	59.1	1164	2	AC2136	multifunctional pe	787	25	56.8	142	2	E84067	hypothetical prote
715	26	59.1	1169	2	AD1069	type 1 site-specif	788	25	56.8	143	2	T05564	conserved hypothet
716	26	59.1	1179	2	AG1101	transcription-repa	789	25	56.8	146	2	B82568	hypothetical prote
717	26	59.1	1179	2	AG1463	transcription-repa	790	25	56.8	146	2	T14667	hypothetical prote
718	26	59.1	1185	2	T39734	pyruvate-carboxyla	791	25	56.8	151	2	T14948	hypothetical prote
719	26	59.1	1188	1	NDECKR	type 1 site-specif	792	25	56.8	153	2	S53544	hypothetical prote
720	26	59.1	1199	2	T29145	hypothetical prote	793	25	56.8	160	2	A10435	protein-Npi-phosph
721	26	59.1	1200	2	T48194	hypothetical prote	794	25	56.8	164	2	T30407	hypothetical prote
722	26	59.1	1225	1	B64234	hypothetical prote	795	25	56.8	165	2	G90142	hypothetical prote
723	26	59.1	1234	2	T14515	hypothetical prote	796	25	56.8	166	2	E96663	probable RING zinc
724	26	59.1	1274	2	S55050	cardiac myosin-bin	797	25	56.8	170	2	T08155	ribosomal protein
725	26	59.1	1276	2	T02711	probable calmoduli	798	25	56.8	170	2	E95358	hypothetical prote
726	26	59.1	1291	1	S05465	retrovirus-related	799	25	56.8	171	2	AE0670	probable acetyltra
727	26	59.1	1325	1	S73723	probable lipoprote	800	25	56.8	172	1	C64897	probable phosphino
728	26	59.1	1332	2	D84669	aldehyde oxidase I	801	25	56.8	172	2	C85733	probable resistanc
729	26	59.1	1356	2	E87311	DNA-directed RNA p	802	25	56.8	172	2	D90885	probable resistanc
730	26	59.1	1369	1	JC4860	protein-tyrosine k	803	25	56.8	174	2	S30200	ribosomal protein
731	26	59.1	1374	2	T17124	dna-directed RNA p	804	25	56.8	176	2	F71064	micrococcal nuclea
732	26	59.1	1419	2	T32970	hypothetical prote	805	25	56.8	176	2	S30199	ribosomal protein
733	26	59.1	1420	2	S54471	probable membrane	806	25	56.8	179	2	H82549	hypothetical prote
734	26	59.1	1441	2	T13717	CRAG protein - fru	807	25	56.8	182	2	AD2331	50S ribosomal prot
735	26	59.1	1451	2	D64203	DNA polymerase III	808	25	56.8	182	2	A72854	probable histidino
736	26	59.1	1476	2	A45773	kelch protein, lon	809	25	56.8	186	1	B64203	hypothetical prote
737	26	59.1	1493	2	A38218	GAP-associated pro	810	25	56.8	187	2	C53394	ribosomal protein
738	26	59.1	1496	2	I51170	carbamyl phosphate	811	25	56.8	188	2	F97074	hypothetical prote
739	26	59.1	1544	2	G96904	DNA segregation Ar	812	25	56.8	188	2	B42983	hypothetical prote
740	26	59.1	1741	2	S74910	hemolysin - Synec	813	25	56.8	189	2	B84347	hypothetical prote
741	26	59.1	1744	2	JH0720	tanabin - African	814	25	56.8	190	2	AB2031	hypothetical prote
742	26	59.1	1824	2	T07589	disease resistance	815	25	56.8	191	2	A53394	ribosomal protein
743	26	59.1	1927	2	T25604	hypothetical prote	816	25	56.8	193	2	B83811	hypothetical prote
744	26	59.1	2274	2	T30258	adenomatous polyo	817	25	56.8	200	1	A39741	cytochrome c bioge
745	26	59.1	2278	1	S56274	FAB1 protein - yea	818	25	56.8	201	2	E70211	hypothetical prote
746	26	59.1	2290	1	GNVYE	genome polyprotein	819	25	56.8	207	2	I46084	interleukin 6 - ca
747	26	59.1	2292	2	A41519	capsid polyprotein	820	25	56.8	208	1	S29549	interleukin-6 - sh
748	26	59.1	2315	2	A41519	posterior-group pr	821	25	56.8	209	2	B83954	inhibition of Cher
749	26	59.1	2700	2	D88450	protein F2iH11.2 [	822	25	56.8	209	2	G70091	conserved hypothet
750	26	59.1	3137	2	A37797	collagen alpha 3(V	823	25	56.8	209	2	AB3979	ABC transporter (A
751	26	59.1	3164	1	WMBEH6	polyketide synthas	824	25	56.8	213	2	AB2392	hypothetical prote
752	26	59.1	4613	2	T17409	mycosubtilin synth	825	25	56.8	214	2	AD2932	hypothetical prote
753	26	59.1	5369	2	T44807	hypothetical prote	826	25	56.8	215	2	AD0263	nicotinamide (EC
754	25.5	58.0	346	2	C84449	alpha-1-microglobu	827	25	56.8	217	2	AB4810	probable guanilate
755	25.5	58.0	352	1	HCHU	F28K20.14 protein	828	25	56.8	218	2	S76385	hypothetical prote
756	25.5	58.0	406	2	H86437	hypothetical prote	829	25	56.8	219	2	H82840	orotate phosphorib
757	25.5	58.0	550	2	T32560	conserved hypothet	830	25	56.8	219	2	D35216	FP26 protein - fow
758	25.5	58.0	564	2	H82919	probable calcium-b	831	25	56.8	219	2	D70838	hypothetical prote
759	25	56.8	50	2	S29110		832	25	56.8	219	2	B47152	probable fimbrial

833	25	56.8	219	2	S49428	hypothetical prote	906	25	56.8	275	2	T12937	probable phosphoe
834	25	56.8	220	1	S22516	S-allele-associate	907	25	56.8	276	2	H75169	abc transporter PA
835	25	56.8	220	2	T23817	hypothetical prote	908	25	56.8	276	2	B97142	ribosomal protein
836	25	56.8	221	2	S31637	rep protein - Lact	909	25	56.8	276	2	C71045	probable membrane
837	25	56.8	221	2	D33294	hypothetical prote	910	25	56.8	281	2	T42669	hypothetical prote
838	25	56.8	224	2	A49543	maltodextrase util	911	25	56.8	283	1	LNPHLS	lectin precursor -
839	25	56.8	224	2	E83859	hypothetical prote	912	25	56.8	283	2	T38532	hypothetical prote
840	25	56.8	224	2	B87657	conserved hypotet	913	25	56.8	284	2	B84146	transglutaminase t
841	25	56.8	225	2	S67772	hypothetical prote	914	25	56.8	284	2	T39397	probable methyltra
842	25	56.8	225	2	T17795	hypothetical prote	915	25	56.8	286	2	A54070	3-hydroxyanthranil
843	25	56.8	226	2	C75141	virr related prote	916	25	56.8	288	2	T21770	hypothetical prote
844	25	56.8	226	2	E83774	hypothetical prote	917	25	56.8	290	2	T02877	probable chlorophy
845	25	56.8	226	2	H97250	probable amidophos	918	25	56.8	290	2	T49631	probable Ni-bindin
846	25	56.8	227	2	C75550	conserved hypotet	919	25	56.8	291	2	T02986	chlorophyll a/b-bi
847	25	56.8	227	2	G97112	probable metal-dep	920	25	56.8	295	2	S67860	gumk protein - xan
848	25	56.8	227	2	AG1314	hypothetical prote	921	25	56.8	295	2	T33535	hypothetical prote
849	25	56.8	227	2	AG1686	hypothetical prote	922	25	56.8	296	1	G64453	conserved hypotet
850	25	56.8	228	2	B38941	cytochrome-c oxida	923	25	56.8	296	2	E90700	allantoinase [limp
851	25	56.8	229	2	S70599	cytochrome-c oxida	924	25	56.8	296	2	H85550	allantoinase [limp
852	25	56.8	229	2	S01503	cytochrome-c oxida	925	25	56.8	297	2	AF0874	chromosome initia
853	25	56.8	229	2	S55007	cytochrome-c oxida	926	25	56.8	297	2	S22098	replication initi
854	25	56.8	229	2	T11277	cytochrome-c oxida	927	25	56.8	297	2	F85947	replication initi
855	25	56.8	230	2	H97160	nucleoside phospho	928	25	56.8	297	2	B91102	replication initia
856	25	56.8	230	2	H72244	conserved hypotet	929	25	56.8	297	2	T35181	hypothetical prote
857	25	56.8	230	2	G84913	probable peptidyl-	930	25	56.8	298	2	E86863	fructose-bisphosph
858	25	56.8	231	2	A99184	conserved hypotet	931	25	56.8	302	2	T23435	hypothetical prote
859	25	56.8	232	2	D89924	conserved hypotet	932	25	56.8	302	2	E83589	probable transcrip
860	25	56.8	233	1	VHVUAV	nucleoprotein N -	933	25	56.8	302	2	AE0112	chromosome initiat
861	25	56.8	233	2	T03329	probable amidase 1	934	25	56.8	303	2	C98191	norq (AB031072) [l
862	25	56.8	235	2	B87147	50S ribosomal prot	935	25	56.8	304	2	E70677	hypothetical prote
863	25	56.8	235	2	F70613	probable ribosomal	936	25	56.8	304	2	A48174	beta-lactamase (EC
864	25	56.8	238	2	G70067	conserved hypotet	937	25	56.8	305	2	T52287	probable histone d
865	25	56.8	239	2	A70633	hypothetical prote	938	25	56.8	307	2	T00687	hypothetical prote
866	25	56.8	240	2	S11056	lectin - winged be	939	25	56.8	307	2	C95171	thiamin biosynthes
867	25	56.8	240	2	A11577	metal cations ABC	940	25	56.8	307	2	C98037	thiamin biosynthes
868	25	56.8	242	2	S40771	ribosomal protein	941	25	56.8	309	2	E87671	cytochrome c oxida
869	25	56.8	242	2	T11790	ribosomal protein	942	25	56.8	310	2	B86825	aspartate carbamoy
870	25	56.8	242	2	AG2046	hypothetical prote	943	25	56.8	310	2	AB0275	arabinose operon r
871	25	56.8	247	2	H69276	L-isoaspartyl-prot	944	25	56.8	310	2	B83331	catechol 1,1,2-diox
872	25	56.8	248	1	Q0B21R	BXRFL (EC-RFL) pro	945	25	56.8	311	2	E83804	protein-export mem
873	25	56.8	250	2	A70175	chaperonin homolog	946	25	56.8	313	2	A45822	beta-lactamase (EC
874	25	56.8	250	2	JE0157	mammalian sec22 pr	947	25	56.8	315	2	D89955	conserved hypotet
875	25	56.8	252	1	G71092	phosphoesterase-re	948	25	56.8	317	2	S63358	hypothetical prote
876	25	56.8	252	2	G90513	hypothetical prote	949	25	56.8	322	2	T40846	uracil-DNA glycosy
877	25	56.8	252	2	A71001	hypothetical prote	950	25	56.8	322	2	AC3492	acetoacetate-CoA l
878	25	56.8	253	2	F83440	probable short-cha	951	25	56.8	326	2	A89842	hypothetical prote
879	25	56.8	253	2	F69134	hypothetical prote	952	25	56.8	331	2	A86278	hypothetical prote
880	25	56.8	253	2	T27720	hypothetical prote	953	25	56.8	333	2	F72282	transcription regu
881	25	56.8	253	2	F64125	ferric enterobacti	954	25	56.8	334	2	E87448	arginine N-succiny
882	25	56.8	258	2	B90121	proliferating cell	955	25	56.8	334	2	AD1186	serine phosphatase
883	25	56.8	259	2	C64059	uridine phosphoryl	956	25	56.8	339	2	A83539	hypothetical prote
884	25	56.8	259	2	B72800	gp2 protein - Myco	957	25	56.8	342	1	C69395	H+-transporting AR
885	25	56.8	260	2	A36402	corticotropin / li	958	25	56.8	342	2	D95906	probable transcrip
886	25	56.8	261	2	T50792	embryonic abundant	959	25	56.8	342	2	D95906	recombination prot
887	25	56.8	261	2	AH2288	hypothetical prote	960	25	56.8	342	2	S18728	hypothetical prote
888	25	56.8	262	2	B86662	hypothetical prote	961	25	56.8	342	2	T22428	hypothetical prote
889	25	56.8	263	2	S05433	corticotropin / li	962	25	56.8	345	2	JC6195	AatII restriction
890	25	56.8	264	2	E95410	probable ABC trans	963	25	56.8	346	2	T19676	hypothetical prote
891	25	56.8	266	2	A95247	malA protein [limp	964	25	56.8	347	2	I55120	rnsF protein - Esc
892	25	56.8	266	2	F98111	malA protein [limp	965	25	56.8	348	2	A55020	recombination prot
893	25	56.8	268	2	S00553	MSS18 protein - ye	966	25	56.8	348	2	JQ0745	recombination prot
894	25	56.8	269	2	S48444	probable temperatu	967	25	56.8	348	2	F81860	RecA protein NMA16
895	25	56.8	269	2	AG3538	ubiquinone/menaqui	968	25	56.8	348	2	F81082	recA protein NMB14
896	25	56.8	270	2	AG3095	nitric oxide reduc	969	25	56.8	349	2	A97124	rECA recombinase,
897	25	56.8	270	2	AD3634	norQ protein [limp	970	25	56.8	350	2	S76212	hypothetical prote
898	25	56.8	270	2	E88402	protein H05C05.3 [	971	25	56.8	351	2	D91080	hypothetical prote
899	25	56.8	270	2	E69337	hypothetical prote	972	25	56.8	351	2	E85925	hypothetical prote
900	25	56.8	272	2	E95348	nitric-oxide reduc	973	25	56.8	352	2	S10499	recombination prot
901	25	56.8	272	2	AB1454	phage protein homo	974	25	56.8	353	2	T25775	hypothetical prote
902	25	56.8	273	2	S48511	MPF4 protein - yea	975	25	56.8	354	1	RGHY02	GTP-binding regula
903	25	56.8	274	2	S24742	recombination prot	976	25	56.8	354	1	RGXLOA	GTP-binding regula
904	25	56.8	274	2	S24745	recombination prot	977	25	56.8	354	1	RGFFO1	GTP-binding regula
905	25	56.8	274	2	H70900	hypothetical prote	978	25	56.8	354	1	RGFFO2	GTP-binding regula

979 25 56.8 354 1 RGHUO2 GTP-binding regula  
980 25 56.8 354 1 RGHUO2 GTP-binding regula  
981 25 56.8 354 1 RGHUO2 GTP-binding regula  
982 25 56.8 354 2 JC4212 nitrilase (EC 3.5.  
983 25 56.8 354 2 T10496 UDPglucose 4-epime  
984 25 56.8 354 2 S24362 GTP-binding regula  
985 25 56.8 354 2 T19476 hypothetical prote  
986 25 56.8 354 2 S27014 GTP-binding regula  
987 25 56.8 354 2 A61035 GTP-binding regula  
988 25 56.8 354 2 D71620 ubiquinone biosynt  
989 25 56.8 354 2 T07342 probable prototyp  
990 25 56.8 354 2 T21241 hypothetical prote  
991 25 56.8 355 1 RGHUGX GTP-binding regula  
992 25 56.8 355 1 RGHUGX GTP-binding regula  
993 25 56.8 355 1 A59473 early switch prote  
994 25 56.8 355 2 A61031 GTP-binding regula  
995 25 56.8 355 2 A48976 GTP-binding regula  
996 25 56.8 356 2 T38408 hypothetical prote  
997 25 56.8 358 2 AB2041 hypothetical prote  
998 25 56.8 359 2 JS0734 endo-1,4-beta-xyla  
999 25 56.8 361 2 B83327 probable transcrip  
1000 25 56.8 361 2 A96261 hypothetical prote

ALIGNMENTS

RESULT 1  
G82526  
ATP-dependent DNA helicase XP2680 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: G82526  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: G82526  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-680 <SIM>  
A:Cross-references: UNIPROT:Q9PA40; UNIPARC:UPI00000C2AF9; GB:AE004074; GB:AE003849; NID  
A:Experimental source: Strain 9a5c  
R:Simpsom, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.B.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XP2680  
C:Superfamily: helicase II

Query Match 79.5%; Score 35; DB 2; Length 680;  
Best Local Similarity 77.8%; Pred. No. 21;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLOLEFDV 9  
Db 114 FLOIHDV 122

RESULT 2  
G64232

hypothetical protein MG296 - Mycoplasma genitalium  
C:Species: Mycoplasma genitalium  
C>Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 05-Oct-2004  
C:Accession: G64232  
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.  
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
C.A.; Venter, J.C.  
Science 270, 397-403, 1995  
A:Title: The minimal gene complement of Mycoplasma genitalium.  
A:Reference number: A64200; MUID:96026346; PMID:7569993  
A:Accession: G64232  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-129 <TIGR>  
A:Cross-references: UNIPROT:P47538; UNIPARC:UPI00001395B2; GB:U39710; GB:L43967; NID:glu  
A:Experimental source: strain G-37  
C:Genetics:  
A:Genetic code: SGC3  
C:Superfamily: uncharacterized conserved protein

Query Match 75.0%; Score 33; DB 2; Length 129;  
Best Local Similarity 77.8%; Pred. No. 8.8;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLOLEFDV 9  
Db 11 FLOTEFQV 19

RESULT 3  
B82096  
conserved hypothetical protein VC2278 [imported] - Vibrio cholerae (strain N16961 serogr  
C:Species: Vibrio cholerae  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: B82096  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: B82096  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-430 <HEI>  
A:Cross-references: UNIPROT:Q9KPT4; UNIPARC:UPI00000C3258; GB:AE004299; GB:AE003852; NID  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC2278  
A:Map position: 1  
C:Superfamily: conserved hypothetical protein HI0125

Query Match 75.0%; Score 33; DB 2; Length 430;  
Best Local Similarity 66.7%; Pred. No. 34;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLEFDV 9  
Db 227 FMOLEFSAV 235

RESULT 4  
G95328  
hypothetical protein Sma0994 [imported] - Sinorhizobium meliloti (strain 1021) magapla  
C:Species: Sinorhizobium meliloti  
C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: G95328  
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow  
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: G95328

A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-154 <KUR>  
 A:Cross-references: UNIPROT:Q92ZF1; UNIPARC:UPI00000CB10E; GB:AE006469; PIDN:AAK65193.1;  
 A:Experimental source: strain 1021, megaplasmid pSYMA  
 R:Galibert P.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
 hebaault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
 A>Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: SMA0994  
 A:Genome: plasmid

Query Match 72.7%; Score 32; DB 2; Length 154;  
 Best Local Similarity 87.5%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLFDDAV 9  
 ||| ||||  
 Db 109 LQLAFDAV 116

RESULT 5  
 T09802  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - African malaria mosquito mitochondrion  
 C:Species: mitochondrion Anopheles gambiae (African malaria mosquito)  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Dec-2004  
 C:Accession: T09802  
 R:Beard, C.B.; Hamm, D.M.; Collins, F.H.  
 Insect Mol. Biol. 2, 103-124, 1993  
 A>Title: The mitochondrial genome of the mosquito *Anopheles gambiae*: DNA sequence, genom  
 A:Reference number: 216863; MUID:97242550; PMID:9087549  
 A:Accession: T09802  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-228 <BEA>  
 A:Cross-references: UNIPROT:P34840; UNIPARC:UPI0000127FCF; EMBL:L20934; NID:g309056; PID  
 A:Experimental source: strain G3  
 C:Genetics:  
 A:Genome: mitochondrion  
 A:Genetic code: SGC4  
 C:Superfamily: cytochrome-c oxidase, subunit II, mitochondrial type; cytochrome-c oxidas  
 C:Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner  
 F:9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F:161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
 F:196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F:198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 72.7%; Score 32; DB 2; Length 228;  
 Best Local Similarity 75.0%; Pred. No. 27;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLFFDA 8  
 ||| ||||  
 Db 113 FLNLEFDS 120

RESULT 6  
 T12000  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - Anopheles quadrimaculatus A mitochondrion  
 C:Species: mitochondrion Anopheles quadrimaculatus A  
 C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 31-Dec-2004  
 C:Accession: T12000  
 R:Cockburn, A.P.; Mitchell, S.E.; Seawright, J.A.  
 Arch. Insect Biochem. Physiol. 14, 31-36, 1990  
 A>Title: Cloning of the mitochondrial genome of *Anopheles quadrimaculatus*.  
 A:Reference number: 217375; MUID:92190510; PMID:2134168  
 A:Accession: T12000

A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-228 <COC>  
 A:Cross-references: UNIPARC:UPI0000127FDO; EMBL:L04272; NID:g342501; PID:g507281; PIDN  
 A:Experimental source: strain Orlando  
 C:Genetics:  
 A:Genome: mitochondrion  
 A:Note: COXII  
 C:Superfamily: cytochrome-c oxidase, subunit II, mitochondrial type; cytochrome-c oxid  
 C:Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner  
 F:161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
 F:196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F:198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 72.7%; Score 32; DB 2; Length 228;  
 Best Local Similarity 75.0%; Pred. No. 27;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLFFDA 8  
 ||| ||||  
 Db 113 FLNLEFDS 120

RESULT 7  
 S50328  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - Katharina tunicata mitochondrion  
 C:Species: mitochondrion Katharina tunicata  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Dec-2004  
 C:Accession: S50328  
 R:Boore, J.L.; Brown, W.M.  
 Genetics 138, 423-443, 1994  
 A>Title: Complete DNA sequence of the mitochondrial genome of the black chiton, Kathari  
 A:Reference number: S50327; MUID:95129806; PMID:7828825  
 A:Accession: S50328  
 A:Molecule type: DNA  
 A:Residues: 1-229 <BOO>  
 A:Cross-references: UNIPROT:Q37534; UNIPARC:UPI0000091ECE; EMBL:U09810; NID:g557273; PI  
 C:Genetics:  
 A:Genome: mitochondrion  
 A:Genetic code: SGC4  
 C:Superfamily: cytochrome-c oxidase, subunit II, mitochondrial type; cytochrome-c oxid  
 C:Keywords: copper; electron transfer; heme; membrane-associated complex; mitochondrial  
 ein

F:9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F:161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
 F:196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F:198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 72.7%; Score 32; DB 2; Length 229;  
 Best Local Similarity 75.0%; Pred. No. 28;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLFFDA 8  
 ||| ||||  
 Db 113 FLNLEFDS 120

RESULT 8  
 G97034  
 probable metal-dependent phosphoesterase (PHP family), Yciv ortholog [imported] - Clost  
 C:Species: Clostridium acetobutylicum  
 C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: G97034  
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee  
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
 A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: G97034  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-274 <KUR>  
 A:Cross-references: UNIPROT:Q97K29; UNIPARC:UPI00000CA0AC; GB:AB001437; PIDN:AAK79066.1

A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CHC1092  
C:Superfamily: hypothetical protein HI1400

Query Match 72.7%; Score 32; DB 2; Length 274;  
Best Local Similarity 55.6%; Pred. No. 34;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLPFDV 9  
|||:|:|:  
Db 205 FLKLDPDGI 213

RESULT 9  
JH0259  
prostaglandin-endoperoxide synthase (EC 1.14.99.1) 1 precursor - human  
N:Alternate names: cyclooxygenase; prostaglandin G/H synthase; prostaglandin H synthase  
N:Contains: prostaglandin-endoperoxide synthase 1, splice form 2  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: JH0259; PH0225; A39937; B38146; A38146; S50181; A36746; S69169  
R:Takahashi, Y.; Ueda, N.; Yoshimoto, T.; Yamamoto, S.; Yokoyama, C.; Miyata, A.; Tanabe  
Biochem. Biophys. Res. Commun. 182, 433-438, 1992  
A:Title: Immunofluorescence purification and cDNA cloning of human platelet prostaglandin en  
A:Reference number: JH0259; MUID:92134251; PMID:1734857  
A:Accession: JH0259  
A:Molecule type: mRNA  
A:Residues: 1-599 <TAKE>  
A:Cross-references: UNIPROT:P23219; UNIPARC:UPI0000012DF; GB:S78220; NID:g243971; PIDN:  
A:Accession: PH0225  
A:Molecule type: protein  
A:Residues: 24-31 <TAKE>  
A:Cross-references: UNIPARC:UPI000017528B  
R:Funk, C.D.; Funk, L.B.; Kennedy, M.E.; Pong, A.S.; Fitzgerald, G.A.  
FASEB J. 5, 2304-2312, 1991  
A:Title: Human platelet/erythrocytopenia cell prostaglandin G/H synthase: cDNA cloning, e  
A:Reference number: A39937; MUID:91317397; PMID:1907252  
A:Accession: A39937  
A:Molecule type: mRNA  
A:Residues: 1-599 <FUN>  
A:Cross-references: UNIPARC:UPI0000012DF; GB:M59979; NID:g189886; PIDN:AAA03630.1; PID:  
R:Diaz, A.; Reginato, A.M.; Jimenez, S.A.  
J. Biol. Chem. 267, 10816-10822, 1992  
A:Title: Alternative splicing of human prostaglandin G/H synthase mRNA and evidence of d  
nd tumor necrosis factor alpha.  
A:Reference number: A38146; MUID:92268138; PMID:1587858  
A:Accession: B38146  
A:Molecule type: mRNA  
A:Residues: 1-599 <DIAL>  
A:Cross-references: UNIPARC:UPI0000012DF; GB:S36271; NID:g249625; PIDN:AAB22217.1; PID:  
A:Experimental source: lung fibroblast  
A:Note: sequence extracted from NCBI backbone (NCBIN:103945, NCBIP:103946)  
A:Accession: A38146  
A:Molecule type: mRNA  
A:Residues: 1-395,433-599 <DIA2>  
A:Cross-references: UNIPARC:UPI000002B0F3; GB:S36219; NID:g249623; PIDN:AAB22216.1; PID:  
A:Experimental source: lung fibroblast  
A:Note: sequence extracted from NCBI backbone (NCBIN:103825, NCBIP:103826)  
R:Barnett, J.; Chow, J.; Ives, D.; Chiou, M.; Mackenzie, R.; Osen, E.; Nguyen, B.; Tsing  
Biochim. Biophys. Acta 1209, 130-139, 1994  
A:Title: Purification, characterization and selective inhibition of human prostaglandin  
A:Reference number: S50181; MUID:95035046; PMID:7947975  
A:Accession: S50181  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 24-32 <BAR>  
A:Cross-references: UNIPARC:UPI000017528C  
R:Yokoyama, C.; Tanabe, T.  
Biochem. Biophys. Res. Commun. 165, 888-894, 1989  
A:Title: Cloning of human gene encoding prostaglandin endoperoxide synthase and primary  
A:Reference number: A36746; MUID:90088508; PMID:2512924  
A:Accession: A36746

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-11, 'L', '13-112, 'L', '114-377, 'T', '379-599 <YOK>  
A:Cross-references: UNIPARC:UPI00001562E5; GB:M31822; NID:g189898; PIDN:AAA36439.1; PID:  
R:Ren, Y.; Loose-Mitchell, D.S.; Kulmacz, R.J.  
Arch. Biochem. Biophys. 316, 751-757, 1995  
A:Title: Prostaglandin H synthase-1: evaluation of C-terminus function.  
A:Reference number: S69169; MUID:95168861; PMID:7864630  
A:Accession: S69169  
A:Molecule type: protein  
A:Residues: 585-599 <REN>  
A:Cross-references: UNIPARC:UPI000017528D  
C:Genetics:  
A:Gene: GDB:PTGS1  
A:Cross-references: GDB:128070; OMIM:176805  
A:Map position: 9q32-9q33.3  
C:Function:  
A:Description: catalyzes the oxidative cyclization by oxygen of arachidonic acid to pro:  
A:Pathway: prostaglandin biosynthesis  
C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
C:Keywords: alternative splicing; chromoprotein; endoplasmic reticulum; glycoprotein; he  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-599/Product: prostaglandin-endoperoxide synthase 1 #status experimental <MAT1>  
F:24-395,433-599/Product: prostaglandin-endoperoxide synthase 1, splice form 2 #status  
F:35-68/Domain: EGF homology <EGF>  
F:103,143,409/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:308/Binding site: heme iron (His) (axial ligand) #status predicted  
F:384,529/Active site: Tyr, Ser #status predicted

Query Match 72.7%; Score 32; DB 2; Length 599;  
Best Local Similarity 85.7%; Pred. No. 81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLPFD 7  
|||:|:|:  
Db 355 FLQLKFD 361

RESULT 10  
A29947  
prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - sheep  
N:Alternate names: prostaglandin endoperoxide synthetase  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: A29947  
R:Merlie, J.P.; Fagan, D.; Mudd, J.; Needleman, P.  
J. Biol. Chem. 263, 3550-3553, 1988  
A:Title: Isolation and characterization of the complementary DNA for sheep seminal vesic  
A:Reference number: A29947; MUID:88153641; PMID:2831188  
A:Accession: A29947  
A:Molecule type: mRNA  
A:Residues: 1-599 <MER>  
A:Cross-references: UNIPROT:P05979; UNIPARC:UPI000016C5E8; GB:M18243; NID:g165843; PIDN:  
C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
C:Keywords: oxidoreductase  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-599/Product: prostaglandin-endoperoxide synthase #status predicted <MAT>  
F:35-68/Domain: EGF homology <EGF>

Query Match 72.7%; Score 32; DB 2; Length 599;  
Best Local Similarity 85.7%; Pred. No. 81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLPFD 7  
|||:|:|:  
Db 355 FLQLKFD 361

RESULT 11  
S00561  
prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 10-Dec-1999



C;Accession: S00561  
R;Yokoyama, C.; Takai, T.; Tanabe, T.  
FEBS Lett. 231, 347-351, 1988  
A;Title: Primary structure of sheep prostaglandin endoperoxide synthase deduced from cDN  
A;Reference number: S00561; MUID:88196421; PMID:3129310  
A;Accession: S00561  
A;Molecule type: mRNA  
A;Residues: 1-600 <YOK>  
A;Cross-references: UNIPARC:UPI000016C4DE; EMBL:Y00750; NID:g1361; PID:CAA68719.1; PID:  
A;Note: part of this sequence, including the amino end of the mature protein, was confir  
A;Note: 97-His, 164-Gly, 456-Gln, 520-Gln, 520-Lys, and 525-Ile were also found  
C;Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
C;Keywords: oxidoreductase  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-600/Product: prostaglandin-endoperoxide synthase #status experimental <MAT>  
F;36-69/Domain: EGF homology <EGF>

Query Match 72.7%; Score 32; DB 2; Length 600;  
Best Local Similarity 85.7%; Pred. No. 81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||||  
Db 356 FLQLKFD 362

RESULT 12  
A28960  
prostaglandin-endoperoxide synthase (EC 1.14.99.1) G/H precursor - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: A28960  
R;Dewitt, D.L.; Smith, W.L.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1412-1416, 1988  
A;Title: Primary structure of prostaglandin G/H synthase from sheep vesicular gland dete  
A;Reference number: A28960; MUID:8814447; PMID:3125548  
A;Accession: A28960  
A;Molecule type: mRNA  
A;Residues: 1-600 <DEW>  
A;Cross-references: UNIPROT:P05979; UNIPARC:UPI000016C5F1; GB:J03599; NID:g166035; PID:  
C;Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
C;Keywords: oxidoreductase  
F;36-69/Domain: EGF homology <EGF>

Query Match 72.7%; Score 32; DB 2; Length 600;  
Best Local Similarity 85.7%; Pred. No. 81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||||  
Db 356 FLQLKFD 362

RESULT 13  
S39782  
cyclooxygenase 1 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Dec-1999  
C;Accession: S39782  
R;Feng, L.; Sun, W.; Xia, Y.; Tang, W.W.; Channmugam, P.; Soyoola, E.; Wilson, C.B.; Hwan  
Arch. Biochem. Biophys. 307, 361-368, 1993  
A;Title: Cloning two isoforms of rat cyclooxygenase: differential regulation of their ex  
A;Reference number: S39782; MUID:94099619; PMID:8274023  
A;Accession: S39782  
A;Molecule type: mRNA  
A;Residues: 1-602 <FEN>  
A;Cross-references: UNIPARC:UPI0000175290; GB:S67721; NID:g460555; PID:AA29400.1; PID:  
C;Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
F;38-71/Domain: EGF homology <EGF>

Query Match 72.7%; Score 32; DB 2; Length 602;  
Best Local Similarity 85.7%; Pred. No. 82;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||||  
Db 358 FLQLKFD 364

RESULT 14  
A35564  
prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C;Accession: A35564  
R;Dewitt, D.L.; El-Harith, E.A.; Kraemer, S.A.; Andrews, M.J.; Yao, E.F.; Armstrong, R.  
J. Biol. Chem. 265, 5192-5198, 1990  
A;Title: The aspirin and heme-binding sites of ovine and murine prostaglandin endoperox  
A;Reference number: A35564; MUID:90203007; PMID:2108169  
A;Accession: A35564  
A;Molecule type: mRNA  
A;Residues: 1-602 <DEW>  
A;Cross-references: UNIPROT:P22437; UNIPARC:UPI000000188A; GB:M34141; NID:g200302; PID:  
C;Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
C;Keywords: oxidoreductase  
F;1-26/Domain: signal sequence #status predicted <SIG>  
F;27-602/Product: prostaglandin-endoperoxide synthase #status predicted <MAT>  
F;38-71/Domain: EGF homology <EGF>

Query Match 72.7%; Score 32; DB 2; Length 602;  
Best Local Similarity 85.7%; Pred. No. 82;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||||  
Db 358 FLQLKFD 364

RESULT 15  
S69198  
prostaglandin G/H synthase 1 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S69198; S69199  
R;Kitzler, J.W.  
submitted to the EMBL Data Library, December 1994  
A;Reference number: S69198  
A;Accession: S69198  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-602 <KIT>  
A;Cross-references: UNIPROT:Q63921; UNIPARC:UPI0000131799; EMBL:U18060; NID:g603051; PI:  
R;Kitzler, J.; Hill, E.; Hardman, R.; Reddy, N.; Philpot, R.; Eling, T.E.  
Arch. Biochem. Biophys. 316, 856-863, 1995  
A;Title: Analysis and quantitation of splicing variants of the TPA-inducible PGHS-1 mRN  
A;Reference number: S69199; MUID:95168876; PMID:7864644  
A;Accession: S69199  
A;Molecule type: mRNA  
A;Residues: 61-602 <KIT>  
A;Cross-references: UNIPARC:UPI0000175280; EMBL:U18060  
A;Note: only a part of the nucleic acid sequence is shown  
C;Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
C;Keywords: alternative splicing  
F;38-71/Domain: EGF homology <EGF>

Query Match 72.7%; Score 32; DB 2; Length 602;  
Best Local Similarity 85.7%; Pred. No. 82;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||||  
Db 358 FLQLKFD 364

RESULT 16  
F83704

homosystein methyl transferase BH0438 [imported] - Bacillus halodurans (strain C-125)  
 C:Species: Bacillus halodurans  
 C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C:Accession: F83704  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A:Reference number: A83650; MUID:20512582; PMID:11058132  
 A:Accession: F83704  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-756 <STO>  
 A:Cross-references: UNIPROT:O9KFP1; UNIPARC:UPI000012EF6A; GB:AP001508; GB:BA0000004; NID  
 A:Experimental source: strain C-125  
 C:Genetics:  
 C:Superfamily: cobalamin-independent methionine synthase

Query Match 72.7%; Score 32; DB 2; Length 756;  
 Best Local Similarity 77.8%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
 ||| ||||  
 DB 235 FLQTVFDV 243

RESULT 17  
 A32252  
 Probable phosphoesterase (EC 3.1.1.-) L - Acinetobacter calcoaceticus (fragment)  
 N:Alternate names: gene L protein  
 C:Species: Acinetobacter calcoaceticus  
 C>Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 31-Dec-2004  
 C:Accession: A32252; T01631  
 R:Goosen, N.; Horsman, H.P.A.; Huinen, R.G.M.; van de Putte, P.  
 J. Bacteriol. 171, 447-455, 1989  
 A:Title: Acinetobacter calcoaceticus genes involved in biosynthesis of the coenzyme pyruvate  
 A:Reference number: A32252; MUID:89123056; PMID:2536663  
 A:Accession: A32252  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-204 <GOO>  
 A:Cross-references: UNIPROT:P07778; UNIPARC:UPI000013BE17; GB:X06452; NID:g38740; PIDN:C  
 A:Experimental source: strain LMD 79.41  
 C:Comment: this sequence has motifs characteristic of a variety of phosphoesterases.  
 C:Keywords: hydrolase  
 F:43-139/Domain: phosphoesterase core homology <PEC>

Query Match 70.5%; Score 31; DB 2; Length 204;  
 Best Local Similarity 62.5%; Pred. No. 40;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
 :||:||||  
 DB 128 IQIDFDV 135

RESULT 18  
 A40979  
 temperature shock-inducible protein TIPI precursor - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: protein YBR0622; protein YBR067c  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 13-May-1992 #sequence\_revision 13-May-1992 #text\_change 09-Jul-2004  
 C:Accession: A40979; S45928; A57263  
 R:Kondo, K.; Inouye, M.  
 J. Biol. Chem. 266, 17537-17544, 1991  
 A:Title: TIPI, a cold shock-inducible gene of Saccharomyces cerevisiae.  
 A:Reference number: A40979  
 A:Accession: A40979  
 A:Molecule type: DNA  
 A:Residues: 1-210 <KON>  
 A:Cross-references: UNIPROT:P27654; UNIPARC:UPI0000136FB0; GB:M71216; NID:gl72983; PIDN:  
 R.Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.

submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45927  
 A:Accession: S45928  
 A:Molecule type: DNA  
 A:Residues: 1-210 <FEU>  
 A:Cross-references: UNIPARC:UPI0000136FB0; EMBL:Z35936; NID:g536313; PIDN:CAA85011.1; PI  
 R:Van Der Vaart, J.M.; Caro, L.H.P.; Chapman, J.W.; Klis, F.M.; Verrips, C.T.  
 J. Bacteriol. 177, 3104-3110, 1995  
 A:Title: Identification of three mannoproteins in the cell wall of Saccharomyces cerevisiae  
 A:Reference number: A57263; MUID:95286490; PMID:7768807  
 A:Accession: A57263  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-210 <VAN>  
 A:Cross-references: UNIPARC:UPI0000136FB0  
 C:Genetics:  
 A:Gene: SGD:TIP1  
 A:Cross-references: SGD:S0000271; MIPS:YBR067c  
 A:Map position: 2R  
 C:Superfamily: serine-rich protein  
 C:Keywords: cell wall; transmembrane protein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-210/Product: temperature shock-inducible protein TIPI #status predicted <MAT>  
 F:194-210/Domain: transmembrane #status predicted <TM>

Query Match 70.5%; Score 31; DB 2; Length 210;  
 Best Local Similarity 55.6%; Pred. No. 41;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
 |||:||||  
 DB 78 FSELDFDAI 86

RESULT 19  
 G70415  
 nucleotide sugar epimerase - Aquifex aeolicus  
 C:Species: Aquifex aeolicus  
 C>Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 C:Accession: G70415  
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov  
 V.  
 Nature 392, 353-358, 1998  
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A:Reference number: A70300; MUID:98196866; PMID:9537320  
 A:Accession: G70415  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-321 <AQF>  
 A:Cross-references: UNIPROT:O67354; UNIPARC:UPI00000565C3; GB:AE000735; NID:g2983749; PI  
 A:Experimental source: strain VF5  
 C:Genetics:  
 A:Gene: nse  
 C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology  
 F:3-316/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 70.5%; Score 31; DB 2; Length 321;  
 Best Local Similarity 66.7%; Pred. No. 66;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
 |||:||||  
 DB 72 FOEFDFDAV 80

RESULT 20  
 T06786  
 6a-hydroxymaackia in methyltransferase (EC 2.1.1.-) - garden pea  
 C:Species: Pisum sativum (garden pea)  
 C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T06786  
 R:Wu, Q.; Preisig, C.L.; VanEtten, H.D.  
 Plant Mol. Biol. 35, 551-560, 1997

A;Title: Isolation of the cDNAs encoding (+)6a-hydroxymaackiain 3-O-methyltransferase, d  
A;Reference number: Z15813; MUID:98009990; PMID:9349277  
A;Accession: T06786  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-360 <WU>  
A;Cross-references: UNIPROT:O24305; UNIPARC:UPI000000A483B; EMBL:U69554; NID:gl586636; PT  
C;Genetics:  
A;Note: hnm6  
C;Function:  
A;Description: catalyzes the methylation of (+)6a-hydroxymaackiain to (+)pisatin  
A;Pathway: the terminal step in the pisatin biosynthesis  
C;Superfamily: O-methyltransferase  
C;Keywords: methyltransferase

Query Match 70.5%; Score 31; DB 2; Length 360;  
Best Local Similarity 75.0%; Pred. No. 75;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
|||:|  
Db 310 LQLEYDV 317

RESULT 21  
A86324  
protein F14D16.19 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: A86324  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: A86324  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-384 <STO>  
A;Cross-references: UNIPROT:Q9LMC3; UNIPARC:UPI000009F99E; GB:AE005172; NID:g8778280; PT  
C;Genetics:  
A;Gene: F14D16.19  
A;Map position: 1

Query Match 70.5%; Score 31; DB 2; Length 384;  
Best Local Similarity 71.4%; Pred. No. 81;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||:|  
Db 91 FLRIEFD 97

RESULT 22  
F81393  
probable altronate hydrolase C-terminus Cj0483 [imported] - Campylobacter jejuni (strain  
C;Species: Campylobacter jejuni  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: F81393  
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
Nature 403, 665-668, 2000  
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A;Reference number: A81250; MUID:20150912; PMID:10688204  
A;Accession: F81393  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-390 <PAR>  
A;Cross-references: UNIPROT:Q9PI26; UNIPARC:UPI00000C214A; GB:AL139075; GB:AL1111168; NI  
A;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: uxaA'; Cj0483

Query Match 70.5%; Score 31; DB 2; Length 390;  
Best Local Similarity 85.7%; Pred. No. 83;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFDV 9  
|||:|  
Db 56 QLEFDAL 62

RESULT 23  
B90139  
phosphomethylpyrimidine kinase (thiD-1) [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: B90139  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,  
arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: B90139  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-400 <KUR>  
A;Cross-references: UNIPROT:Q981E3; UNIPARC:UPI000006415A; GB:AE006641; NID:gl3813129;  
C;Genetics:  
A;Gene: thiD-1

Query Match 70.5%; Score 31; DB 2; Length 400;  
Best Local Similarity 55.6%; Pred. No. 85;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
|||:|  
Db 60 FIEAQFDV 68

RESULT 24  
T44444  
hypothetical protein [imported] - Flavobacterium johnsoniae (fragment)  
C;Species: Flavobacterium johnsoniae  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T44444  
R;Agarwal, S.; Hunicutt, D.W.; McBride, M.J.  
Proc. Natl. Acad. Sci. U.S.A. 94, 12139-12144, 1997  
A;Title: Cloning and characterization of the Flavobacterium johnsoniae (Cytophaga john  
A;Reference number: Z22770; MUID:98004537; PMID:9342376  
A;Accession: T44444  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-578 <AGA>  
A;Cross-references: UNIPROT:O30490; UNIPARC:UPI000000AE74A; EMBL:AF007381; NID:g2281662;  
A;Experimental source: strain ATCC17061

Query Match 70.5%; Score 31; DB 2; Length 578;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFDV 9  
|||:|  
Db 278 QLEFDV 284

RESULT 25  
T19678

hypothetical protein C33D9.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T19678  
 R:Lloyd, C.  
 submitted to the EMBL Data Library, December 1995  
 A:Reference number: Z19162  
 A:Accession: T19678  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-875 <WIL>  
 A:Cross-references: UNIPROT:Q18372; UNIPARC:UPI000017B7FE; EMBL:Z68159; PIDN:CAA92282.1;  
 A:Experimental source: clone C33D9  
 C:Genetics:  
 A:Gene: CESP:C33D9.1  
 A:Map position: 4  
 A:introns: 14/1; 74/3; 129/3; 171/3; 198/1; 241/2; 269/3; 352/3; 403/2; 515/3; 595/3; 65/3

Query Match 70.5%; Score 31; DB 2; Length 875;  
 Best Local Similarity 85.7%; Pred. No. 2e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFDVAV 9  
 ||:||||  
 Db 47 QLEFDVAV 53

RESULT 26  
 G64514  
 type I restriction enzyme homolog - *Methanococcus jannaschii* plasmid PURB800  
 C:Species: *Methanococcus jannaschii*  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C:Accession: G64514  
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
 Science 273, 1058-1073, 1996  
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
 A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*  
 A:Reference number: A64300; MUID:96337999; PMID:8688087  
 A:Accession: G64514  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1042 <BUL>  
 A:Cross-references: UNIPROT:Q60295; UNIPARC:UPI0000136793; GB:L77118; NID:g1500644; TIGR  
 C:Genetics:  
 A:Map position: ECLREV52581-49453  
 A:Genome: plasmid  
 A:Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachromoso  
 C:Superfamily: type I site-specific deoxyribonuclease chain hsdR  
 C:Keywords: ATP; nucleotide binding; P-loop  
 F:336-343/Region: nucleotide-binding motif A (P-loop)  
 F:439-440/Region: nucleotide-binding motif B  
 F:439-442/Region: DEAH motif

Query Match 70.5%; Score 31; DB 2; Length 1042;  
 Best Local Similarity 55.6%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FQLEFDDVAV 9  
 ||:||||  
 Db 517 FQLEFDDVAV 525

RESULT 27  
 JCS546  
 chitin synthase (EC 2.4.1.16) csma - *Emericella nidulans*  
 N:Alternate names: chitin-UDP N-acetylglucosaminyltransferase  
 C:Species: *Emericella nidulans*, *Aspergillus nidulans*  
 C>Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
 C:Accession: JCS546  
 R:Fujiwara, M.; Horiuchi, H.; Ohta, A.; Takagi, M.  
 Biochem. Biophys. Res. Commun. 236, 75-78, 1997

A:Title: A novel fungal gene encoding chitin synthase with a myosin motor-like domain.  
 A:Reference number: JCS546; MUID:97366599; PMID:9223429  
 A:Accession: JCS546  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1852 <FUJ>  
 A:Cross-references: UNIPROT:O13281; UNIPARC:UPI000006C82A; DDBJ:AB000125; NID:g2308976;  
 C:Comment: This enzyme is a membrane-bound protein. It is involved in the catalytic poly  
 C:Genetics:  
 A:Gene: csma  
 C:Keywords: ATP; glycosyltransferase; hexosyltransferase  
 F:102-110/Domain: ATP-binding #status predicted <ATP>

Query Match 70.5%; Score 31; DB 2; Length 1852;  
 Best Local Similarity 62.5%; Pred. No. 4.8e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQLEFDFA 8  
 ||:||||  
 Db 158 FQLEQYDA 165

RESULT 28  
 AE2073  
 hypothetical protein alr2139 [imported] - *Nostoc* sp. (strain PCC 7120)  
 C:Species: *Nostoc* sp. PCC 7120  
 A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AE2073  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AE2073  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-100 <KUR>  
 A:Cross-references: UNIPROT:Q8YV42; UNIPARC:UPI00000CE326; GB:BA000019; PIDN:BAE73838.1;  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr2139

Query Match 68.2%; Score 30; DB 2; Length 100;  
 Best Local Similarity 85.7%; Pred. No. 29;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEFDFA 8  
 ||:||||  
 Db 34 LQLEFDFA 40

RESULT 29  
 E84198  
 hypothetical protein Vng0399h [imported] - *Halobacterium* sp. NRC-1  
 C:Species: *Halobacterium* sp. NRC-1  
 C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: E84198  
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
 ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc  
 Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omar, A.D.; Ebhardt, H.; Lowe, T.M.; La  
 A:Title: Genome sequence of *Halobacterium* species NRC-1.  
 A:Reference number: A84160; MUID:20504483; PMID:11016950  
 A:Accession: E84198  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-155 <STO>  
 A:Cross-references: UNIPROT:Q9HS55; UNIPARC:UPI0000063609; GB:AE004437; NID:g10580011; F  
 C:Genetics:  
 A:Gene: VNG0399h

Query Match 68.2%; Score 30; DB 2; Length 155;  
 Best Local Similarity 62.5%; Pred. No. 48;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
 |||||  
 Db 77 LQLQFDGI 84

RESULT 30  
 D69888  
 micrococcal nuclease homolog yncB - Bacillus subtilis  
 C;Species: Bacillus subtilis  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C;Accession: D69888  
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni, F.; Bolland, C.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chao, C.; Bron, S.; Broutin, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chao, C.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997  
 A;Authors: Foulger, D.; Frittz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, M.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maues, Y., M.; Ogasawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Serod, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A;Reference number: A69580; MUID:98044033; PMID:9384377  
 A;Accession: D69888  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-211 <KUN>  
 A;Cross-references: UNIPROT:P94492; UNIPARC:UPI0000060463; GB:Z99113; GB:AL009126; NID:9  
 A;Experimental source: strain 168  
 C;Genetics:  
 A;Gene: yncB  
 C;Superfamily: micrococcal nuclease

Query Match 68.2%; Score 30; DB 2; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEFD 7  
 |||||  
 Db 127 LQLEFD 132

RESULT 31  
 G45170  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - ant (Lasius sp.) mitochondrion  
 C;Species: mitochondrion Lasius sp. (ant)  
 C;Date: 18-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 31-Dec-2004  
 C;Accession: G45170  
 R;Liu, H.; Beckenbach, A.T.  
 Mol. Phylogenet. Evol. 1, 41-52, 1992  
 A;Title: Evolution of the mitochondrial cytochrome oxidase II gene among 10 orders of in  
 A;Reference number: A45170; MUID:94115687; PMID:1342923  
 A;Accession: G45170  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-226 <LIU>  
 A;Cross-references: UNIPARC:UPI0000128033; GB:M83960; NID:9340659; PIDN:AAA31885.1; PID:  
 C;Genetics:  
 A;Gene: COII  
 A;Genome: mitochondrion  
 A;Genetic code: SGC4  
 C;Superfamily: cytochrome-c oxidase, subunit II, mitochondrial type; cytochrome-c oxidase  
 C;Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner  
 F;8-213/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F;160,195,199,206/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted

F;195,197,199,203/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F;197/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 68.2%; Score 30; DB 2; Length 226;  
 Best Local Similarity 62.5%; Pred. No. 74;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8  
 |||||  
 Db 112 FLNIEFDS 119

RESULT 32  
 G90730  
 antitermination protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0  
 C;Species: Escherichia coli  
 C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Nov-2003  
 C;Accession: G90730  
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 gagawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: G90730  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-229 <HAY>  
 A;Cross-references: UNIPARC:UPI00001653D1; GB:BA000007; PIDN:BA034238.1; PID:gl3360274;  
 A;Experimental source: strain O157:H7, substrain RIMD 050952  
 C;Genetics:  
 A;Gene: ECs0815  
 C;Superfamily: antitermination protein Q

Query Match 68.2%; Score 30; DB 2; Length 229;  
 Best Local Similarity 66.7%; Pred. No. 75;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDA 9  
 |||||  
 Db 198 FLQLDSAL 206

RESULT 33  
 B81870  
 probable membrane protein NMA1051 [imported] - Neisseria meningitidis (strain Z2491 ser:  
 C;Species: Neisseria meningitidis  
 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
 C;Accession: B81870  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More  
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream  
 Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A;Reference number: A81775; MUID:20222556; PMID:10761919  
 A;Accession: B81870  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-237 <PAR>  
 A;Cross-references: UNIPROT:Q9JVL1; UNIPARC:UPI0000030DPD; GB:AL162755; GB:AL157959; NTI  
 A;Experimental source: serogroup A, strain Z2491  
 C;Genetics:  
 A;Gene: NMA1051

Query Match 68.2%; Score 30; DB 2; Length 237;  
 Best Local Similarity 85.7%; Pred. No. 78;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFDV 9  
 |||||  
 Db 142 QLEFEAV 148

RESULT 34  
 D85581

hypothetical protein Z0956 [imported] - Escherichia coli (strain O157:H7, substrain EDL9  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 03-Nov-2003  
 C:Accession: D85581  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: D85581  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-257 <STO>  
 A:Cross-references: UNIPARC:UPI0000D0984; GB:AE005174; NID:gl2513721; PIDN:AA055112.1;  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z0956  
 C:Superfamily: antitermination protein Q

Query Match 68.2%; Score 30; DB 2; Length 257;  
 Best Local Similarity 66.7%; Pred. No. 85;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
 |||||:  
 Db 226 FLQLSDAL 234

RESULT 35  
 G82076  
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) cpdA-type VC2433 [similarity] -  
 N:Alternate names: icc protein  
 C:Species: Vibrio cholerae  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: G82076  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B  
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: A82035; MUID:20406833; PMID:10952301  
 A:Accession: G82076  
 A:Molecule type: DNA  
 A:Residues: 1-272 <HEI>  
 A:Cross-references: UNIPROT:Q9KDP7; UNIPARC:UPI00000C32CE; GB:AE004313; GB:AE003852; NID  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC2433  
 A:Map position: 1  
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, Icc type; 3',5'-cyclic-nucleot  
 C:Keywords: iron; metalloprotein; phosphoric diester hydrolase  
 F:13-202/Domain: 3',5'-cyclic-nucleotide phosphodiesterase cpdA homology <CPDA>  
 F:13-93/Domain: phosphoesterase core homology <PEC>

Query Match 68.2%; Score 30; DB 1; Length 272;  
 Best Local Similarity 71.4%; Pred. No. 91;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFDV 9  
 |||||:  
 Db 50 QVEFDV 56

RESULT 36  
 T38816  
 hypothetical protein SPAC4F10.12 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: T38816  
 R:Connor, R.; Churcher, C.M.; Barrrell, B.G.; Rajandream, M.A.; Wood, V.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z21813  
 A:Accession: T38816

A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-280 <CON>  
 A:Cross-references: UNIPROT:O36024; UNIPARC:UPI000006C03B; EMBL:Z98980; NID:el060691; PI  
 A:Experimental source: strain 972h-; cosmid c4F10  
 C:Genetics:  
 A:Gene: SPDB:SPAC4F10.12  
 A:Map position: 1

Query Match 68.2%; Score 30; DB 2; Length 280;  
 Best Local Similarity 85.7%; Pred. No. 94;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
 |||||:  
 Db 145 FLQQEF 151

RESULT 37  
 B97100  
 pyridoxal kinase related protein [imported] - Clostridium acetobutylicum  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: B97100  
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: B97100  
 A:Molecule type: DNA  
 A:Residues: 1-290 <KUR>  
 A:Cross-references: UNIPROT:O97IL8; UNIPARC:UPI00000CA276; GB:AE001437; PIDN:AAK79589.9  
 A:Experimental source: Clostridium acetobutylicum ATCC924  
 C:Genetics:  
 A:Gene: CAC1622

Query Match 68.2%; Score 30; DB 2; Length 290;  
 Best Local Similarity 62.5%; Pred. No. 97;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
 |||||:  
 Db 73 INLEFDV 80

RESULT 38  
 T12770  
 probable endonuclease YokF - Bacillus subtilis phage SPBc2  
 C:Species: Bacillus subtilis phage SPBc2  
 C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
 C:Accession: T12770; B69908  
 R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.  
 submitted to the EMBL Data Library, August 1997  
 A:Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 proph  
 A:Reference number: Z17593  
 A:Accession: T12770  
 A:Status: translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-296 <LAZ>  
 A:Cross-references: UNIPROT:O64020; UNIPARC:UPI00000605E9; EMBL:AF020713; NID:g3025478;  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
 C:Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
 ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F  
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: B69908  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-296 <KUN>  
 A:Cross-references: UNIPARC:UPI00000605E9; GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CA  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: YokP  
 C:Superfamily: micrococcal nuclease

Query Match 68.2%; Score 30; DB 2; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLEFD 7  
 |||||  
 Db 129 LQLEFD 134

## RESULT 39

T23932

hypothetical protein R05D7.4 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T23932

R:Dobson, R.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19819

A:Accession: T23932

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-299 &lt;WIL&gt;

A:Cross-references: UNIPROT:O45707; UNIPARC:UPI000007A29D; EMBL:Z81105; PIDN:CAB03219.1;

A:Experimental source: clone R05D7

C:Genetics:

A:Gene: CESP:R05D7.4

A:Map position: 1

A:Introns: 29/3; 122/1; 162/1; 231/2; 268/3

C:Superfamily: tropinesterase

Query Match 68.2%; Score 30; DB 2; Length 299;  
 Best Local Similarity 55.6%; Pred. No. 1e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLEFD 9  
 |||||  
 Db 266 FPQVQFD 274

## RESULT 40

C69857

formyltetrahydrofolate deformylase homolog ykK - *Bacillus subtilis*C:Species: *Bacillus subtilis*

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-Oct-2004

C:Accession: C69857

R:Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.

Koether, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

V. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: C69857  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-300 <KUN>  
 A:Cross-references: UNIPROT:O34990; UNIPARC:UPI00000330DE; GB:Z99110; GB:AL009126; NID  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: ykK  
 C:Superfamily: formyltetrahydrofolate deformylase; phosphoribosylglycinamide formyltransferase  
 F:106-298/Domain: phosphoribosylglycinamide formyltransferase homology <PRGF>

Query Match 68.2%; Score 30; DB 2; Length 300;  
 Best Local Similarity 71.4%; Pred. No. 1e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFD 7  
 |||||  
 Db 63 FLRIEFD 69

## RESULT 41

C85574

probable LysR-like transcription regulator Z0885 [imported] - *Escherichia coli* (strainC:Species: *Escherichia coli*

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C:Accession: C85574

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: C85574

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-301 &lt;STO&gt;

A:Cross-references: UNIPROT:Q8X4W1; UNIPARC:UPI000000D0D66; GB:AE005174; NID:g12513649;

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z0885

C:Superfamily: regulatory protein ampr

Query Match 68.2%; Score 30; DB 2; Length 301;  
 Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLEFD 9  
 |||||  
 Db 137 FLNREYDAV 145

## RESULT 42

C90723

probable transcription regulator ECs0755 [imported] - *Escherichia coli* (strain O157:H7;C:Species: *Escherichia coli*

C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C:Accession: C90723

R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: C90723

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-301 &lt;HAY&gt;

A:Cross-references: UNIPROT:Q8X4W1; UNIPARC:UPI000000D0D66; GB:BA000007; PIDN:BA034178.1

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs0755

C:Superfamily: regulatory protein ampr

Query Match 68.2%; Score 30; DB 2; Length 301;  
 Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEPDAV 9  
 ||| |  
 Db 137 FLNREYDAV 145

## RESULT 43

T04247

hypothetical protein F20B18.30 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004

C:Accession: T04247

R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X

A:Reference number: Z15263

A:Accession: T04247

A:Molecule type: DNA

A:Residues: 1-365 <BEV>

A:Cross-references: UNIPROT:Q9SZG7; UNIPARC:UPI0000A2E33; EMBL:AL049483

A:Experimental source: cultivar Columbia; BAC clone F20B18

C:Genetics:

A:Map position: 4

A:Introns: 21/1; 246/2

A:Note: F20B18.30

C:Superfamily: Arabidopsis hypothetical protein F20B18.30

## Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 365;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEPD 7

||:|||||

Db 205 FVELEPD 211

## RESULT 44

T01551

receptor kinase homolog A.TM018A10.19 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004

C:Accession: T01551

R:Dempsey, S.; Harper, M.

A:Description: The sequence of A. thaliana TM018A10.

A:Reference number: Z14348

A:Accession: T01551

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-372 <DEM>

A:Cross-references: UNIPROT:Q23082; UNIPARC:UPI000009CFFF; EMBL:AF013294; NID:g2252848;

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 4

A:Introns: 28/1; 72/3; 139/2; 217/2; 267/3

A:Note: A.TM018A10.19

C:Superfamily: kinase-related transforming protein; protein kinase homology

## Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 372;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEPDAV 9

|||:||||

Db 42 LQLDFDTI 49

## RESULT 45

T51874

hypothetical protein DKFZp762P233.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004

C:Accession: T51874

R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Weil, B.; Wiemann, S.

A:Reference number: Z25855

A:Accession: T51874

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-420 <AAA>

A:Cross-references: UNIPROT:Q9NPU8; UNIPARC:UPI0000071E65; EMBL:AL390155

A:Experimental source: adult melanoma (MeWo cell line); clone DKFZp762P233

C:Genetics:

A:Note: DKFZp762P233.1

C:Superfamily: Neurospora cytosolic leucine-tRNA ligase

## Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 420;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEPD 7

|||||

Db 254 LQLEPD 259

## RESULT 46

T01550

receptor kinase homolog A.TM018A10.18 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004

C:Accession: T01550

R:Dempsey, S.; Harper, M.

A:Description: The sequence of A. thaliana TM018A10.

A:Reference number: Z14348

A:Accession: T01550

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-429 <DEM>

A:Cross-references: UNIPROT:Q23081; UNIPARC:UPI000009F717; EMBL:AF013294; NID:g2252848;

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 4

A:Introns: 89/1; 133/3; 204/1; 276/2; 326/3

C:Superfamily: kinase-related transforming protein; protein kinase homology

## Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 429;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEPDAV 9

|||||

Db 103 LQLEPDTI 110

## RESULT 47

T31511

hypothetical protein Y116A8C.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004

C:Accession: T31511

R:McMurray, A.

A:Reference number: Z21041

A:Accession: T31511

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-433 <WIL>

A:Cross-references: UNIPROT:Q9U2T2; UNIPARC:UPI0000179440; EMBL:AL117204; PIDN:CAB55145

A:Experimental source: clone Y116A8C

C:Genetics:

A:Gene: CESP:Y116A8C.9

A:Introns: 16/2; 42/2; 75/2; 107/3; 173/3; 230/3; 262/3; 318/3; 373/1; 398/1



Query Match 68.2%; Score 30; DB 2; Length 433;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
 |:|:|:|  
 Db 105 FIKLEFD 111

## RESULT 48

G70116  
 histidine-tRNA ligase (EC 6.1.1.21) hisS - Lyme disease spirochete  
 N;Alternate names: histidyl-tRNA synthetase  
 C;Species: Borrelia burgdorferi (Lyme disease spirochete)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: G70116  
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
 Nature 390, 580-586, 1997  
 A;Authors: Smith, H.O.; Venter, J.C.  
 A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
 A;Reference number: A70100; MUID:98065943; PMID:9403685  
 A;Accession: G70116  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-457 <KLE>  
 A;Cross-references: UNIPROT:O51160; UNIPARC:UPI0000057372; GB:AE001125; GB:AE000783; NID  
 A;Experimental source: strain B31  
 C;Superfamily: histidyl-tRNA synthetase; histidine-tRNA ligase homology  
 C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis  
 F;8-418/Domain: histidine-tRNA ligase homology <HTL>

Query Match 68.2%; Score 30; DB 1; Length 457;  
 Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEFD 9  
 |:|:|:|  
 Db 121 FMQFDFDIV 129

## RESULT 49

D70917  
 probable tkt protein - Mycobacterium tuberculosis (strain H37RV)  
 C;Species: Mycobacterium tuberculosis  
 C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 C;Accession: D70917  
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A;Reference number: A70500; MUID:98295987; PMID:9634230  
 A;Accession: D70917  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-700 <COL>  
 A;Cross-references: UNIPROT:O06811; UNIPARC:UPI0000137006; GB:Z95844; GB:AL123456; NID:9  
 A;Experimental source: strain H37RV  
 C;Genetics:  
 A;Gene: tkt  
 C;Superfamily: transketolase; thiamin pyrophosphate-binding domain homology

Query Match 68.2%; Score 30; DB 2; Length 700;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFDA 8  
 |:|:|:|  
 Db 332 QLEFDA 337

## RESULT 50

T15742  
 hypothetical protein C32D5.11 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: T15742  
 R;Miller, N.  
 submitted to the EMBL Data Library, July 1995  
 A;Description: The sequence of C. elegans cosmid C32D5.  
 A;Reference number: Z18396  
 A;Accession: T15742  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-770 <MTL>  
 A;Cross-references: UNIPROT:Q18355; UNIPARC:UPI0000077C07; EMBL:U23511; NID:G746463; PI  
 A;Experimental source: strain Bristol N2  
 C;Genetics:  
 A;Gene: CESP:C32D5.11  
 A;Introns: 40/2; 75/2; 129/2; 175/2; 189/3; 222/2; 283/3; 328/3; 586/3; 610/3; 747/1  
 F;64-115/Domain: RING finger homology <RRN>

Query Match 68.2%; Score 30; DB 2; Length 770;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEFD 9  
 |:|:|:|  
 Db 271 FLIAEFD 279

Search completed: May 9, 2006, 02:24:50  
 Job time : 34.4 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:06:12 ; Search time 99.6 Seconds  
(without alignments)  
63.753 Million cell updates/sec

Title: US-09-870-216C-5  
Perfect score: 44  
Sequence: 1 FLOLEFNAV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Uniprot\_05.80.\*  
1: uniprot\_trembl.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	84.1	124	2	Q94TV4_9EUCA
2	37	84.1	140	2	Q94TU9_9EUCA
3	37	84.1	142	2	Q94TU8_9EUCA
4	37	84.1	147	2	Q94TU6_9EUCA
5	37	84.1	155	2	Q94TV7_9EUCA
6	37	84.1	163	2	Q94TV6_9EUCA
7	37	84.1	166	2	Q8WFY3_9EUCA
8	37	84.1	170	2	Q8WFY4_9EUCA
9	37	84.1	171	2	Q94TU3_9EUCA
10	37	84.1	172	2	Q94TU7_9EUCA
11	37	84.1	174	2	Q94TU2_9EUCA
12	37	84.1	178	2	Q94TV3_9EUCA
13	37	84.1	179	2	Q94TU1_9EUCA
14	37	84.1	180	2	Q6PLV2_9EUCA
15	37	84.1	180	2	Q94TV0_9EUCA
16	37	84.1	181	2	Q94TV2_9EUCA
17	37	84.1	183	2	Q8WFZ3_9EUCA
18	37	84.1	183	2	Q94TV5_9EUCA
19	37	84.1	184	2	Q8WFY8_9EUCA
20	37	84.1	185	2	Q8WFY7_9EUCA
21	37	84.1	188	2	Q94TV1_9EUCA
22	37	84.1	189	2	Q6PLS9_9EUCA
23	37	84.1	189	2	Q6PLT0_9EUCA
24	37	84.1	189	2	Q6PLT1_9EUCA
25	37	84.1	189	2	Q6PLT3_9EUCA
26	37	84.1	189	2	Q6PLT4_9EUCA
27	37	84.1	189	2	Q6PLT5_9EUCA
28	37	84.1	189	2	Q6PLT6_9EUCA
29	37	84.1	189	2	Q6PLT7_9EUCA
30	37	84.1	189	2	Q6PLT9_9EUCA
31	37	84.1	189	2	Q6PLU0_9EUCA

32	37	84.1	189	2	Q6PLU1_9EUCA	O6plu1 aegla sp. k
33	37	84.1	189	2	Q6PLU2_9EUCA	O6plu2 aegla ringu
34	37	84.1	189	2	Q6PLU4_9EUCA	O6plu4 aegla sanlo
35	37	84.1	189	2	Q6PLU5_9EUCA	O6plu5 aegla sanlo
36	37	84.1	189	2	Q6PLU6_9EUCA	O6plu6 aegla jujuy
37	37	84.1	189	2	Q6PLU8_9EUCA	O6plu8 aegla septu
38	37	84.1	189	2	Q6PLV0_9EUCA	O6plv0 aegla scamo
39	37	84.1	189	2	Q6PLV3_9EUCA	O6plv3 aegla obati
40	37	84.1	189	2	Q6PLV5_9EUCA	O6plv5 aegla plate
41	37	84.1	189	2	Q6PLV6_9EUCA	O6plv6 aegla plate
42	37	84.1	189	2	Q6PLV8_9EUCA	O6plv8 aegla margi
43	37	84.1	189	2	Q6PLV9_9EUCA	O6plv9 aegla strin
44	37	84.1	189	2	Q6PLW1_9EUCA	O6plw1 aegla leptu
45	37	84.1	189	2	Q6PLW3_9EUCA	O6plw3 aegla caver
46	37	84.1	189	2	Q6PLW5_9EUCA	O6plw5 aegla prado
47	37	84.1	189	2	Q6PLW7_9EUCA	O6plw7 aegla urugu
48	37	84.1	189	2	Q6PLW9_9EUCA	O6plw9 aegla sp. k
49	37	84.1	189	2	Q6PLX0_9EUCA	O6plx0 aegla sp. k
50	37	84.1	189	2	Q6PLX1_9EUCA	O6plx1 aegla plate
51	37	84.1	189	2	Q6PLX3_9EUCA	O6plx3 aegla viola
52	37	84.1	189	2	Q6PLX5_9EUCA	O6plx5 aegla rossi
53	37	84.1	189	2	Q6PLX7_9EUCA	O6plx7 aegla inerm
54	37	84.1	189	2	Q6PLX0_9EUCA	O6plx0 aegla leptu
55	37	84.1	189	2	Q6PLX2_9EUCA	O6plx2 aegla serra
56	37	84.1	189	2	Q6PLX3_9EUCA	O6plx3 aegla grise
57	37	84.1	189	2	Q6PLX4_9EUCA	O6plx4 aegla spini
58	37	84.1	189	2	Q6PLX5_9EUCA	O6plx5 aegla singu
59	37	84.1	189	2	Q6PLX7_9EUCA	O6plx7 aegla grise
60	37	84.1	189	2	Q6PLX9_9EUCA	O6plx9 aegla logir
61	37	84.1	189	2	Q6PLZ0_9EUCA	O6plz0 aegla logir
62	37	84.1	189	2	Q6PLZ1_9EUCA	O6plz1 aegla logir
63	37	84.1	189	2	Q6PLZ2_9EUCA	O6plz2 aegla serra
64	37	84.1	189	2	Q6PLZ5_9EUCA	O6plz5 aegla incon
65	37	84.1	189	2	Q6PLZ7_9EUCA	O6plz7 aegla plana
66	37	84.1	189	2	Q6PM00_9EUCA	O6pm00 aegla itaco
67	37	84.1	189	2	Q6PM02_9EUCA	O6pm02 aegla sp. k
68	37	84.1	189	2	Q6PM03_9EUCA	O6pm03 aegla sp. k
69	37	84.1	189	2	Q6PM05_9EUCA	O6pm05 aegla jarai
70	37	84.1	189	2	Q6PM07_9EUCA	O6pm07 aegla parva
71	37	84.1	189	2	Q6PM09_9EUCA	O6pm09 aegla camar
72	37	84.1	189	2	Q6PM11_9EUCA	O6pm11 aegla parob
73	37	84.1	189	2	Q6PM13_9EUCA	O6pm13 aegla castr
74	37	84.1	189	2	Q6PM14_9EUCA	O6pm14 aegla paula
75	37	84.1	189	2	Q6PM16_9EUCA	O6pm16 aegla schmi
76	37	84.1	189	2	Q6PM17_9EUCA	O6pm17 aegla jarai
77	37	84.1	189	2	Q6PM18_9EUCA	O6pm18 aegla jarai
78	37	84.1	189	2	Q6PM19_9EUCA	O6pm19 aegla camar
79	37	84.1	189	2	Q6PM21_9EUCA	O6pm21 aegla jarai
80	37	84.1	189	2	Q6PM22_9EUCA	O6pm22 aegla spino
81	37	84.1	189	2	Q6PM23_9EUCA	O6pm23 aegla spino
82	37	84.1	189	2	Q6PM24_9EUCA	O6pm24 aegla sp. k
83	37	84.1	189	2	Q6PM25_9EUCA	O6pm25 aegla sp. k
84	37	84.1	189	2	Q6PM26_9EUCA	O6pm26 aegla jarai
85	37	84.1	189	2	Q6PM27_9EUCA	O6pm27 aegla odebr
86	37	84.1	189	2	Q6PM29_9EUCA	O6pm29 aegla jarai
87	37	84.1	189	2	Q6PM30_9EUCA	O6pm30 aegla jarai
88	37	84.1	189	2	Q6PM31_9EUCA	O6pm31 aegla jarai
89	37	84.1	189	2	Q6PM32_9EUCA	O6pm32 aegla sp. k
90	37	84.1	189	2	Q6PM33_9EUCA	O6pm33 aegla sp. k
91	37	84.1	189	2	Q6PM34_9EUCA	O6pm34 aegla paran
92	37	84.1	189	2	Q6PM35_9EUCA	O6pm35 aegla paran
93	37	84.1	189	2	Q6PM37_9EUCA	O6pm37 aegla castr
94	37	84.1	189	2	Q6PM38_9EUCA	O6pm38 aegla castr
95	37	84.1	189	2	Q6PM39_9EUCA	O6pm39 aegla strin
96	37	84.1	189	2	Q6PM40_9EUCA	O6pm40 aegla margi
97	37	84.1	189	2	Q6PM46_9EUCA	O6pm46 aegla viola
98	37	84.1	189	2	Q6PM49_9EUCA	O6pm49 aegla plate
99	37	84.1	189	2	Q8W7E3_9EUCA	O8w7e3 aegla rostr
100	37	84.1	189	2	Q8W7H0_9EUCA	O8w7h0 aegla laevi
101	37	84.1	189	2	Q8W7J0_9EUCA	O8w7j0 aegla laevi
102	37	84.1	189	2	Q8W7M9_9EUCA	O8w7m9 aegla abtao
103	37	84.1	189	2	Q8W7P2_9EUCA	O8w7p2 aegla chalc
104	37	84.1	189	2	Q8W7T5_9EUCA	O8w7t5 aegla abtao

105	37	84.1	189	2	Q8W7Z9_9EUA	Q8w7z9 aegla arauc	178	32	72.7	121	2	Q6PVN5_9DIPT	Q6pvn5 arachnocamp
106	37	84.1	189	2	Q8W899_9EUA	Q8w899 aegla pwen	179	32	72.7	121	2	Q6PVN7_9DIPT	Q6pvn7 arachnocamp
107	37	84.1	189	2	Q8W8K0_9EUA	Q8w8k0 aegla manni	180	32	72.7	121	2	Q6PVN8_9DIPT	Q6pvn8 arachnocamp
108	37	84.1	189	2	Q8W8M1_9EUA	Q8w8m1 aegla affin	181	32	72.7	128	2	Q9N2C8_HORSE	Q9n2c8 equus cabal
109	37	84.1	189	2	Q8W8M4_9EUA	Q8w8m4 aegla hucic	182	32	72.7	130	2	Q7GF56_9DIPT	Q7gf56 anopheles a
110	37	84.1	189	2	Q8W8Q9_9EUA	Q8w8q9 aegla denti	183	32	72.7	133	2	Q5FX74_9DIPT	Q5fx74 anopheles c
111	37	84.1	189	2	Q8W8R0_9EUA	Q8w8r0 aegla denti	184	32	72.7	135	2	Q7GF41_9DIPT	Q7gf41 anopheles a
112	37	84.1	189	2	Q8W8D0_9EUA	Q8w8d0 aegla denti	185	32	72.7	138	2	Q7GF41_9DIPT	Q7gf41 anopheles s
113	37	84.1	189	2	Q8WAD1_9EUA	Q8wad1 aegla alaca	186	32	72.7	139	2	Q03566_9DIPT	Q03566 anopheles i
114	37	84.1	189	2	Q8WAD2_9EUA	Q8wad2 aegla alaca	187	32	72.7	140	2	Q03431_9DIPT	Q03431 anopheles b
115	37	84.1	189	2	Q8WAD3_9EUA	Q8wad3 aegla rioli	188	32	72.7	140	2	Q03446_9DIPT	Q03446 anopheles s
116	37	84.1	189	2	Q8WAD4_9EUA	Q8wad4 aegla spect	189	32	72.7	140	2	Q7GF49_9DIPT	Q7gf49 anopheles d
117	37	84.1	189	2	Q8WAD5_9EUA	Q8wad5 aegla cholic	190	32	72.7	146	2	Q7GF43_9DIPT	Q7gf43 anopheles n
118	37	84.1	189	2	Q8WAD6_9EUA	Q8wad6 aegla cholic	191	32	72.7	150	2	Q03420_9DIPT	Q03420 anopheles d
119	37	84.1	189	2	Q8WAD7_9EUA	Q8wad7 aegla sp. k	192	32	72.7	154	2	Q03436_9DIPT	Q03436 anopheles g
120	37	84.1	189	2	Q8WAD8_9EUA	Q8wad8 aegla sp. k	193	32	72.7	154	2	Q7GF55_9DIPT	Q7gf55 anopheles a
121	37	84.1	189	2	Q8WAD9_9EUA	Q8wad9 aegla baham	194	32	72.7	154	2	Q922F1_RHIME	Q922f1 rhizobium m
122	37	84.1	189	2	Q8WAE0_9EUA	Q8wae0 aegla laevi	195	32	72.7	156	2	Q5UCT9_CAVPO	Q5uct9 cavia porce
123	37	84.1	189	2	Q8WFL1_9EUA	Q8wfl1 discoropag	196	32	72.7	158	2	Q03445_9DIPT	Q03445 anopheles r
124	37	84.1	204	2	Q8M3A5_9NEOP	Q8m3a5 nannochoris	197	32	72.7	160	2	Q5QCR0_9DIPT	Q5qcr0 anopheles c
125	37	84.1	1278	2	Q8U4K0_PYRFU	Q8u4k0 pyrococcus	198	32	72.7	167	2	Q94TU5_9EUA	Q94tu5 paralthode
126	35	79.5	183	2	Q94TW0_9EUA	Q94tw0 emerita ana	199	32	72.7	169	2	Q03418_9DIPT	Q03418 anopheles b
127	35	79.5	189	2	Q8WAC9_9EUA	Q8wac9 munida subr	200	32	72.7	169	2	Q03435_9DIPT	Q03435 anopheles e
128	35	79.5	192	2	Q8WFX9_9EUA	Q8wfx9 pagurigates	201	32	72.7	171	2	Q6E883_9HEMI	Q6e883 campylenchi
129	35	79.5	224	2	Q92ZZ9_9HEXA	Q92zz9 isotomurus	202	32	72.7	171	2	Q6E885_9HEMI	Q6e885 campylenchi
130	35	79.5	229	2	Q9MGD8_PENMO	Q9mgd8 penaeus mon	203	32	72.7	172	2	Q03442_9DIPT	Q03442 anopheles o
131	35	79.5	680	2	Q9PA40_XYLFA	Q9pa40 xytiella fas	204	32	72.7	174	2	Q8HI46_9DIPT	Q8hi46 anopheles c
132	35	79.5	1612	2	Q9VM11_DROME	Q9vm11 drosophila	205	32	72.7	175	2	Q03447_9DIPT	Q03447 anopheles t
133	35	79.5	1613	2	Q9XZU2_DROME	Q9xzuz2 drosophila	206	32	72.7	175	2	Q03448_9DIPT	Q03448 anopheles t
134	34	77.3	171	2	Q8SFT6_HOMGA	Q8sft6 homarus gam	207	32	72.7	175	2	Q03567_9DIPT	Q03567 anopheles d
135	34	77.3	173	2	Q8WFXZ6_9EUA	Q8wfxz6 neotrypaea	208	32	72.7	176	2	Q85UD4_9DIPT	Q8sud4 anopheles c
136	34	77.3	187	2	Q8WFXZ1_9EUA	Q8wfxz2 jaxea noctu	209	32	72.7	176	2	Q85GL3_9DIPT	Q8sgl3 anopheles c
137	34	77.3	188	2	Q8WFXZ1_9EUA	Q8wfxz1 upogebia af	210	32	72.7	176	2	Q85GL2_9DIPT	Q8sgl2 anopheles c
138	34	77.3	189	2	Q6PLZ3_9EUA	Q6plz3 aegla franc	211	32	72.7	176	2	Q85GL1_9DIPT	Q8sgl1 anopheles c
139	34	77.3	189	2	Q6PLZ4_9EUA	Q6plz4 aegla franc	212	32	72.7	179	2	Q03429_9DIPT	Q03429 anopheles a
140	34	77.3	189	2	Q6PM36_9EUA	Q6pm36 aegla schmi	213	32	72.7	181	2	Q7GF39_9DIPT	Q7gf39 anopheles t
141	34	77.3	189	2	Q6PM42_9EUA	Q6pm42 aegla ligul	214	32	72.7	182	2	Q5Q0Z9_9HEXA	Q5q0z9 orchesella
142	34	77.3	189	2	Q6PM43_9EUA	Q6pm43 aegla ligul	215	32	72.7	182	2	Q5Q101_9HEXA	Q5q101 orchesella
143	34	77.3	189	2	Q8WAE1_9EUA	Q8wae1 aegla papud	216	32	72.7	182	2	Q5Q103_9HEXA	Q5q103 orchesella
144	34	77.3	189	2	Q8WAE2_9EUA	Q8wae2 aegla papud	217	32	72.7	182	2	Q5Q104_9HEXA	Q5q104 orchesella
145	34	77.3	192	1	UREE_ALCEU	Q93038 alcaligenes	218	32	72.7	182	2	Q5Q105_9HEXA	Q5q105 orchesella
146	34	77.3	229	2	Q9XM11_FARNO	Q9xm11 farfantepen	219	32	72.7	182	2	Q5Q108_9HEXA	Q5q108 orchesella
147	34	77.3	229	2	Q5OHN9_PENJP	Q5ohn9 penaeus jap	220	32	72.7	182	2	Q5Q109_9HEXA	Q5q109 orchesella
148	34	77.3	229	2	Q76178_9EUA	Q76178 euphausia s	221	32	72.7	182	2	Q5Q110_9HEXA	Q5q110 orchesella
149	34	77.3	231	2	Q53E77_ERISI	Q53e77 eriocheir s	222	32	72.7	182	2	Q5Q112_9HEXA	Q5q112 orchesella
150	34	77.3	268	2	Q4G0S7_HUMAN	Q4g0s7 homo sapien	223	32	72.7	184	2	Q8WFZ9_PROCL	Q8wfz9 procamparur
151	34	77.3	445	2	Q67KF2_SYMTH	Q67kf2 symbiobacte	224	32	72.7	186	2	Q03421_9DIPT	Q03421 anopheles k
152	33	75.0	129	1	Y296_MYCGE	P47538 mycoplasma	225	32	72.7	187	2	Q5EGH3_9DIPT	Q5egh3 anopheles s
153	33	75.0	142	2	Q6CTJ7_KLULA	Q6ctj7 kluyveromyc	226	32	72.7	187	2	Q5EGH4_9DIPT	Q5egh4 anopheles s
154	33	75.0	192	2	Q8DF88_VIBVU	Q8df88 vibrio vulin	227	32	72.7	187	2	Q7GF42_9DIPT	Q7gf42 anopheles r
155	33	75.0	198	2	Q8WFX7_9EUA	Q8wfx7 calcinus ob	228	32	72.7	189	2	Q5EGH1_9DIPT	Q5egh1 anopheles s
156	33	75.0	198	2	Q94TV8_9EUA	Q94tv8 clibanarius	229	32	72.7	189	2	Q7GF44_9DIPT	Q7gf44 anopheles n
157	33	75.0	228	2	Q8M692_9NEOP	Q8m692 paratennopt	230	32	72.7	189	2	Q7GF50_9DIPT	Q7gf50 anopheles a
158	33	75.0	229	2	Q9MNY0_PAGLO	Q9mny0 pagurus lon	231	32	72.7	190	2	Q7GF51_9DIPT	Q7gf51 anopheles d
159	33	75.0	230	2	Q9MD12_LOLBI	Q9mdi2 loligo bleee	232	32	72.7	191	2	Q5GCH6_9DIPT	Q5gch6 aedes furci
160	33	75.0	280	2	Q7WN63_VIBVY	Q7wm63 vibrio vulin	233	32	72.7	192	2	Q5GCH6_9DIPT	Q5gch6 aedes furci
161	33	75.0	291	2	Q4IRE6_GIBZE	Q4ire6 gibberella	234	32	72.7	192	2	Q03409_9DIPT	Q03409 anopheles m
162	33	75.0	374	2	Q5A974_CANAL	Q5a974 candida alb	235	32	72.7	192	2	Q03413_9DIPT	Q03413 anopheles a
163	33	75.0	394	2	Q5AVK1_EMENI	Q5avk1 aspergillus	236	32	72.7	193	2	Q03417_9DIPT	Q03417 anopheles b
164	33	75.0	401	2	Q6Q028_BACFR	Q6q028 bacteroides	237	32	72.7	193	2	Q7GF38_9DIPT	Q7gf38 anopheles t
165	33	75.0	401	2	Q41L8D_STAHJ	Q41ld8 staphylococ	238	32	72.7	193	2	Q5E405_VIBF1	Q5e405 vibrio fisc
166	33	75.0	430	2	Q61Q19_CABBR	Q61q19 caenorhabdi	239	32	72.7	194	2	Q03423_9DIPT	Q03423 anopheles r
167	33	75.0	430	2	Q9KPT4_VIECH	Q9kpt4 vibrio chol	240	32	72.7	194	2	Q03444_9DIPT	Q03444 anopheles r
168	33	75.0	466	2	Q5UNS3_HALMA	Q5uns3 haloarcula	241	32	72.7	197	2	Q8HP17_9DIPT	Q8hp17 anopheles p
169	33	75.0	511	2	Q6BVS4_DEBHA	Q6bvs4 debaryomyc	242	32	72.7	198	2	Q8HP12_9DIPT	Q8hp12 chagasia ba
170	33	75.0	662	2	Q8EH04_SHEON	Q8eh04 shewanella	243	32	72.7	198	2	Q8HPJ3_9DIPT	Q8hpj3 anopheles c
171	33	75.0	1231	2	Q41JY9_9EUREK	Q41jy9 burkholderi	244	32	72.7	199	2	Q8HPK6_9DIPT	Q8hpk6 anopheles t
172	32	72.7	96	2	Q7GF47_9DIPT	Q7gf47 anopheles d	245	32	72.7	200	2	Q9T4V9_9DIPT	Q9t4v9 anopheles d
173	32	72.7	96	2	Q7GF52_9DIPT	Q7gf52 anopheles m	246	32	72.7	201	2	Q03412_9DIPT	Q03412 anopheles a
174	32	72.7	112	2	Q9T4Z2_9DIPT	Q9t4z2 anopheles k	247	32	72.7	201	2	Q5GCD2_AEDAE	Q5gcd2 aedes aegypt
175	32	72.7	115	2	Q9T4Z2_9DIPT	Q9t4z2 anopheles a	248	32	72.7	201	2	Q5GCD5_AEDAE	Q5gcd5 aedes aegypt
176	32	72.7	120	2	Q7GF53_9DIPT	Q7gf53 anopheles m	249	32	72.7	201	2	Q5GCE0_AEDAE	Q5gce0 aedes aegypt
177	32	72.7	121	2	Q6PVN3_9DIPT	Q6pvn3 arachnocamp	250	32	72.7	201	2	Q5GCE1_AEDAE	Q5gce1 aedes aegypt

251	32	72.7	201	2	Q5GCB4_AEDAE	Q5gce4 aedes aegypt	324	72.7	221	2	003866_9DIPT	003866 anopheles a
252	32	72.7	201	2	Q5GCB5_AEDAE	Q5gce5 aedes aegypt	325	72.7	221	2	003877_9DIPT	003877 anopheles m
253	32	72.7	201	2	Q5GCB6_9DIPT	Q5gce6 aedes vexan	326	72.7	221	2	Q8HAS7_9DIPT	Q8has7 anopheles s
254	32	72.7	201	2	Q5GCB7_9DIPT	Q5gce7 aedes vexan	327	72.7	221	2	Q6VV92_9ASIL	Q6vv92 obelophorus
255	32	72.7	201	2	Q5GCB8_9DIPT	Q5gce8 aedes luteo	328	72.7	221	2	Q6VV96_9ASIL	Q6vv96 obelophorus
256	32	72.7	201	2	Q5GCB9_9DIPT	Q5gce9 aedes luteo	329	72.7	222	2	Q4ZJY5_9DIPT	Q4zjy5 anopheles a
257	32	72.7	201	2	Q5GCB9_9DIPT	Q5gce9 aedes furci	330	72.7	223	2	Q03884_9DIPT	003884 bironella h
258	32	72.7	201	2	Q5GCB9_9DIPT	Q5gch3 aedes furci	331	72.7	225	2	003874_9DIPT	003874 anopheles k
259	32	72.7	201	2	Q5GCB9_9DIPT	Q5gch7 aedes furci	332	72.7	225	2	003876_9DIPT	003876 anopheles l
260	32	72.7	201	2	Q5GCB9_9DIPT	Q5gch9 aedes furci	333	72.7	225	2	Q37353_9HEXA	Q37353 isotomurus
261	32	72.7	201	2	Q5GCB9_9DIPT	Q5gch9 aedes furci	334	72.7	225	2	Q9MEY9_9HEXA	Q9mey9 isotomurus
262	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp12 aedes trise	335	72.7	227	2	Q9T2X8_9DIPT	Q9t2x8 anopheles m
263	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp14 anopheles a	336	72.7	227	2	Q9T339_9DIPT	Q9t339 anopheles m
264	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp16 anopheles j	337	72.7	227	2	Q9T340_9DIPT	Q9t340 anopheles m
265	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp18 anopheles p	338	72.7	227	2	Q9T344_9DIPT	Q9t344 anopheles v
266	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp19 anopheles p	339	72.7	227	2	Q9T4J8_9DIPT	Q9t4j8 anopheles a
267	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp20 anopheles i	340	72.7	227	2	Q9T6C1_9DIPT	Q9t6c1 anopheles c
268	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp21 anopheles f	341	72.7	227	2	Q9T7A5_9DIPT	Q9t7a5 anopheles m
269	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp22 anopheles e	342	72.7	227	2	Q9T7A6_9DIPT	Q9t7a6 anopheles m
270	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp24 anopheles a	343	72.7	227	2	Q9T7A8_9DIPT	Q9t7a8 anopheles m
271	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp25 anopheles s	344	72.7	227	2	Q9T7A9_9DIPT	Q9t7a9 anopheles m
272	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp26 anopheles s	345	72.7	227	2	Q8HN13_9DIPT	Q8hn13 prosimulium
273	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp27 anopheles s	346	72.7	227	2	Q8HN17_9DIPT	Q8hn17 cramptonomy
274	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp28 anopheles m	347	72.7	228	1	COX2_AEDAE	P50692 aedes aegypt
275	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp30 anopheles f	348	72.7	228	1	COX2_AEDAE	P34840 anopheles g
276	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp31 anopheles d	349	72.7	228	1	COX2_AEDAE	P33505 anopheles q
277	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp32 anopheles g	350	72.7	228	1	COX2_AEDAE	Q03852 anopheles a
278	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp33 anopheles a	351	72.7	228	2	003853_9DIPT	003853 anopheles a
279	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp34 anopheles b	352	72.7	228	2	003854_9DIPT	003854 anopheles a
280	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp35 anopheles c	353	72.7	228	2	003855_9DIPT	003855 anopheles a
281	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp36 anopheles c	354	72.7	228	2	003856_9DIPT	003856 anopheles f
282	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp37 anopheles r	355	72.7	228	2	003857_9DIPT	003857 anopheles f
283	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp38 anopheles n	356	72.7	228	2	003858_9DIPT	003858 anopheles f
284	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp39 anopheles d	357	72.7	228	2	003859_9DIPT	003859 anopheles f
285	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp40 anopheles d	358	72.7	228	2	003860_9DIPT	003860 anopheles f
286	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp41 anopheles a	359	72.7	228	2	003861_9DIPT	003861 anopheles f
287	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp42 anopheles a	360	72.7	228	2	003862_9DIPT	003862 anopheles k
288	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp43 anopheles a	361	72.7	228	2	003863_9DIPT	003863 anopheles l
289	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp44 anopheles m	362	72.7	228	2	003864_9DIPT	003864 anopheles s
290	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp45 anopheles n	363	72.7	228	2	003865_9DIPT	003865 anopheles s
291	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp46 anopheles s	364	72.7	228	2	003866_9DIPT	003866 anopheles b
292	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp47 anopheles s	365	72.7	228	2	003867_9DIPT	003867 anopheles b
293	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp48 anopheles s	366	72.7	228	2	003868_9DIPT	003868 anopheles b
294	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp49 anopheles s	367	72.7	228	2	003869_9DIPT	003869 anopheles f
295	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp50 anopheles s	368	72.7	228	2	003870_9DIPT	003870 anopheles f
296	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp51 anopheles m	369	72.7	228	2	003871_9DIPT	003871 anopheles f
297	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp52 anopheles m	370	72.7	228	2	003872_9DIPT	003872 anopheles h
298	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp53 anopheles s	371	72.7	228	2	003873_9DIPT	003873 anopheles k
299	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp54 anopheles s	372	72.7	228	2	003874_9DIPT	003874 anopheles m
300	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp55 anopheles s	373	72.7	228	2	003875_9DIPT	003875 anopheles m
301	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp56 anopheles b	374	72.7	228	2	003876_9DIPT	003876 anopheles p
302	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp57 anopheles b	375	72.7	228	2	003877_9DIPT	003877 anopheles p
303	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp58 anopheles a	376	72.7	228	2	003878_9DIPT	003878 anopheles s
304	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp59 anopheles a	377	72.7	228	2	003879_9DIPT	003879 anopheles s
305	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp60 anopheles l	378	72.7	228	2	003880_9DIPT	003880 anopheles s
306	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp61 anopheles l	379	72.7	228	2	003881_9DIPT	003881 anopheles s
307	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp62 anopheles v	380	72.7	228	2	003882_9DIPT	003882 anopheles s
308	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp63 anopheles p	381	72.7	228	2	003883_9DIPT	003883 anopheles t
309	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp64 anopheles p	382	72.7	228	2	003884_9DIPT	003884 anopheles t
310	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp65 anopheles m	383	72.7	228	2	003885_9DIPT	003885 anopheles t
311	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp66 anopheles l	384	72.7	228	2	003886_9DIPT	003886 anopheles t
312	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp67 anopheles l	385	72.7	228	2	003887_9DIPT	003887 anopheles t
313	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp68 anopheles r	386	72.7	228	2	003888_9DIPT	003888 anopheles t
314	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp69 anopheles a	387	72.7	228	2	003889_9DIPT	003889 anopheles t
315	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp70 anopheles a	388	72.7	228	2	003890_9DIPT	003890 anopheles t
316	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp71 anopheles a	389	72.7	228	2	003891_9DIPT	003891 anopheles t
317	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp72 anopheles a	390	72.7	228	2	003892_9DIPT	003892 anopheles t
318	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp73 anopheles t	391	72.7	228	2	003893_9DIPT	003893 anopheles t
319	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp74 anopheles t	392	72.7	228	2	003894_9DIPT	003894 anopheles t
320	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp75 anopheles o	393	72.7	228	2	003895_9DIPT	003895 anopheles t
321	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp76 anopheles d	394	72.7	228	2	003896_9DIPT	003896 anopheles d
322	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp77 anopheles d	395	72.7	228	2	003897_9DIPT	003897 anopheles d
323	32	72.7	201	2	Q8HPH8_AEDTR	Q8hp78 anopheles m	396	72.7	228	2	003898_9DIPT	003898 anopheles l

397	32	72.7	228	2	Q5XLJ6_9DIPT	Q5xlj6 anopheles l	470	32	72.7	233	2	Q94U08_9DIPT	Q94u08 anopheles m
398	32	72.7	228	2	Q5XLJ7_9DIPT	Q5xlj7 anopheles s	471	32	72.7	233	2	Q94U09_9DIPT	Q94u09 anopheles m
399	32	72.7	228	2	Q6SZR9_9DIPT	Q6szr9 anopheles p	472	32	72.7	233	2	Q94U10_9DIPT	Q94u10 anopheles m
400	32	72.7	228	2	Q702X3_9DIPT	Q702x3 anopheles a	473	32	72.7	233	2	Q94U11_9DIPT	Q94u11 anopheles m
401	32	72.7	228	2	Q702L8_9DIPT	Q702l8 anopheles a	474	32	72.7	233	2	Q94U12_9DIPT	Q94u12 anopheles m
402	32	72.7	228	2	Q702L8_9DIPT	Q702l8 anopheles a	475	32	72.7	234	2	Q94U03_9DIPT	Q94u03 anopheles m
403	32	72.7	228	2	Q703P1_9DIPT	Q703p1 anopheles j	476	32	72.7	235	2	Q94U02_9DIPT	Q94u02 anopheles m
404	32	72.7	228	2	Q703P7_9DIPT	Q703p7 anopheles j	477	32	72.7	259	1	PGH1_BOVIN	Q62664 bos taurus
405	32	72.7	228	2	Q703R3_9DIPT	Q703r3 anopheles j	478	32	72.7	261	2	Q65ML3_BACLD	Q65ml3 bacillus li
406	32	72.7	228	2	Q703R9_9DIPT	Q703r9 anopheles j	479	32	72.7	274	2	Q97K29_CLOAB	Q97k29 clostridium
407	32	72.7	228	2	Q703S7_9DIPT	Q703s7 anopheles j	480	32	72.7	292	2	Q5LGH1_BACFN	Q5lgh1 bacteroides
408	32	72.7	228	2	Q703T2_9DIPT	Q703t2 anopheles j	481	32	72.7	300	2	Q5KZ65_GBOCA	Q5kz65 geobacillus
409	32	72.7	228	2	Q703T4_9DIPT	Q703t4 anopheles j	482	32	72.7	319	2	Q8EL22_OCEIH	Q8el22 oceanobacil
410	32	72.7	228	2	Q703T9_9DIPT	Q703t9 anopheles j	483	32	72.7	355	2	Q8D7J5_VIRVU	Q8d7j5 vibrio vuln
411	32	72.7	228	2	Q85UW4_9DIPT	Q85uw4 anopheles s	484	32	72.7	359	2	Q8KB98_CHLTE	Q8kb98 chlorobium
412	32	72.7	228	2	Q8HKX6_9DIPT	Q8hkx6 anopheles v	485	32	72.7	362	2	Q7MEK4_VIRBY	Q7mek4 vibrio vuln
413	32	72.7	228	2	Q8HKX9_9DIPT	Q8hkx9 anopheles p	486	32	72.7	412	2	Q6BXH7_DEBHA	Q6bxh7 debaryomyce
414	32	72.7	228	2	Q8HKX1_9DIPT	Q8hkx1 anopheles m	487	32	72.7	414	2	Q8HZR0_CANFA	Q8hzo0 canis famil
415	32	72.7	228	2	Q8HKX2_9DIPT	Q8hkx2 anopheles m	488	32	72.7	500	2	Q97AL2_THEVO	Q97al2 thermoplasma
416	32	72.7	228	2	Q8HKX3_9DIPT	Q8hkx3 anopheles m	489	32	72.7	500	2	Q7URH7_RHOBA	Q7urh7 rhodopirell
417	32	72.7	228	2	Q8HKX4_9DIPT	Q8hkx4 anopheles m	490	32	72.7	562	2	Q5T7T8_HUMAN	Q5t7t8 homo sapien
418	32	72.7	228	2	Q8HKX5_9DIPT	Q8hkx5 anopheles j	491	32	72.7	599	1	PGH1_HUMAN	P23219 homo sapien
419	32	72.7	228	2	Q8HKX7_9DIPT	Q8hkx7 anopheles f	492	32	72.7	599	1	PGH1_SHEEP	P05979 ovis aries
420	32	72.7	228	2	Q8HKX8_9DIPT	Q8hkx8 anopheles f	493	32	72.7	600	1	PGH1_MOUSE	P22437 mus musculus
421	32	72.7	228	2	Q8HKX9_9DIPT	Q8hkx9 anopheles f	494	32	72.7	602	1	PGH1_MOUSE	P22437 mus musculus
422	32	72.7	228	2	Q8HCQ6_9DIPT	Q8hcq6 anopheles d	495	32	72.7	602	1	PGH1_RAT	Q63921 rattus norv
423	32	72.7	228	2	Q8HCQ7_9DIPT	Q8hcq7 anopheles c	496	32	72.7	602	2	Q66HK3_RAT	Q66hk3 rattus norv
424	32	72.7	228	2	Q8HCQ7_9DIPT	Q8hcq7 anopheles a	497	32	72.7	602	2	Q543T1_MOUSE	Q543t1 mus musculus
425	32	72.7	228	2	Q8W8S4_9DIPT	Q8w8s4 anopheles w	498	32	72.7	606	2	Q97554_RABIT	Q97554 oryctolagus
426	32	72.7	228	2	Q8W8S5_9DIPT	Q8w8s5 anopheles m	499	32	72.7	617	2	Q8CIL6_MOUSE	Q8cil6 mus musculus
427	32	72.7	228	2	Q8W8S6_9DIPT	Q8w8s6 anopheles d	500	32	72.7	633	2	Q8HZR1_CANFA	Q8hzo1 canis famil
428	32	72.7	228	2	Q8WBL6_9DIPT	Q8wbl6 anopheles p	501	32	72.7	727	2	Q4HNB8_CAMUP	Q4hnb8 campylobact
429	32	72.7	228	2	Q8WBL7_9DIPT	Q8wbl7 anopheles s	502	32	72.7	756	1	METE_BACHD	Q9kfp1 bacillus ha
430	32	72.7	228	2	Q8WBL8_9DIPT	Q8wbl8 anopheles m	503	32	72.7	1047	2	Q5ZCH3_MAGGR	Q5zch3 magnaporthe
431	32	72.7	228	2	Q9B8L1_9DIPT	Q9b8l1 anopheles s	504	32	72.7	1447	2	Q4QDT7_LEIMA	Q4qdt7 leishmania
432	32	72.7	228	2	Q9B8L7_AEDAL	Q9b8l7 aedes albop	505	32	72.7	1638	2	Q9C162_NEUCR	Q9c162 neurospora
433	32	72.7	228	2	Q9XKD5_9NEOP	Q9xkd5 statilia ma	506	32	72.7	2289	2	Q4PBD1_USTMA	Q4pbd1 ustilago ma
434	32	72.7	228	2	Q56185_9DIPT	Q56185 anopheles m	507	32	72.7	2289	2	Q9HFW4_USTMA	Q9hfw4 ustilago ma
435	32	72.7	228	2	Q56186_9DIPT	Q56186 anopheles m	508	32	72.7	3414	2	Q61E74_CABBR	Q61e74 caenorhabdi
436	32	72.7	228	2	Q56187_9DIPT	Q56187 anopheles m	509	32	72.7	8545	1	ANCL_CABEL	Q9n4m4 caenorhabdi
437	32	72.7	228	2	Q56189_9DIPT	Q56189 anopheles m	510	32	72.7	8545	2	Q6IMP3_CABEL	Q6imp3 caenorhabdi
438	32	72.7	228	2	Q56193_9DIPT	Q56193 anopheles m	511	31	70.5	36	2	Q53SJ8_HUMAN	Q53sj8 homo sapien
439	32	72.7	228	2	Q56194_9DIPT	Q56194 anopheles v	512	31	70.5	145	2	Q9G7N4_9DIOP	Q9g7n4 cyrtodiopsi
440	32	72.7	228	2	Q56196_9DIPT	Q56196 anopheles i	513	31	70.5	159	2	Q8WFX5_9EUCA	Q8wfx5 coenobita c
441	32	72.7	228	2	Q5JCK7_AEDAL	Q5jck7 aedes albop	514	31	70.5	160	2	Q5BJY0_9DIOP	Q5bjy0 cyrtodiopsi
442	32	72.7	228	2	Q642V6_RIFPA	Q642v6 riftia pach	515	31	70.5	163	2	Q5BJX3_9DIOP	Q5bjx3 cyrtodiopsi
443	32	72.7	228	2	Q8HN15_9DIPT	Q8hn15 sylvicola f	516	31	70.5	164	2	Q5EJY1_9DIOP	Q5ejy1 cyrtodiopsi
444	32	72.7	228	2	Q4JIE3_9DIPT	Q4jie3 anopheles p	517	31	70.5	169	2	Q5EJY2_9DIOP	Q5ejy2 cyrtodiopsi
445	32	72.7	228	2	Q4JIE4_9DIPT	Q4jie4 anopheles p	518	31	70.5	169	2	Q5EJX8_9DIOP	Q5ejx8 cyrtodiopsi
446	32	72.7	229	2	Q79792_9DIPT	Q79792 helodon ony	519	31	70.5	171	2	Q6E8K5_9HEMI	Q6e8k5 oxyrhachis
447	32	72.7	229	2	Q79793_9DIPT	Q79793 prosimulium	520	31	70.5	179	2	Q94TU4_PARCM	Q94tu4 paralichode
448	32	72.7	229	2	Q79794_9DIPT	Q79794 cneiphia sp.	521	31	70.5	185	2	Q8WFX6_9EUCA	Q8wfy6 lomix hirta
449	32	72.7	229	2	Q79795_9DIPT	Q79795 simulium au	522	31	70.5	187	2	Q6JGD7_9NEOP	Q6jgd7 melliera br
450	32	72.7	229	2	Q79797_9DIPT	Q79797 simulium pi	523	31	70.5	187	2	Q6JGG1_9NEOP	Q6jgg1 supella lon
451	32	72.7	229	2	Q79798_9DIPT	Q79798 simulium ja	524	31	70.5	187	2	Q6JGG4_GROPO	Q6jgg4 gromphadori
452	32	72.7	229	2	Q79799_9DIPT	Q79799 simulium lu	525	31	70.5	188	1	COMD1_CANFA	Q8ymd0 canis famil
453	32	72.7	229	2	Q79800_9DIPT	Q79800 simulium co	526	31	70.5	188	1	COMD1_MOUSE	Q8k4m5 mus musculus
454	32	72.7	229	2	Q37534_KATTU	Q37534 katharina t	527	31	70.5	190	1	COMD1_HUMAN	Q8n668 homo sapien
455	32	72.7	229	2	Q5C851_9INSE	Q5c851 nesomachili i	528	31	70.5	190	1	Y1120_XANAC	Q8pnf1 xanthomonas
456	32	72.7	229	2	Q623T7_CABBR	Q623t7 caenorhabdi	529	31	70.5	190	2	Q53EN2_HUMAN	Q53en2 homo sapien
457	32	72.7	229	2	Q7J3E2_9DIPT	Q7j3e2 simulium au	530	31	70.5	201	2	Q5GCP5_9DIPT	Q5gcf5 aedes luteo
458	32	72.7	229	2	Q9T3G3_9DIPT	Q9t3g3 simulium au	531	31	70.5	204	1	YPOL_ACICA	P07778 acinetobact
459	32	72.7	229	2	Q9T5E3_9DIPT	Q9t5e3 cneiphia sp.	532	31	70.5	204	2	Q5DGD9_SCHJA	Q5dgd9 schistosoma
460	32	72.7	229	2	Q9T5E4_9DIPT	Q9t5e4 cneiphia sp.	533	31	70.5	204	2	Q7VUD4_BORPE	Q7vud4 bordetella
461	32	72.7	229	2	Q8RB10_THETN	Q8rb10 thermoanaer	534	31	70.5	205	2	Q7W418_BORBA	Q7w418 bordetella
462	32	72.7	230	2	Q9T7A4_9DIPT	Q9t7a4 anopheles m	535	31	70.5	205	2	Q7WFF2_BORBR	Q7wff2 bordetella
463	32	72.7	230	2	Q62Y06_BACLD	Q62y06 bacillus li	536	31	70.5	208	2	Q9GAK3_9NEOP	Q9gak3 kaloterme
464	32	72.7	233	2	Q94NZ9_9DIPT	Q94nz9 anopheles m	537	31	70.5	208	2	Q9GAK4_9NEOP	Q9gak4 kaloterme
465	32	72.7	233	2	Q94P17_9DIPT	Q94p17 anopheles m	538	31	70.5	208	2	Q9GAK6_9NEOP	Q9gak6 glyptoterm
466	32	72.7	233	2	Q94U04_9DIPT	Q94u04 anopheles m	539	31	70.5	208	2	Q9GAK8_9NEOP	Q9gak8 glyptoterm
467	32	72.7	233	2	Q94U05_9DIPT	Q94u05 anopheles m	540	31	70.5	210	1	TIP1_YEAST	P27654 saccharomyc
468	32	72.7	233	2	Q94U06_9DIPT	Q94u06 anopheles m	541	31	70.5	216	2	Q86AW0_DICTOI	Q86aw0 dictyosteli
469	32	72.7	233	2	Q94U07_9DIPT	Q94u07 anopheles m	542	31	70.5	228	2	Q76CP9_9NEOP	Q76cp9 sinocaprite

543	31	70.5	228	2	Q9B0V7_9NEOP	Q9b0y7 saalganea pe	616	31	70.5	844	2	Q18372_CAEEL	Q18372 caenorhabdi
544	31	70.5	228	2	Q9B110_9NEOP	Q9b110 saalganea ob	617	31	70.5	902	2	Q7R5D7_GIALA	Q7r5d7 giardia lam
545	31	70.5	228	2	Q9B1N5_9NEOP	Q9b1n5 saalganea am	618	31	70.5	934	2	Q6NH63_CORDI	Q6nh63 corynebacte
546	31	70.5	228	2	Q9B648_9NEOP	Q9b648 saalganea ro	619	31	70.5	978	2	Q874G6_KLULA	Q874g6 kluyveromyc
547	31	70.5	228	2	Q9B650_9NEOP	Q9b650 saalganea ta	620	31	70.5	1027	2	Q6CL64_KLULA	Q6cl64 kluyveromyc
548	31	70.5	228	2	Q9B651_9NEOP	Q9b651 saalganea ta	621	31	70.5	1042	1	T1RH_MENJA	Q50295 methanococc
549	31	70.5	228	2	Q9B673_9NEOP	Q9b673 saalganea cr	622	31	70.5	1067	2	Q7QV77_GIALA	Q7qv77 giardia lam
550	31	70.5	228	2	Q9B6A1_9NEOP	Q9b6a1 caeparia cr	623	31	70.5	1106	2	Q5ATU2_EMENI	Q5atu2 aspergillus
551	31	70.5	228	2	Q8LV09_9NEOP	Q8lv09 paratemnopte	624	31	70.5	1683	2	Q4RLP9_TETNG	Q4rlp9 tetraodon ma
552	31	70.5	228	2	Q8LV84_9NEOP	Q8lv84 neotemnopte	625	31	70.5	1774	2	Q4P7Q0_USTWA	Q4p7q0 ustilago ma
553	31	70.5	228	2	Q8LVF8_9NEOP	Q8lvf8 paratemnopte	626	31	70.5	1852	2	Q5AZG2_EMENI	Q5azg2 aspergillus
554	31	70.5	228	2	Q8LVW5_9NEOP	Q8lvw5 neotemnopte	627	31	70.5	1852	2	Q13281_EMERIC	Q13281 emericella
555	31	70.5	228	2	Q8M690_9NEOP	Q8m690 neotemnopte	628	31	70.5	4540	2	Q7PS35_ANOGA	Q7ps35 anopheles g
556	31	70.5	228	2	Q8M691_9NEOP	Q8m691 neotemnopte	629	31	70.5	58	2	Q4TF22_TETNG	Q4tf22 tetraodon n
557	31	70.5	228	2	Q8M693_9NEOP	Q8m693 paratemnopte	630	30	68.2	34	2	Q8PF8W2_LEPIN	Q8pf8w2 leptospira
558	31	70.5	228	2	Q8M694_9NEOP	Q8m694 paratemnopte	631	30	68.2	60	2	Q5SW97_HUMAN	Q5sw97 homo sapien
559	31	70.5	228	2	Q8M695_9NEOP	Q8m695 paratemnopte	632	30	68.2	68	2	Q54UX8_DICDI	Q54ux8 dictyosteli
560	31	70.5	228	2	Q8M697_9NEOP	Q8m697 paratemnopte	633	30	68.2	77	2	Q53RB4_ORYSA	Q53rb4 oryza sativ
561	31	70.5	228	2	Q8M699_9NEOP	Q8m699 paratemnopte	634	30	68.2	100	2	Q8YV42_ANASP	Q8yv42 anabaena sp
562	31	70.5	228	2	Q8M6A1_9NEOP	Q8m6a1 paratemnopte	635	30	68.2	120	2	Q6PVP2_9DIPT	Q6pvp2 arachnocamp
563	31	70.5	228	2	Q8M6A2_9NEOP	Q8m6a2 paratemnopte	636	30	68.2	120	2	Q5GVW0_XANOR	Q5gvw0 xanthomonas
564	31	70.5	228	2	Q8M6A3_9NEOP	Q8m6a3 paratemnopte	637	30	68.2	121	2	Q6PVP4_9DIPT	Q6pvp4 arachnocamp
565	31	70.5	228	2	Q8M6A4_9NEOP	Q8m6a4 paratemnopte	638	30	68.2	121	2	Q6PVP6_9DIPT	Q6pvp6 arachnocamp
566	31	70.5	228	2	Q8M6A5_9NEOP	Q8m6a5 paratemnopte	639	30	68.2	121	2	Q6PVQ0_9DIPT	Q6pvq0 arachnocamp
567	31	70.5	228	2	Q8M6A6_9NEOP	Q8m6a6 paratemnopte	640	30	68.2	121	2	Q6PVQ6_9DIPT	Q6pvq6 arachnocamp
568	31	70.5	228	2	Q8M6A7_9NEOP	Q8m6a7 paratemnopte	641	30	68.2	121	2	Q6PVQ8_9DIPT	Q6pvq8 arachnocamp
569	31	70.5	228	2	Q8M6A8_9NEOP	Q8m6a8 paratemnopte	642	30	68.2	121	2	Q6PVQ9_9DIPT	Q6pvq9 arachnocamp
570	31	70.5	228	2	Q8M6A9_9NEOP	Q8m6a9 paratemnopte	643	30	68.2	121	2	Q8SG39_9ASIL	Q8sg39 comptosia s
571	31	70.5	228	2	Q8M6B0_9NEOP	Q8m6b0 paratemnopte	644	30	68.2	121	2	Q8SH41_9ASIL	Q8sh41 heterospilo
572	31	70.5	228	2	Q8M6B1_9NEOP	Q8m6b1 paratemnopte	645	30	68.2	122	2	Q4P2G2_USTWA	Q4p2g2 ustilago ma
573	31	70.5	228	2	Q8M6B2_9NEOP	Q8m6b2 paratemnopte	646	30	68.2	122	2	Q8SG41_9ASIL	Q8sg41 ectinorhinc
574	31	70.5	228	2	Q8M6B3_9NEOP	Q8m6b3 paratemnopte	647	30	68.2	123	2	Q8SH45_9ASIL	Q8sh45 villa sp. 1
575	31	70.5	228	2	Q8M6B4_9NEOP	Q8m6b4 paratemnopte	648	30	68.2	123	2	Q8SH46_9ASIL	Q8sh46 ectinorhinc
576	31	70.5	228	2	Q8M6B5_9NEOP	Q8m6b5 paratemnopte	649	30	68.2	126	2	Q8SG34_9ASIL	Q8sg34 heterospilo
577	31	70.5	228	2	Q8M6B6_9NEOP	Q8m6b6 paratemnopte	650	30	68.2	131	2	Q5SW98_HUMAN	Q5sw98 homo sapien
578	31	70.5	228	2	Q8M6B7_9NEOP	Q8m6b7 paratemnopte	651	30	68.2	133	2	Q6JCW0_LASPU	Q6jcw0 prenolepis
579	31	70.5	229	2	Q8HD91_PANJA	Q8hd91 panulirus j	652	30	68.2	133	2	Q6JCW2_LASPU	Q6jcw2 lasius fuli
580	31	70.5	229	2	Q9ZXZ2_PANAR	Q9zxz2 panulirus a	653	30	68.2	133	2	Q6JCW4_9HYME	Q6jcw4 myrmecocyst
581	31	70.5	243	2	Q8V186_MOUSE	Q8v186 mus musculu	654	30	68.2	133	2	Q6JCW6_9HYME	Q6jcw6 myrmecocyst
582	31	70.5	290	2	Q5L920_BACFN	Q5l920 bacteroides	655	30	68.2	133	2	Q6JCW8_9HYME	Q6jcw8 myrmecocyst
583	31	70.5	290	2	Q64Q97_BACFR	Q64q97 bacteroides	656	30	68.2	133	2	Q6JCX0_9HYME	Q6jcx0 myrmecocyst
584	31	70.5	313	2	Q5ZH28_CHICK	Q5zh28 gallus gall	657	30	68.2	133	2	Q6JCX2_9HYME	Q6jcx2 myrmecocyst
585	31	70.5	320	2	Q7VX03_HELHP	Q7vk03 helicobacte	658	30	68.2	133	2	Q6JCX4_9HYME	Q6jcx4 myrmecocyst
586	31	70.5	321	2	Q67354_AQUAE	Q67354 aquifex aeo	659	30	68.2	133	2	Q6JCX6_9HYME	Q6jcx6 myrmecocyst
587	31	70.5	328	2	Q542C6_DICDI	Q54zc6 dictyosteli	660	30	68.2	133	2	Q6JCX8_9HYME	Q6jcx8 myrmecocyst
588	31	70.5	350	2	Q8D7T0_VIBVU	Q8d7t0 vibrio vuln	661	30	68.2	133	2	Q6JCY0_9HYME	Q6jcy0 myrmecocyst
589	31	70.5	359	2	Q5AWF4_EMENI	Q5awf4 aspergillus	662	30	68.2	133	2	Q6JCZ0_9HYME	Q6jcz0 myrmecocyst
590	31	70.5	360	2	Q24305_FEA	Q24305 pisum sativ	663	30	68.2	133	2	Q6JCZ2_9HYME	Q6jcz2 myrmecocyst
591	31	70.5	378	2	Q7MEU4_VIBVY	Q7meu4 vibrio vuln	664	30	68.2	133	2	Q6JCZ4_9HYME	Q6jcz4 myrmecocyst
592	31	70.5	384	2	Q9LMC3_ARATH	Q9lmc3 arabidopsis	665	30	68.2	133	2	Q6JCZ8_9HYME	Q6jcz8 myrmecocyst
593	31	70.5	388	2	Q4HE05_CAMCO	Q4he05 campylobact	666	30	68.2	133	2	Q6JD00_9HYME	Q6jd00 myrmecocyst
594	31	70.5	390	2	Q9P126_CAMJE	Q9pi26 campylobact	667	30	68.2	133	2	Q6JD04_9HYME	Q6jd04 myrmecocyst
595	31	70.5	390	2	Q7MY62_PHOLL	Q7my62 photorhabdu	668	30	68.2	133	2	Q6JD06_9HYME	Q6jd06 myrmecocyst
596	31	70.5	392	2	Q7Q5C3_ANOGA	Q7q5c3 anopheles g	669	30	68.2	133	2	Q6JD08_9HYME	Q6jd08 myrmecocyst
597	31	70.5	393	2	Q66W61_CAMCO	Q66w61 campylobact	670	30	68.2	140	2	Q8SH76_9DIPT	Q8sh76 austrochlus
598	31	70.5	400	2	Q981E3_SULSO	Q981e3 sulfolobus	671	30	68.2	141	2	Q8SH90_9DIPT	Q8sh90 austrochlus
599	31	70.5	402	2	Q96V37_SULTO	Q96v37 sulfolobus	672	30	68.2	141	2	Q6JH11_9DIPT	Q6jhl1 anopheles p
600	31	70.5	408	2	Q54L99_DICDI	Q54l99 dictyosteli	673	30	68.2	145	2	Q9G7Q0_9DIPT	Q9g7q0 teloglalabr
601	31	70.5	419	2	Q9F776_CAMJE	Q9f776 campylobact	674	30	68.2	145	2	Q9G7Q1_9DIPT	Q9g7q1 teloglalabr
602	31	70.5	433	2	Q06708_BORBR	Q06708 bordetella	675	30	68.2	145	2	Q9G7Q2_9DIPT	Q9g7q2 sphyracepha
603	31	70.5	441	2	Q4NFP81_9DELT	Q4np81 anaeromyxob	676	30	68.2	147	2	Q753G5_ASIGO	Q753g5 ashyba gose
604	31	70.5	459	2	Q7NCF0_GLOVI	Q7ncf0 gloebacter	677	30	68.2	147	2	Q8SH82_9DIPT	Q8sh82 afrochlus h
605	31	70.5	461	2	Q4LWH8_9BURK	Q4lwh8 burkholderi	678	30	68.2	154	2	Q8SH91_9DIPT	Q8sh91 austrochlus
606	31	70.5	496	2	Q8KJA5_RHILO	Q8kja5 rhizobium l	679	30	68.2	155	2	Q9HS55_HALSA	Q9hs55 halobacteri
607	31	70.5	496	2	Q98AN2_RHILO	Q98an2 rhizobium l	680	30	68.2	155	2	Q8SCQ7_9DIPT	Q8scq7 austrochlus
608	31	70.5	578	2	Q3O490_CYTUO	Q3o490 cytophaga j	681	30	68.2	155	2	Q85CQ9_9DIPT	Q85cq9 austrochlus
609	31	70.5	593	2	Q4HZQ1_GIBZE	Q4hzq1 gibberella	682	30	68.2	155	2	Q85CQ9_9DIPT	Q85cq9 austrochlus
610	31	70.5	608	2	Q9VV99_DROME	Q9vv99 drosophila	683	30	68.2	155	2	Q8SH83_9DIPT	Q8sh83 archaechllu
611	31	70.5	647	2	Q4PI91_USTWA	Q4pi91 ustilago ma	684	30	68.2	155	2	Q8SH84_9DIPT	Q8sh84 archaechllu
612	31	70.5	658	2	Q87928_XYLFT	Q87928 xylella fas	685	30	68.2	155	2	Q8SH85_9DIPT	Q8sh85 archaechllu
613	31	70.5	707	2	Q620V3_CAEER	Q620v3 caenorhabdi	686	30	68.2	155	2	Q8SH86_9DIPT	Q8sh86 austrochlus
614	31	70.5	718	2	Q81I78_PLAF7	Q81i78 plasmodium	687	30	68.2	155	2	Q8SH87_9DIPT	Q8sh87 austrochlus
615	31	70.5	826	2	Q968Z5_CAEEL	Q968z5 caenorhabdi	688	30	68.2	155	2	Q8SH88_9DIPT	Q8sh88 austrochlus

689	30	68.2	155	2	Q85H92_9DIPT	Q85H92 austrochilus	762	30	68.2	208	2	Q8M3A3_9NEOP	Q8M3A3 panorama cog
690	30	68.2	155	2	Q85H93_9DIPT	Q85H93 austrochilus	763	30	68.2	208	2	Q8M3C3_9NEOP	Q8M3C3 caurinus de
691	30	68.2	158	2	Q4XL38_PLACH	Q4XL38 plaemodium	764	30	68.2	208	2	Q9B216_9DIPT	Q9B216 chironomus
692	30	68.2	159	2	Q8WAC8_9EUC	Q8WAC8 pachycheles	765	30	68.2	208	2	Q9GAL7_9NEOP	Q9GAL7 cryptoterme
693	30	68.2	160	2	Q6YMY9_9HYME	Q6YMY9 camponotus	766	30	68.2	208	2	Q9GAL8_9NEOP	Q9GAL8 cryptoterme
694	30	68.2	160	2	Q6YMZ5_9HYME	Q6YMZ5 camponotus	767	30	68.2	208	2	Q9GAL9_9NEOP	Q9GAL9 cryptoterme
695	30	68.2	160	2	Q6YMZ6_9HYME	Q6YMZ6 camponotus	768	30	68.2	208	2	Q6VYB2_9ASIL	Q6VYB2 ozodiceromy
696	30	68.2	163	2	Q5E181_VIBF1	Q5E181 vibrio fisc	769	30	68.2	209	2	Q6Q7Z4_9HEXA	Q6Q7Z4 folsomia ca
697	30	68.2	164	2	Q85H75_9DIPT	Q85H75 procladius	770	30	68.2	209	2	Q6Q7Z5_9HEXA	Q6Q7Z5 folsomia ca
698	30	68.2	166	2	Q8M390_9NEOP	Q8M390 panorama ban	771	30	68.2	209	2	Q8M398_9NEOP	Q8M398 panorama bic
699	30	68.2	171	2	Q6E8A9_9HEMI	Q6E8A9 bolbonota s	772	30	68.2	209	2	Q8M3C8_9DIPT	Q8M3C8 bittacus st
700	30	68.2	171	2	Q6E8B3_9HEMI	Q6E8B3 bolbonota i	773	30	68.2	209	2	Q8M3D2_9NEOP	Q8M3D2 bittacus wa
701	30	68.2	176	2	Q85H81_9DIPT	Q85H81 bolbonota h	774	30	68.2	209	2	Q8M3E5_9DIPT	Q8M3E5 epiphragma
702	30	68.2	181	2	Q85H78_9DIPT	Q85H78 austrochilus	775	30	68.2	210	2	Q8M388_9NEOP	Q8M388 panorama str
703	30	68.2	182	2	Q85H77_9DIPT	Q85H77 austrochilus	776	30	68.2	210	2	Q8M389_9NEOP	Q8M389 panorama jap
704	30	68.2	183	2	Q8M3E0_9NEOP	Q8M3E0 pycnopsysche	777	30	68.2	210	2	Q8M395_9NEOP	Q8M395 panorama hel
705	30	68.2	185	2	Q6KLMO_LITLI	Q6KLMO littorina l	778	30	68.2	210	2	Q8M3A4_9NEOP	Q8M3A4 panorama flu
706	30	68.2	185	2	Q85H79_9DIPT	Q85H79 afrochilus h	779	30	68.2	210	2	Q8M3A7_9NEOP	Q8M3A7 merope tube
707	30	68.2	185	2	Q8WFZ0_9EUC	Q8WFZ0 pachycheles	780	30	68.2	210	2	Q8M3D5_9NEOP	Q8M3D5 bittacus pu
708	30	68.2	186	2	Q85H74_9DIPT	Q85H74 procladius	781	30	68.2	210	2	Q6JH12_9DIPT	Q6JH12 anopheles f
709	30	68.2	187	2	Q5UC87_9HYME	Q5UC87 pristomyrme	782	30	68.2	211	2	Q8M394_9NEOP	Q8M394 panorama neb
710	30	68.2	187	2	Q6UGB5_9NEOP	Q6UGB5 statilia ap	783	30	68.2	211	2	Q8M3D1_9DIPT	Q8M3D1 bittacus pi
711	30	68.2	187	2	Q6JGB6_9NEOP	Q6JGB6 bantia sp.	784	30	68.2	211	2	P94492_BACSU	P94492 bacillus su
712	30	68.2	187	2	Q6JGF4_9NEOP	Q6JGF4 hymenopus c	785	30	68.2	212	2	Q8M392_9NEOP	Q8M392 panorama ger
713	30	68.2	187	2	Q8M3A0_PANCO	Q8M3A0 panorama com	786	30	68.2	212	2	Q8M399_9NEOP	Q8M399 panorama ara
714	30	68.2	188	2	Q6VCS5_9DIPT	Q6VCS5 tephritis b	787	30	68.2	214	2	Q8M391_9NEOP	Q8M391 panorama acu
715	30	68.2	188	2	Q6VCS9_9DIPT	Q6VCS9 tephritis b	788	30	68.2	214	2	Q8M3D0_9NEOP	Q8M3D0 hylobittacu
716	30	68.2	188	2	Q6VCT1_9DIPT	Q6VCT1 tephritis b	789	30	68.2	214	2	Q8M3D4_9NEOP	Q8M3D4 harpobittac
717	30	68.2	188	2	Q6VCV7_9DIPT	Q6VCV7 tephritis b	790	30	68.2	215	2	Q5K542_9NEOP	Q5K542 salganea ma
718	30	68.2	188	2	Q6VCV3_9DIPT	Q6VCV3 tephritis b	791	30	68.2	215	2	Q8M396_9NEOP	Q8M396 panorama cia
719	30	68.2	188	2	Q5B4N2_9HYME	Q5B4N2 diadasia en	792	30	68.2	215	2	Q8M3D6_APTAP	Q8M3D6 apterobitta
720	30	68.2	188	2	Q5YSH8_NOCFA	Q5YSH8 nocardia fa	793	30	68.2	215	2	Q8M3D7_9NEOP	Q8M3D7 apteropanor
721	30	68.2	189	2	Q6E6Q6_9HYME	Q6E6Q6 gonatocerus	794	30	68.2	217	2	Q6VV73_9ASIL	Q6VV73 stenopogon
722	30	68.2	189	2	Q6E6Q7_9HYME	Q6E6Q7 gonatocerus	795	30	68.2	217	2	Q6VV75_9ASIL	Q6VV75 laphia sp.
723	30	68.2	189	2	Q6E6R3_9HYME	Q6E6R3 gonatocerus	796	30	68.2	217	2	Q6VV78_9ASIL	Q6VV78 efferia nem
724	30	68.2	189	2	Q9B1X1_9HYME	Q9B1X1 diadasia bi	797	30	68.2	218	2	O21467_CULTO	O21467 culex torre
725	30	68.2	189	2	Q4U0B1_9HYME	Q4U0B1 cardiocondy	798	30	68.2	221	2	Q8HFA6_9DIPT	Q8HFA6 anopheles s
726	30	68.2	189	2	Q4U0A1_9HYME	Q4U0A1 cardiocondy	799	30	68.2	222	2	Q9MGC7_9NEOP	Q9MGC7 panesthia c
727	30	68.2	189	2	Q4U095_9HYME	Q4U095 cardiocondy	800	30	68.2	222	2	Q6VV91_9ASIL	Q6VV91 saropogon f
728	30	68.2	189	2	Q4U033_9HYME	Q4U033 cardiocondy	801	30	68.2	222	2	Q6VVA0_9ASIL	Q6VVA0 maira sp. d
729	30	68.2	189	2	Q4U019_9HYME	Q4U019 cardiocondy	802	30	68.2	223	2	Q5IZV5_9DIPT	Q5IZV5 sphaerocera
730	30	68.2	189	2	Q4U0B5_9HYME	Q4U0B5 cardiocondy	803	30	68.2	223	2	Q5IZV6_9DIPT	Q5IZV6 somatia sp.
731	30	68.2	189	2	Q4U0A3_9HYME	Q4U0A3 cardiocondy	804	30	68.2	223	2	Q5IZW0_9DIPT	Q5IZW0 rainieria a
732	30	68.2	189	2	Q4U021_9HYME	Q4U021 cardiocondy	805	30	68.2	223	2	Q5IZW1_9DIPT	Q5IZW1 pyrgota und
733	30	68.2	189	2	Q4U0B9_9HYME	Q4U0B9 cardiocondy	806	30	68.2	223	2	Q5IZW7_9DIPT	Q5IZW7 physoccephal
734	30	68.2	189	2	Q4U089_9HYME	Q4U089 cardiocondy	807	30	68.2	223	2	Q5IZX0_9DIPT	Q5IZX0 otites cent
735	30	68.2	190	2	Q5UC85_9HYME	Q5UC85 cardiocondy	808	30	68.2	223	2	Q5IZX3_9DIPT	Q5IZX3 myopa bucca
736	30	68.2	190	2	Q5UC95_9HYME	Q5UC95 pheidoole no	809	30	68.2	223	2	Q5IZY1_ERITN	Q5IZY1 eristalis c
737	30	68.2	191	2	Q5H4J1_XANOR	Q5H4J1 xanthomonas	810	30	68.2	223	2	Q5IZY7_9DIPT	Q5IZY7 compsobata
738	30	68.2	191	2	Q8DBD7_VIBVU	Q8DBD7 vibrio vuln	811	30	68.2	223	2	Q5IZY9_9DIPT	Q5IZY9 blepharoneu
739	30	68.2	193	2	Q6VVA1_9ASIL	Q6VVA1 promachus s	812	30	68.2	223	2	Q7YD04_9DIPT	Q7YD04 rhaqoletis
740	30	68.2	194	2	Q8TWFS_METKA	Q8TWFS methanopyru	813	30	68.2	224	2	O99999_9HEXA	O99999 isotomurus
741	30	68.2	195	2	Q8M397_9NEOP	Q8M397 neopanorpa	814	30	68.2	224	2	Q7YCZ4_9DIPT	Q7YCZ4 rhaqoletis
742	30	68.2	198	2	Q8M3D3_9NEOP	Q8M3D3 bittacus se	815	30	68.2	224	2	O63467_9NEOP	O63467 thyridia ps
743	30	68.2	199	2	Q8M386_9NEOP	Q8M386 brachypodes	816	30	68.2	225	2	Q9B0W4_9DIPT	Q9B0W4 chironomus
744	30	68.2	199	2	Q8M385_9NEOP	Q8M385 brachypodes	817	30	68.2	225	2	Q9B6R2_9DIPT	Q9B6R2 cricotopus
745	30	68.2	200	2	Q8HP11_9DIPT	Q8HP11 toxorhynchi	818	30	68.2	226	1	COX2_LASSP	P29875 lasius sp.
746	30	68.2	200	2	Q6VVA2_9ASIL	Q6VVA2 promachus b	819	30	68.2	226	2	Q9B647_9NEOP	Q9B647 salganea ca
747	30	68.2	201	2	Q5GCF2_9DIPT	Q5GCF2 culx decen	820	30	68.2	226	2	Q6VV85_9ASIL	Q6VV85 hypenetes c
748	30	68.2	201	2	Q8HP10_9DIPT	Q8HP10 uranotaenia	821	30	68.2	227	2	Q5V8R9_9DIPT	Q5V8R9 euktefferie
749	30	68.2	201	2	Q8HP13_9DIPT	Q8HP13 bironella g	822	30	68.2	227	2	Q5V8S0_9DIPT	Q5V8S0 diplociadu
750	30	68.2	201	2	Q8HP15_9DIPT	Q8HP15 anopheles s	823	30	68.2	227	2	Q5V8S1_9DIPT	Q5V8S1 diplociadu
751	30	68.2	201	2	Q8HP19_9DIPT	Q8HP19 anopheles f	824	30	68.2	227	2	Q5V8S2_9DIPT	Q5V8S2 prodianesa
752	30	68.2	202	2	Q8M393_9NEOP	Q8M393 panorama lat	825	30	68.2	227	2	Q5V8S3_9DIPT	Q5V8S3 prodianesa
753	30	68.2	202	2	Q8M3A2_9NEOP	Q8M3A2 panorama car	826	30	68.2	227	2	Q6L8E0_9MAXI	Q6L8E0 tetracalia
754	30	68.2	202	2	Q6VV81_9ASIL	Q6VV81 hemipenthes	827	30	68.2	227	2	Q7HCJ9_9DIPT	Q7HCJ9 cheilosia h
755	30	68.2	202	2	Q6VV94_9ASIL	Q6VV94 holopogon c	828	30	68.2	227	2	Q94N09_9DIPT	Q94N09 cheilosia c
756	30	68.2	202	2	Q6VVA3_9ASIL	Q6VVA3 mydas clava	829	30	68.2	227	2	Q9T308_9NEOP	Q9T308 salganea ta
757	30	68.2	202	2	Q84MG9_ORYSA	Q84MG9 oryza sativ	830	30	68.2	227	2	Q9T9L6_9NEOP	Q9T9L6 salganea ta
758	30	68.2	203	2	Q8M3A1_9NEOP	Q8M3A1 panorama deb	831	30	68.2	227	2	Q9T9L7_9NEOP	Q9T9L7 salganea ta
759	30	68.2	203	2	Q6VV93_9ASIL	Q6VV93 smeryngolap	832	30	68.2	227	2	Q9XKC6_9NEOP	Q9XKC6 salganea ta
760	30	68.2	203	2	Q6VV98_9ASIL	Q6VV98 diognites g	833	30	68.2	227	2	Q4H0R1_9DIPT	Q4H0R1 themira ann
761	30	68.2	206	2	Q8M3D9_9NEOP	Q8M3D9 limnephilus	834	30	68.2	228	1	COX2_CULQU	P50693 culex quing





981 30 68.2 429 1 ASB10\_HUMAN  
 982 30 68.2 429 2 O23081\_ARATH  
 983 30 68.2 438 2 Q9HAM7\_HUMAN  
 984 30 68.2 441 2 Q4LWP7\_BURK  
 985 30 68.2 447 2 Q5N4W0\_SYNP6  
 986 30 68.2 452 2 Q6ZUL6\_HUMAN  
 987 30 68.2 456 2 Q662M6\_BORGA  
 988 30 68.2 457 1 SYH\_BOBU  
 989 30 68.2 462 2 Q6S8X6\_DEBHA  
 990 30 68.2 469 2 Q742M3\_ASHGO  
 991 30 68.2 482 2 Q7Q132\_ANOGA  
 992 30 68.2 487 2 Q652L9\_ORYSA  
 993 30 68.2 505 1 Y4NJ\_RHISN  
 994 30 68.2 507 2 Q982L9\_RHILO  
 995 30 68.2 527 2 Q5P3E0\_LACAC  
 996 30 68.2 533 2 Q8H6T2\_CHURE  
 997 30 68.2 543 2 Q5BH19\_EMENI  
 998 30 68.2 556 2 Q8ROW5\_MOUSE  
 999 30 68.2 577 2 Q7YVR9\_CRYPV  
 1000 30 68.2 577 2 Q5CJT9\_CRYHO

## ALIGNMENTS

RESULT 1  
 Q94TV4\_9EUCA  
 ID Q94TV4\_9EUCA PRELIMINARY; PRT; 124 AA.  
 AC Q94TV4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Haplogaster dentata.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
 OC Lithodidae; Haplogaster.  
 OX NCBI\_TaxID=174385;  
 RN [1]  
 RA Zaklan S.D., Cunningham C.W.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 3 form the functional core of the enzyme complex. Subunit 2  
 transfers the electrons from cytochrome c via its binuclear copper  
 A center to the bimetallic center of the catalytic subunit 1 (By  
 similarity).  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 EMBL; AF425366; AL26524.1; -; Genomic\_DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR PROSITE; PS00857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 DR Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;

KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 1  
 FT SEQUENCE 124 AA; 14660 MW; 57DC335EF2212FBI CRC64;  
 SQ  
 Query Match 84.1%; Score 37; DB 2; Length 124;  
 Best Local Similarity 87.5%; Pred. No. 9.3;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLFEDA 8  
 DB 93 FLQLFEDS 100  
 RESULT 2  
 Q94TV9\_9EUCA  
 ID Q94TV9\_9EUCA PRELIMINARY; PRT; 140 AA.  
 AC Q94TV9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Labidochirus splendescens.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
 OC Paguridae; Labidochirus.  
 OX NCBI\_TaxID=174388;  
 RN [1]  
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 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 EMBL; AF425371; AL26529.1; -; Genomic\_DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CUA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR PROSITE; PS00857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 DR Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 1  
 FT SEQUENCE 140 AA; 16429 MW; 92400CF6A7FEE00 CRC64;  
 SQ  
 Query Match 84.1%; Score 37; DB 2; Length 140;  
 Best Local Similarity 87.5%; Pred. No. 11;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 FLQLEFDA 8
Db 97 FLQLEFDS 104

RESULT 3
Q94TU8_9EUCA
ID Q94TU8_9EUCA PRELIMINARY; PRT; 142 AA.
AC Q94TU8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
OS Lopholithodes mandtii.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Lithodidae; Lopholithodes.
OX NCBI_TaxID=174396;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zaklan S.D., Cunningham C.W.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AF425372; AAL26530.1; -; Genomic DNA.
CC GO: GO:0019866; C:inner membrane; IEA.
CC GO: GO:0016021; C:integral to membrane; IEA.
CC GO: GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO: GO:0005739; C:mitochondrion; IEA.
CC GO: GO:0005507; F:copper ion binding; IEA.
CC GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO: GO:0016491; F:oxidoreductase activity; IEA.
CC GO: GO:0006810; P:transport; IEA.
CC InterPro: IPR0011505; Copper_CuA.
CC InterPro: IPR011759; COX2_TM.
CC Pfam: PF00116; COX2; 1.
CC PRINTS: PF02790; COX2; 1.
CC PROSITE: PS00857; COX2_CUA; 1.
CC PROSITE: PS50999; COX2_TM; 1.
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON_TER 1 1
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 16485 MW; E00E56EB30703D02 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 142;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFDA 8
Db 90 FLQLEFDS 97

RESULT 4
Q94TU6_9EUCA
ID Q94TU6_9EUCA PRELIMINARY; PRT; 147 AA.
AC Q94TU6;

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DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
OS Pagurus bernhardus (common hermit crab).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Paguridae; Pagurus.
OX NCBI_TaxID=174397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zaklan S.D., Cunningham C.W.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AF425374; AAL26532.1; -; Genomic DNA.
CC GO: GO:0019866; C:inner membrane; IEA.
CC GO: GO:0016021; C:integral to membrane; IEA.
CC GO: GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO: GO:0005739; C:mitochondrion; IEA.
CC GO: GO:0005507; F:copper ion binding; IEA.
CC GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO: GO:0016491; F:oxidoreductase activity; IEA.
CC GO: GO:0006810; P:transport; IEA.
CC GO: GO:0008810; P:transport; IEA.
CC InterPro: IPR0011505; Copper_CuA.
CC InterPro: IPR011759; COX2_TM.
CC Pfam: PF00116; COX2; 1.
CC PRINTS: PF02790; COX2; 1.
CC PROSITE: PS00857; COX2_CUA; 1.
CC PROSITE: PS50999; COX2_TM; 1.
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON_TER 1 1
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 17357 MW; 51BE16CED00DA004 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 147;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFDA 8
Db 97 FLQLEFDS 104

RESULT 5
Q94TV7_9EUCA
ID Q94TV7_9EUCA PRELIMINARY; PRT; 155 AA.
AC Q94TV7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
OS Cryptolithodes sitchensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Lithodidae; Cryptolithodes.

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OX NCBI\_TaxID=174327;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Zaklan S.D., Cunningham C.W.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1 (By  
 CC similarity).  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferrocytochrome  
 c + 2 H(2)O.  
 CC  
 CC -!- COPACTOR: Copper A (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AF425363; AAL26521.1; -; Genomic\_DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0005739; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:electron transport; IEA.  
 DR GO; GO:0006810; P:electron transport; IEA.  
 DR InterPro; IPR001505; Copper\_CUA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 1 155  
 FT NON\_TER 155 155  
 SQ SEQUENCE 155 AA; 17780 MW; 663801A37950E345 CRC64;  
  
 Query Match 84.1%; Score 37; DB 2; Length 155;  
 Best Local Similarity 87.5%; Pred. No. 12;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 FLQLEFDA 8  
 Db ||||| :  
 76 FLQLEFDS 83  
  
 RESULT 6  
 Q94TV6 9EUCA  
 ID Q94TV6\_9EUCA PRELIMINARY; PRT; 163 AA.  
 AC Q94TV6;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Cryptolithodes typicus.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
 OC Lithodidae; Cryptolithodes.  
 OX NCBI\_TaxID=174328;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Zaklan S.D., Cunningham C.W.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper

CC A center to the bimetallic center of the catalytic subunit 1 (By  
 CC similarity).  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferrocytochrome  
 c + 2 H(2)O.  
 CC  
 CC -!- COPACTOR: Copper A (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AF425364; AAL26522.1; -; Genomic\_DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0006118; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:electron transport; IEA.  
 DR InterPro; IPR001505; Copper\_CUA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 1 163  
 FT NON\_TER 163 163  
 SQ SEQUENCE 163 AA; 18747 MW; B569F4CF5A80FDA8 CRC64;  
  
 Query Match 84.1%; Score 37; DB 2; Length 163;  
 Best Local Similarity 87.5%; Pred. No. 12;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 FLQLEFDA 8  
 Db ||||| :  
 79 FLQLEFDS 86  
  
 RESULT 7  
 Q8WFY3 9EUCA  
 ID Q8WFY3\_9EUCA PRELIMINARY; PRT; 166 AA.  
 AC Q8WFY3;  
 DT 01-MAR-2002 (TRENBLrel. 20, Created)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Lepidopa californica.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Hippoidea;  
 OC Alboneidae; Lepidopa.  
 OX NCBI\_TaxID=177228;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;  
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
 RA Cunningham C.W.;  
 RA "Mitochondrial gene rearrangements confirm the parallel evolution of  
 the crab-like form.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350(2002).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1 (By  
 CC similarity).  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferrocytochrome  
 c + 2 H(2)O.  
 CC  
 CC -!- COPACTOR: Copper A (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AF431588.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transmembrane; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR PRODOM; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON TER 1  
 FT TER 166 166  
 SQ SEQUENCE 166 AA; 19030 MW; C207194A2159CDB2 CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 166;  
 Best Local Similarity 87.5%; Pred. No. 13;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLEFDA 8  
 Db 89 FLQLEFDS 96  
 RESULT 8  
 Q8WFY4 9EUCA  
 ID Q8WFY4 9EUCA PRELIMINARY; PRT; 170 AA.  
 AC Q8WFY4  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Blepharipoda occidentalis.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Hippoidea;  
 OC Alpheidae; Blepharipoda.  
 OX NCBI\_TaxID=177216;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;  
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
 RA Cunningham C.W.;  
 RT "Mitochondrial gene rearrangements confirm the parallel evolution of  
 the crab-like form.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350(2002).  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1 (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AF431588.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transmembrane; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR PRODOM; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON TER 1  
 FT TER 166 166  
 SQ SEQUENCE 166 AA; 19030 MW; C207194A2159CDB2 CRC64;

DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transmembrane; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR PRODOM; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON TER 170 170  
 FT TER 170 170  
 SQ SEQUENCE 170 AA; 19721 MW; D4F5895D1AE7CA83 CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 170;  
 Best Local Similarity 87.5%; Pred. No. 13;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLEFDA 8  
 Db 113 FLQLEFDS 120  
 RESULT 9  
 Q94TU3 9EUCA  
 ID Q94TU3 9EUCA PRELIMINARY; PRT; 171 AA.  
 AC Q94TU3  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Paralomis granulosa.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
 OC Lithodidae; Paralomis.  
 OX NCBI\_TaxID=174405;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Zaklan S.D., Cunningham C.W.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1 (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AF425377; AAL26535.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transmembrane; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR011759; COX2\_TM.

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DR InterPro: IPR002429; Cyt_c_ox_2.
DR Pfam: PF00116; COX2; 1.
DR Pfam: PF02790; COX2_TM; 1.
DR PRINTS: PR01166; CYCOXIDASEII.
DR ProDom: PD000131; Copper_Cua; 1.
DR PROSITE: PS00857; COX2_CUA; 1.
DR PROSITE: PS00999; COX2_TM; 1.
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; transport.
FT NON_TER 1
FT NON_TER 171
SQ SEQUENCE 171 AA; 19619 MW; D26EEBDDDD906235 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 171;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8
Db 94 FLQLEFDS 101
|||||:

RESULT 10
Q94TU7_9EUA
ID Q94TU7_9EUA PRELIMINARY; PRT; 172 AA.
AC Q94TU7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
OS Oedignathus inermis.
OG Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Lithodidae; Phylloolithodes.
OX NCBI_TaxID=6743;
RN [1]
RA Zaklan S.D., Cunningham C.W.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COPACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AF425373; AAL26531.1; -; Genomic DNA.
CC GO; GO:0019866; C:inner membrane; IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005739; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005739; C:mitochondrion; IEA.
CC GO; GO:0005507; F:copper ion binding; IEA.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO; GO:0005507; F:oxidoreductase activity; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro: IPR001505; Copper_Cua.
CC InterPro: IPR011759; COX2_TM.
CC InterPro: IPR002429; Cyt_c_ox_2.
CC Pfam: PF00116; COX2; 1.
CC PRINTS: PR01166; CYCOXIDASEII.
CC ProDom: PD000131; Copper_Cua; 1.
CC PROSITE: PS00857; COX2_CUA; 1.
CC PROSITE: PS00999; COX2_TM; 1.
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; transport.
FT NON_TER 1
FT NON_TER 171
SQ SEQUENCE 171 AA; 19619 MW; D26EEBDDDD906235 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 171;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8
Db 94 FLQLEFDS 101
|||||:

RESULT 11
Q94TU2_9EUA
ID Q94TU2_9EUA PRELIMINARY; PRT; 174 AA.
AC Q94TU2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
OS Phylloolithodes papillosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Lithodidae; Phylloolithodes.
OX NCBI_TaxID=174407;
RN [1]
RA Zaklan S.D., Cunningham C.W.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COPACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AF425378; AAL26536.1; -; Genomic DNA.
CC GO; GO:0019866; C:inner membrane; IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005739; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005739; C:mitochondrion; IEA.
CC GO; GO:0005507; F:copper ion binding; IEA.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO; GO:0005507; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro: IPR001505; Copper_Cua.
CC InterPro: IPR011759; COX2_TM.
CC InterPro: IPR002429; Cyt_c_ox_2.
CC Pfam: PF00116; COX2; 1.
CC PRINTS: PR01166; CYCOXIDASEII.
CC ProDom: PD000131; Copper_Cua; 1.
CC PROSITE: PS00857; COX2_CUA; 1.
CC PROSITE: PS00999; COX2_TM; 1.
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; transport.
FT NON_TER 1
FT NON_TER 174
SQ SEQUENCE 174 AA; 19948 MW; EB262FBEF0CED389 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 174;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8

```

Db |||||:  
90 FLQLEFDS 97

## RESULT 12

Q94TV3\_9EUCA PRELIMINARY; PRT; 178 AA.  
AC Q94TV3;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
OS Hapalogaster mertensii.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
OC Lithodidae; Hapalogaster.  
OX NCBI\_TaxID=174386;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Zaklan S.D., Cunningham C.W.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1 (By  
CC similarity).  
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -1- COFACTOR: Copper A (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
DR EMBL: AF425367; AAL26525.1; -; Genomic DNA.  
DR GO: GO:0019866; C:inner membrane; IEA.  
DR GO: GO:0005746; C:mitochondrion; IEA.  
DR GO: GO:0005739; C:mitochondrion; IEA.  
DR GO: GO:0005507; F:copper ion binding; IEA.  
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR GO: GO:0005507; F:copper ion binding; IEA.  
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR GO: GO:0005507; F:copper ion binding; IEA.  
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR001505; Copper\_CUA.  
DR InterPro: IPR002429; Cyt\_c\_ox\_2.  
DR Pfam: PF00116; COX2; 1.  
DR PRINTS: PR01166; CYCOXIDASEII.  
DR PRODOM: PD000131; Copper\_CUA; 1.  
DR PROSITE: PS50857; COX2\_CUA; 1.  
DR PROSITE: PS50999; COX2\_TM; 1.  
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
FT NON\_TER 1 178  
FT NON\_TER 178 178  
SQ SEQUENCE 178 AA; 20305 MW; D21D40F3CE64D94F CRC64;

Query Match 84.1%; Score 37; DB 2; Length 178;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFDS 8

Db |||||:  
90 FLQLEFDS 97

## RESULT 13

Q94TU1\_9EUCA PRELIMINARY; PRT; 179 AA.  
AC Q94TU1;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
OS Rhinolithodes wosnessenskii.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
OC Lithodidae; Rhinolithodes.  
OX NCBI\_TaxID=174409;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Zaklan S.D., Cunningham C.W.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1 (By  
CC similarity).  
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -1- COFACTOR: Copper A (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
DR EMBL: AF425379; AAL26537.1; -; Genomic DNA.  
DR GO: GO:0019866; C:inner membrane; IEA.  
DR GO: GO:0016021; C:integral to membrane; IEA.  
DR GO: GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO: GO:0005739; C:mitochondrion; IEA.  
DR GO: GO:0005507; F:copper ion binding; IEA.  
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR GO: GO:0005507; F:copper ion binding; IEA.  
DR InterPro: IPR001505; Copper\_CUA.  
DR InterPro: IPR002429; Cyt\_c\_ox\_2.  
DR Pfam: PF00116; COX2; 1.  
DR PRINTS: PR01166; CYCOXIDASEII.  
DR PRODOM: PD000131; Copper\_CUA; 1.  
DR PROSITE: PS50857; COX2\_CUA; 1.  
DR PROSITE: PS50999; COX2\_TM; 1.  
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
FT NON\_TER 1 179  
FT NON\_TER 179 179  
SQ SEQUENCE 179 AA; 20598 MW; 18058F40B6B1B2A8 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 179;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFDS 8  
Db |||||:  
93 FLQLEFDS 100

RESULT 14  
Q6PLV2\_9EUCA PRELIMINARY; PRT; 180 AA.  
AC Q6PLV2;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN Name=COII;  
OS Aegla scamosa.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aegidae; Aegla.

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OX NCBI_TaxID=273843;
RN [1]_NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1545254; DOI=10.1080/10635150490522331;
RT Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RT "Molecular systematics and biogeography of the southern South American
RT freshwater 'crabs' Aegla (Decapoda; Anomura: Aegliidae) using multiple
RT heuristic tree search approaches";
RL Syst. Biol. 53:767-780(2004).
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL: AY595772; AAT08408.1; -; Genomic DNA.
CC GO: GO:0019866; C:inner membrane; IEA.
CC GO: GO:0016021; C:integral to membrane; IEA.
CC GO: GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO: GO:0005739; C:mitochondrion; IEA.
CC GO: GO:0005507; F:copper ion binding; IEA.
CC GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO: GO:0016491; F:oxidoreductase activity; IEA.
CC GO: GO:0006118; P:electron transport; IEA.
CC GO: GO:0006810; P:transport; IEA.
CC InterPro: IPR001505; Copper_CuA.
CC InterPro: IPR002429; Cyt_c_ox_2.
CC Pfam: PF02790; COX2_TM; 1.
CC PRINTS: PR01166; CYCOXIDASEII.
CC ProDom: PD000131; Copper_CuA; 1.
CC PROSITE: PS50857; COX2_CUA; 1.
CC PROSITE: PS50999; COX2_TM; 1.
CC Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 180
FT SEQUENCE 180 AA; 20778 MW; C827D7E7F4CA2C0B CRC64;
SQ
Query Match 84.1%; Score 37; DB 2; Length 180;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEPDA 8
Db 92 FLQLEFDS 99

RESULT 15
Q94TV0_9EUCA
ID Q94TV0_9EUCA PRELIMINARY; PRT; 180 AA.
AC Q94TV0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
OS Lithodes santolla.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Lithodidae; Lithodes.
OC NCBI_TaxID=174394;
RN [1]_NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RL Zaklan S.D., Cunningham C.W.;
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).

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CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL: AF25370; AAL26528.1; -; Genomic DNA.
CC GO: GO:0019866; C:inner membrane; IEA.
CC GO: GO:0016021; C:integral to membrane; IEA.
CC GO: GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO: GO:0005739; C:mitochondrion; IEA.
CC GO: GO:0005507; F:copper ion binding; IEA.
CC GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO: GO:0016491; F:oxidoreductase activity; IEA.
CC GO: GO:0006118; P:electron transport; IEA.
CC GO: GO:0006810; P:transport; IEA.
CC InterPro: IPR001505; Copper_CuA.
CC InterPro: IPR002429; Cyt_c_ox_2.
CC Pfam: PF00116; COX2; 1.
CC PRINTS: PR01166; CYCOXIDASEII.
CC ProDom: PD000131; Copper_CuA; 1.
CC PROSITE: PS50857; COX2_CUA; 1.
CC PROSITE: PS50999; COX2_TM; 1.
CC Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 180
FT SEQUENCE 180 AA; 20816 MW; F4ED7795D4F090F1 CRC64;
SQ
Query Match 84.1%; Score 37; DB 2; Length 180;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEPDA 8
Db 97 FLQLEFDS 104

RESULT 16
Q94TV2_9EUCA
ID Q94TV2_9EUCA PRELIMINARY; PRT; 181 AA.
AC Q94TV2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
OS Lithodes aequispinus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Lithodidae; Lithodes.
OC NCBI_TaxID=174392;
RN [1]_NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RL Zaklan S.D., Cunningham C.W.;
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).

```



DR GO: GO:0016021; C:integral to membrane; IEA.  
DR GO: GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO: GO:0005739; C:mitochondrion; IEA.  
DR GO: GO:0005507; F:copper ion binding; IEA.  
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR GO: GO:0006810; P:transport; IEA.  
DR InterPro: IPR001505; Copper\_CuA.  
DR InterPro: IPR011759; COX2\_TM.  
DR InterPro: IPR002429; Cyt\_c\_ox\_2.  
DR Pfam: PF00116; COX2; 1.  
DR Pfam: PF02730; COX2\_TM; 1.  
DR PRINTS: PR01166; CYCOXIDASEII.  
DR ProDom: PD000131; Copper\_CuA; 1.  
DR PROSITE: PS50857; COX2\_CUA; 1.  
DR PROSITE: PS50999; COX2\_TM; 1.  
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
FT NON\_TER 1  
FT NON\_TER 183  
SQ SEQUENCE 183 AA; 21190 MW; 083F7ACBA63B6518 CRC64;  
  
Query Match 84.1%; Score 37; DB 2; Length 183;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FLQLEFDA 8  
|||  
Db 99 FLQLEFDS 106  
  
RESULT 18  
Q94TV5\_9EUA  
ID Q94TV5\_9EUA PRELIMINARY; PRT; 183 AA.  
AC Q94TV5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
OS Glycolithodes cristatipes.  
OS Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
OC Lithodidae; Glyptolithodes.  
OC NCBI\_TaxID=174383;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Zaklan S.D., Cunningham C.W.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Subunit 2 transfers the electrons from cytochrome c via its binuclear copper center to the bimetallic center of the catalytic subunit 1 (By similarity).  
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.  
CC -!- COPACTOR: Copper A (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).  
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family. EMBL: AF425365; AL26523.1; -; Genomic DNA.  
DR GO: GO:0019866; C:inner membrane; IEA.  
DR GO: GO:0016021; C:integral to membrane; IEA.  
DR GO: GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO: GO:0005739; C:mitochondrion; IEA.  
DR GO: GO:0005507; F:copper ion binding; IEA.  
DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR GO: GO:0006810; P:transport; IEA.  
DR InterPro: IPR001505; Copper\_CuA.

DR InterPro; IPR011759; COX2\_TM.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS0857; COX2\_CUA; 1.  
 DR PROSITE; PS0999; COX2\_TM; 1.  
 DR PROSITE; PS0999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 1  
 FT NON\_TER 183  
 FT NON\_TER 183  
 SQ SEQUENCE 183 AA; 21102 MW; C15C303F66E4F0 CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 183;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLOLEPDA 8  
 Db 97 FLOLEFDS 104  
 RESULT 19  
 Q8WFY8\_9EUA PRELIMINARY; PRT; 184 AA.  
 ID Q8WFY8\_9EUA PRELIMINARY; PRT; 184 AA.  
 AC Q8WFY8;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Munida quadripinna.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
 OC Galatheoidea; Galatheidae; Munida.  
 OX NCBI\_TaxID=177235;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;  
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
 RA Cunningham C.W.;  
 RT "Mitochondrial gene rearrangements confirm the parallel evolution of  
 the crab-like form.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350(2002).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 3 form the functional core of the enzyme complex. Subunit 2  
 transfers the electrons from cytochrome c via its binuclear copper  
 A center to the bimetallic center of the catalytic subunit 1 (By  
 similarity).  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AF437622; AAL31584.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CUA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR PRINTS; PR01166; CYCOXIDASEII.

DR ProDom; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS0857; COX2\_CUA; 1.  
 DR PROSITE; PS0999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 1  
 FT NON\_TER 184  
 FT NON\_TER 184  
 SQ SEQUENCE 184 AA; 21168 MW; 45AD6A9308516F1E CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLOLEPDA 8  
 Db 99 FLOLEFDS 106  
 RESULT 20  
 Q8WFY7\_9EUA PRELIMINARY; PRT; 185 AA.  
 ID Q8WFY7\_9EUA PRELIMINARY; PRT; 185 AA.  
 AC Q8WFY7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Aegia uruguayana.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
 OC Galatheoidea; Aegidae; Aegia.  
 OX NCBI\_TaxID=177212;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;  
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
 RA Cunningham C.W.;  
 RT "Mitochondrial gene rearrangements confirm the parallel evolution of  
 the crab-like form.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350(2002).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 3 form the functional core of the enzyme complex. Subunit 2  
 transfers the electrons from cytochrome c via its binuclear copper  
 A center to the bimetallic center of the catalytic subunit 1 (By  
 similarity).  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AF437623; AAL31585.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CUA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS0857; COX2\_CUA; 1.  
 DR PROSITE; PS0999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.

FT NON\_TER 1 185  
 SQ SEQUENCE 185 AA; 21419 MW; 6A0C538A7D8A6F82 CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 185;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFDA 8  
 Db 100 FLQLEFDS 107  
 |||||:

RESULT 21  
 Q94TV1\_9EUC  
 ID Q94TV1\_9EUC PRELIMINARY; PRT; 188 AA.  
 AC Q94TV1;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 OS Lithodes maja.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
 OC Lithodidae; Lithodes.  
 OX NCBI\_TaxID=174393;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Zakian S.D., Cunningham C.W.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Subunit 2 transfers the electrons from cytochrome c via its binuclear copper A center to the bimetallic center of the catalytic subunit 1 (By similarity).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family. EMBL; AF425369; AAL26527.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR PRODOM; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 188  
 SQ SEQUENCE 188 AA; 21638 MW; 8F6D57A18ECCAE5C CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 188;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFDA 8  
 Db 1 FLQLEFDS 108  
 |||||:

Query Match 84.1%; Score 37; DB 2; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 102 FLQLEFDS 109  
 |||||:

RESULT 22  
 Q6PLS9\_9EUC  
 ID Q6PLS9\_9EUC PRELIMINARY; PRT; 189 AA.  
 AC Q6PLS9;  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN Name=COII; KACa0541.  
 OS Aegla sp.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
 OC Galatheoidea; Aegliidae; Aegla.  
 OX NCBI\_TaxID=274482;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
 RL "Molecular systematics and biogeography of the southern South American freshwater 'crabs' Aegla (Decapoda; Anomura: Aegliidae) using multiple heuristic tree search approaches."; Syst. Biol. 53:767-780(2004).  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Subunit 2 transfers the electrons from cytochrome c via its binuclear copper A center to the bimetallic center of the catalytic subunit 1 (By similarity).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family. EMBL; AY595795; AAT08431.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR PRODOM; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 189  
 SQ SEQUENCE 189 AA; 21586 MW; 48B356FEFDBF6AD CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFDA 8  
 Db 101 FLQLEFDS 108  
 |||||:

RESULT 23  
 Q6PLT0\_9EUA PRELIMINARY; PRT; 189 AA.  
 ID Q6PLT0\_9EUA PRELIMINARY; PRT; 189 AA.  
 AC Q6PLT0;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN Name=COII;  
 OS Aegla sp. KACa0538.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
 OC Galatheoidea; Aegliidae; Aegla.  
 OC NCBI\_TaxID=274481;  
 OX [1]  
 RP NUCLEOTIDE SEQUENCE  
 RX PubMed=1545254; DOI=10.1080/10635150490522331;  
 RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
 RT "Molecular systematics and biogeography of the southern South American  
 RT freshwater 'crabs' Aegla (decapoda; Anomura: Aegliidae) using multiple  
 RT heuristic tree search approaches.";   
 RL Syst. Biol. 53:767-780(2004).  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1 (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AY595794; AAU08430.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0005070; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CUA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR PRODOM; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 DR KX Oxidoreductase; Inner membrane; Membrane; Mitochondrion;  
 DR KX Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 1 189  
 FT NON\_TER 189 189  
 SQ SEQUENCE 189 AA; 21567 MW; 5D5356FEE7F1F6B7 CRC64;  
  
 Query Match 84.1%; Score 37; DB 2; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 FLQLEFDA 8  
 |||||:  
 Db 101 FLQLEFDS 108  
  
 RESULT 24  
 Q6PLT1\_9EUA  
 ID Q6PLT1\_9EUA PRELIMINARY; PRT; 189 AA.  
 AC Q6PLT1;

DE Cytochrome oxidase subunit II (Fragment).  
GN Name=COII;  
OS Aegla intercalata.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aeglidae; Aegla.  
OX NCBI\_TaxID=273849;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15545254; DOI=10.1080/10635150490522331;  
RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
RT "Molecular systematics and biogeography of the southern South American  
RT freshwater 'crabs' Aegla (Decapoda; Anomura: Aeglidae) using multiple  
RT heuristic tree search approaches.";  
RL Syst. Biol. 53:767-780(2004).  
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1 (By  
CC similarity).  
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -1- COFACTOR: Copper A (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
CC EMBL; AY595791; AY08427.1; -; Genomic\_DNA.  
CC GO; GO:0019866; C:inner membrane; IEA.  
CC GO; GO:0016021; C:integral to membrane; IEA.  
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
CC GO; GO:0005739; C:mitochondrion; IEA.  
CC GO; GO:0005507; F:copper ion binding; IEA.  
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
CC GO; GO:0016491; F:oxidoreductase activity; IEA.  
CC GO; GO:0006810; P:electron transport; IEA.  
CC GO; GO:0006810; P:transport; IEA.  
CC InterPro; IPR001505; Copper\_CUA.  
CC InterPro; IPR011759; COX2\_TM.  
CC InterPro; IPR002429; Cyt\_c\_ox\_2.  
CC Pfam; PF00116; COX2; 1.  
CC PRINTS; PR01166; CYCOXIDASEII.  
CC ProDom; PD000131; Copper\_CUA; 1.  
CC PROSITE; PS50857; COX2\_CUA; 1.  
CC PROSITE; PS50999; COX2\_TM; 1.  
CC Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
CC Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
FT NON\_TER 1 189  
FT NON\_TER 189 189  
SQ SEQUENCE 189 AA; 21731 MW; 76055B4098673CE0 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEPDA 8  
|||||:  
Db 101 FLQLEPDS 108

RESULT 26  
Q6PLT4\_9EUC  
ID Q6PLT4\_9EUC PRELIMINARY; PRT; 189 AA.  
AC Q6PLT4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN Name=COII;  
OS Aegla intercalata.  
OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aeglidae; Aegla.  
OX NCBI\_TaxID=273849;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15545254; DOI=10.1080/10635150490522331;  
RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
RT "Molecular systematics and biogeography of the southern South American  
RT freshwater 'crabs' Aegla (Decapoda; Anomura: Aeglidae) using multiple  
RT heuristic tree search approaches.";  
RL Syst. Biol. 53:767-780(2004).  
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1 (By  
CC similarity).  
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -1- COFACTOR: Copper A (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
CC EMBL; AY595790; AY08426.1; -; Genomic\_DNA.  
CC GO; GO:0019866; C:inner membrane; IEA.  
CC GO; GO:0016021; C:integral to membrane; IEA.  
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
CC GO; GO:0005739; C:mitochondrion; IEA.  
CC GO; GO:0005507; F:copper ion binding; IEA.  
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
CC GO; GO:0016491; F:oxidoreductase activity; IEA.  
CC GO; GO:0006810; P:electron transport; IEA.  
CC GO; GO:0006810; P:transport; IEA.  
CC InterPro; IPR001505; Copper\_CUA.  
CC InterPro; IPR011759; COX2\_TM.  
CC InterPro; IPR002429; Cyt\_c\_ox\_2.  
CC Pfam; PF00116; COX2; 1.  
CC PRINTS; PR01166; CYCOXIDASEII.  
CC ProDom; PD000131; Copper\_CUA; 1.  
CC PROSITE; PS50857; COX2\_CUA; 1.  
CC PROSITE; PS50999; COX2\_TM; 1.  
CC Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
CC Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
FT NON\_TER 1 189  
FT NON\_TER 189 189  
SQ SEQUENCE 189 AA; 21745 MW; 11C1F5D5CADA40CE CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEPDA 8  
|||||:  
Db 101 FLQLEPDS 108

RESULT 27  
Q6PLT5\_9EUC  
ID Q6PLT5\_9EUC PRELIMINARY; PRT; 189 AA.  
AC Q6PLT5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN Name=COII;  
OS Aegla intercalata.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aeglidae; Aegla.  
OX NCBI\_TaxID=273849;

```

RN NUCLEOTIDE SEQUENCE.
RP PubMed=15545254; DOI=10.1080/10635150490522331;
RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RA "Molecular systematics and biogeography of the southern South american
RT freshwater 'crabs' Aegla (decapoda: Anomura: Aegliidae) using multiple
RT heuristic tree search approaches.";
RL Syst. Biol. 53:767-780(2004).
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AY595789; AAT08425.1; -; Genomic_DNA.
CC GO; GO:0019866; C:inner membrane; IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005739; C:mitochondrion; IEA.
CC GO; GO:0005507; F:copper ion binding; IEA.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro; IPR001505; Copper_CuA.
CC InterPro; IPR011759; COX2_TM.
CC InterPro; IPR002429; Cyt_c_ox_2.
CC Pfam; PF00116; COX2; 1.
CC Pfam; PF02790; COX2_TM; 1.
CC PRINTS; PR01166; CYCOXIDASEII.
CC ProDom; PD000131; Copper_CuA; 1.
CC PROSITE; PS50857; COX2_CUA; 1.
CC PROSITE; PS50999; COX2_TM; 1.
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 189
SQ SEQUENCE 189 AA; 21749 MW; 4E3D31809ECB54CC CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8
DB 101 FLQLEFDS 108

RESULT 28
Q6PLT6_9EUCA PRELIMINARY; PRT; 189 AA.
AC Q6PLT6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Aegla platensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC Galatheoidea; Aegliidae; Aegla.
OC NCBI_TaxID=273811;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15545254; DOI=10.1080/10635150490522331;
RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RA "Molecular systematics and biogeography of the southern South american
RT freshwater 'crabs' Aegla (decapoda: Anomura: Aegliidae) using multiple
RT heuristic tree search approaches.";
RL Syst. Biol. 53:767-780(2004).

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RT "Molecular systematics and biogeography of the southern South american
RT freshwater 'crabs' Aegla (decapoda: Anomura: Aegliidae) using multiple
RT heuristic tree search approaches.";
RL Syst. Biol. 53:767-780(2004).
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AY595789; AAT08424.1; -; Genomic_DNA.
CC GO; GO:0019866; C:inner membrane; IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005739; C:mitochondrion; IEA.
CC GO; GO:0005507; F:copper ion binding; IEA.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro; IPR001505; Copper_CuA.
CC InterPro; IPR011759; COX2_TM.
CC InterPro; IPR002429; Cyt_c_ox_2.
CC Pfam; PF00116; COX2; 1.
CC Pfam; PF02790; COX2_TM; 1.
CC PRINTS; PR01166; CYCOXIDASEII.
CC ProDom; PD000131; Copper_CuA; 1.
CC PROSITE; PS50857; COX2_CUA; 1.
CC PROSITE; PS50999; COX2_TM; 1.
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 189
SQ SEQUENCE 189 AA; 21791 MW; 8F22AF85D97325BE CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8
DB 101 FLQLEFDS 108

RESULT 29
Q6PLT7_9EUCA PRELIMINARY; PRT; 189 AA.
AC Q6PLT7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Aegla platensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC Galatheoidea; Aegliidae; Aegla.
OC NCBI_TaxID=273811;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15545254; DOI=10.1080/10635150490522331;
RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RA "Molecular systematics and biogeography of the southern South american
RT freshwater 'crabs' Aegla (decapoda: Anomura: Aegliidae) using multiple
RT heuristic tree search approaches.";
RL Syst. Biol. 53:767-780(2004).

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CC      c + 2 H(2)O.
CC      -!- COFACTOR: Copper A (By similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane (By similarity).
CC      -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
DR      EMBL; AY595784; AAT08420.1; -; Genomic_DNA.
DR      GO; GO:0019866; C:inner membrane; IEA.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      GO; GO:0005507; F:copper ion binding; IEA.
DR      GO; GO:001429; F:cytochrome-c oxidase activity; IEA.
DR      GO; GO:0005739; C:mitochondrion; IEA.
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro; IPR001505; Copper_CuA.
DR      InterPro; IPR011759; COX2_TM.
DR      Pfam; PF00116; COX2; 1.
DR      Pfam; PF02790; COX2_TM; 1.
DR      PRINTS; PR01166; CYCOXIDASEII.
DR      ProDom; PD000131; Copper_CuA; 1.
DR      PROSITE; PS00857; COX2_CUA; 1.
DR      PROSITE; PS0999; COX2_TM; 1.
DR      Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW      Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT      NON_TER 1
FT      NON_TER 189
SQ      SEQUENCE 189 AA; 21685 MW; C737BD06415DB681 CRC64;

Query Match      84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLEPDA 8
Db      101 FLQLEFDS 108

RESULT 32
Q6PLU1_9EUCA
ID      Q6PLU1_9EUCA PRELIMINARY; PRT; 189 AA.
AC      Q6PLU1_
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Cytochrome oxidase subunit II (Fragment).
GN      Name=COII;
OS      Aegla sp. KaCa0479.
OG      Mitochondrion.
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC      Galatheoidea; Aeglidae; Aegla.
OX      NCBI_TaxID=274479;
RN      [1]_
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=15545254; DOI=10.1080/10635150490522331;
RA      Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RT      "Molecular systematics and biogeography of the southern South american
RT      freshwater 'crabs' Aegla (Decapoda: Anomura: Aeglidae) using multiple
RT      heuristic tree search approaches.";
RL      Syst. Biol. 53:767-780(2004).
CC      -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC      chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC      3 form the functional core of the enzyme complex. Subunit 2
CC      transfers the electrons from cytochrome c via its binuclear copper
CC      A center to the bimetallic center of the catalytic subunit 1 (By
CC      similarity).
CC      -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC      c + 2 H(2)O.
CC      -!- COFACTOR: Copper A (By similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane (By similarity).

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CC      -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
DR      EMBL; AY595783; AAT08419.1; -; Genomic_DNA.
DR      GO; GO:0019866; C:inner membrane; IEA.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR      GO; GO:0005739; C:mitochondrion; IEA.
DR      GO; GO:0005507; F:copper ion binding; IEA.
DR      GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro; IPR001505; Copper_CuA.
DR      InterPro; IPR011759; COX2_TM.
DR      InterPro; IPR002429; Cyt_c_ox_2.
DR      Pfam; PF00116; COX2; 1.
DR      Pfam; PF02790; COX2_TM; 1.
DR      PRINTS; PR01166; CYCOXIDASEII.
DR      ProDom; PD000131; Copper_CuA; 1.
DR      PROSITE; PS00857; COX2_CUA; 1.
DR      PROSITE; PS0999; COX2_TM; 1.
DR      Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
KW      Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT      NON_TER 1
FT      NON_TER 189
SQ      SEQUENCE 189 AA; 21685 MW; C737BD06415DB681 CRC64;

Query Match      84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLEPDA 8
Db      101 FLQLEFDS 108

RESULT 33
Q6PLU2_9EUCA
ID      Q6PLU2_9EUCA PRELIMINARY; PRT; 189 AA.
AC      Q6PLU2_
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE      Cytochrome oxidase subunit II (Fragment).
GN      Name=COII;
OS      Aegla ringueleti.
OG      Mitochondrion.
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC      Galatheoidea; Aeglidae; Aegla.
OX      NCBI_TaxID=273847;
RN      [1]_
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=15545254; DOI=10.1080/10635150490522331;
RA      Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RT      "Molecular systematics and biogeography of the southern South american
RT      freshwater 'crabs' Aegla (Decapoda: Anomura: Aeglidae) using multiple
RT      heuristic tree search approaches.";
RL      Syst. Biol. 53:767-780(2004).
CC      -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC      chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC      3 form the functional core of the enzyme complex. Subunit 2
CC      transfers the electrons from cytochrome c via its binuclear copper
CC      A center to the bimetallic center of the catalytic subunit 1 (By
CC      similarity).
CC      -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC      c + 2 H(2)O.
CC      -!- COFACTOR: Copper A (By similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane (By similarity).
CC      -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
DR      EMBL; AY595782; AAT08418.1; -; Genomic_DNA.
DR      EMBL; AY595781; AAT08417.1; -; Genomic_DNA.
DR      GO; GO:0019866; C:inner membrane; IEA.

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GO: GO:0004129; P:cytochrome-c oxidase activity; IEA.  
DR GO: GO:0016491; P:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR GO: GO:0006810; P:transport; IEA.  
DR InterPro: IPR001505; Copper\_CuA.  
DR InterPro: IPR011759; COX2\_TM.  
DR InterPro: IPR002429; Cyt\_c\_ox\_2.  
DR Pfam: PF00116; COX2; 1.  
DR Pfam: PF02790; COX2; 1.  
DR PRINTS: PR01166; CYCOXIDASEII.  
DR ProDom: PD000131; Copper\_CuA; 1.  
DR PROSITE: PS00857; COX2\_CuA; 1.  
DR PROSITE: PS00999; COX2\_TM; 1.  
DR Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
DR NON\_TER 1  
FT NON\_TER 189  
FT NON\_TER 189  
SQ SEQUENCE 189 AA; 21705 MW; 0D6E52B6E1F75110 CRC64;  
  
Query Match 84.1%; Score 37; DB 2; Length 189;  
Best Local Similarity 87.5%; Pred. NO. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 FQLEFDD 8  
|||  
Db 101 FQLEFDS 108  
  
RESULT 35  
Q6PLU5\_9EUC PRELIMINARY; PRT; 189 AA.  
ID Q6PLU5\_9EUC PRELIMINARY; PRT; 189 AA.  
AC Q6PLU5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DT Cytochrome oxidase subunit II (fragment).  
GN Name=COII;  
OS Aegla sanlorenzo.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aegliidae; Aegla.  
OC NCBI\_TaxID=273846;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15545254; DOI=10.1080/10635150490522331;  
RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
RT "Molecular systematics and biogeography of the southern South American  
RT freshwater 'crabs' Aegla (Decapoda: Anomura: Aegliidae) using multiple  
RT heuristic tree search approaches.";  
RL Syst. Biol. 53:767-780 (2004).  
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1 (By  
CC similarity).  
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -1- COFACTOR: Copper A (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
DR EMBL: AY595779; RAT08415.1; -; Genomic\_DNA.  
DR GO: GO:0019666; C:inner membrane; IEA.  
DR GO: GO:0016021; C:integral to membrane; IEA.  
DR GO: GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO: GO:0005739; C:mitochondrion; IEA.  
DR GO: GO:0005507; P:copper ion binding; IEA.  
DR GO: GO:0004129; P:cytochrome-c oxidase activity; IEA.  
DR GO: GO:0016491; P:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR GO: GO:0006810; P:transport; IEA.

DR InterPro; IPR001505; Copper\_Cua.  
DR InterPro; IPR011759; COX2\_TM; 1.  
DR PRINTS; PR01166; CYCOXDASEII.  
DR Pfam; PF00116; COX2; 1; \_c\_ox\_2.  
DR Pfam; PF02790; COX2; 1.  
DR PRINTS; PR01166; CYCOXDASEII.  
DR PRODOM; PD000131; Copper\_CUA; 1.  
DR PROSITE; PS50857; COX2\_CUA; 1.  
DR PROSITE; PS50999; COX2\_TM; 1.  
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
FT NON\_TER 1  
FT NON\_TER 189 189  
SQ SEQUENCE 189 AA; 21747 MW; EB5CC5977BDF151B CRC64;  
  
Query Match 84.1%; Score 37; DB 2; Length 189;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FLOLEPDA 8  
Db 101 FLOLEFDS 108  
|||||:  
101 FLOLEFDS 108

RESULT 36  
Q6PLU6\_9EUCA PRELIMINARY; PRT; 189 AA.  
ID Q6PLU6\_9EUCA  
AC Q6PLU6; 189 AA.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN Name=COI1;  
OS Aegla jujuyana.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aeglidae; Aegla.  
OX NCBI\_TaxID=273845;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15545254; DOI=10.1080/10635150490522331;  
RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
RT "Molecular systematics and biogeography of the southern South American freshwater 'crabs' Aegla (Decapoda: Anomura: Aeglidae) using multiple heuristic tree search approaches.";  
RL Syst. Biol. 53:767-780(2004).  
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Subunit 2 transfers the electrons from cytochrome c via its binuclear copper center to the bimetallic center of the catalytic subunit 1 (By similarity).  
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrom c + O(2) = 4 ferricytochrome c + 2 H(2)O.  
CC -!- COFACTOR: Copper A (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).  
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family. ENMBL; AV595778; AAT08414.1; -; Genomic DNA.  
DR ENMBL; AV595778; AAT08414.1; -; Genomic DNA.  
DR GO; GO:0019866; C:inner membrane; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
DR GO; GO:0005507; F:copper ion binding; IEA.  
DR GO; GO:0016021; F:cytochrome c oxidase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001505; Copper\_CUA.  
DR InterPro; IPR011759; COX2\_TM.  
DR Pfam; PF00116; COX2; 1.  
DR Pfam; PF02790; COX2\_TM; 1.  
DR PRINTS; PR01166; CYCOXDASEII.

DR InterPro; IPR001505; Copper\_Cua.  
DR InterPro; IPR011759; COX2\_TM; 1.  
DR PRINTS; PR01166; CYCOXDASEII.  
DR Pfam; PF00116; COX2; 1; \_c\_ox\_2.  
DR Pfam; PF02790; COX2; 1.  
DR PRINTS; PR01166; CYCOXDASEII.  
DR PRODOM; PD000131; Copper\_CUA; 1.  
DR PROSITE; PS50857; COX2\_CUA; 1.  
DR PROSITE; PS50999; COX2\_TM; 1.  
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
FT NON\_TER 1  
FT NON\_TER 189 189  
SQ SEQUENCE 189 AA; 21747 MW; EB5CC5977BDF151B CRC64;  
  
Query Match 84.1%; Score 37; DB 2; Length 189;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FLOLEPDA 8  
Db 101 FLOLEFDS 108  
|||||:  
101 FLOLEFDS 108

RESULT 36  
Q6PLU6\_9EUCA PRELIMINARY; PRT; 189 AA.  
ID Q6PLU6\_9EUCA  
AC Q6PLU6; 189 AA.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN Name=COI1;  
OS Aegla jujuyana.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aeglidae; Aegla.  
OX NCBI\_TaxID=273845;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15545254; DOI=10.1080/10635150490522331;  
RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
RT "Molecular systematics and biogeography of the southern South American freshwater 'crabs' Aegla (Decapoda: Anomura: Aeglidae) using multiple heuristic tree search approaches.";  
RL Syst. Biol. 53:767-780(2004).  
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Subunit 2 transfers the electrons from cytochrome c via its binuclear copper center to the bimetallic center of the catalytic subunit 1 (By similarity).  
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrom c + O(2) = 4 ferricytochrome c + 2 H(2)O.  
CC -!- COFACTOR: Copper A (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).  
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family. ENMBL; AV595778; AAT08414.1; -; Genomic DNA.  
DR ENMBL; AV595778; AAT08414.1; -; Genomic DNA.  
DR GO; GO:0019866; C:inner membrane; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
DR GO; GO:0005507; F:copper ion binding; IEA.  
DR GO; GO:0016021; F:cytochrome c oxidase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001505; Copper\_CUA.  
DR InterPro; IPR011759; COX2\_TM.  
DR Pfam; PF00116; COX2; 1.  
DR Pfam; PF02790; COX2\_TM; 1.  
DR PRINTS; PR01166; CYCOXDASEII.

DR ProDom; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS50857; COX2\_TM; 1.  
 FT NON\_TER 189 189  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 189 189  
 SQ SEQUENCE 189 AA; 21703 MW; EOCFA9E101F7A8B3 CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQLEFDDA 8  
 |||||:  
 Db 101 FQLEFDD 108

RESULT 38  
 Q6PLV0\_9EUA  
 ID Q6PLV0\_9EUA PRELIMINARY; PRT; 189 AA.  
 AC Q6PLV0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN Name=COII;  
 OS Aegla scamosa.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
 OC Galatheoidea; Aegliidae; Aegla.  
 OX NCBI\_TaxID=273843;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE  
 RA PubMed:15545254; DOI=10.1080/10635150490522331;  
 RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
 RT "Molecular systematics and biogeography of the southern South american  
 RT freshwater 'crabs' Aegla (Decapoda: Anomura: Aegliidae) using multiple  
 RT heuristic tree search approaches.";  
 RL Syst. Biol. 53:767-780(2004).  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1 (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AY595774; AAT08410.1; -; Genomic DNA.  
 DR EMBL; AY595773; AAT08409.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CUA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.

KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 189 189  
 FT NON\_TER 189 189  
 SQ SEQUENCE 189 AA; 21701 MW; 8DBE6D0D987A8772 CRC64;  
 Query Match 84.1%; Score 37; DB 2; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQLEFDDA 8  
 |||||:  
 Db 101 FQLEFDD 108

RESULT 39  
 Q6PLV3\_9EUA  
 ID Q6PLV3\_9EUA PRELIMINARY; PRT; 189 AA.  
 AC Q6PLV3;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN Name=COII;  
 OS Aegla obstipa.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
 OC Galatheoidea; Aegliidae; Aegla.  
 OX NCBI\_TaxID=273842;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE  
 RA PubMed:15545254; DOI=10.1080/10635150490522331;  
 RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
 RT "Molecular systematics and biogeography of the southern South american  
 RT freshwater 'crabs' Aegla (Decapoda: Anomura: Aegliidae) using multiple  
 RT heuristic tree search approaches.";  
 RL Syst. Biol. 53:767-780(2004).  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1 (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 DR EMBL; AY595771; AAT08407.1; -; Genomic DNA.  
 DR EMBL; AY595770; AAT08406.1; -; Genomic DNA.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CUA.  
 DR InterPro; IPR011759; COX2\_TM.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CUA; 1.  
 DR PROSITE; PS50857; COX2\_CUA; 1.  
 DR PROSITE; PS50999; COX2\_TM; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
 FT NON\_TER 189 189

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FT NON TER 189 189
SQ SEQUENCE 189 AA; 21685 MW; F44E05F703289A73 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEPDA 8
Db 101 FLQLEPDS 108

RESULT 40
Q6PLV5_9EUCA
ID Q6PLV5_9EUCA PRELIMINARY; PRT; 189 AA.
AC Q6PLV5;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Aegla platensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC Galatheoidea; Aeglidae; Aegla.
OC NCBI_TaxID=273811;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15545254; DOI=10.1080/10635150490522331;
RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RA "Molecular systematics and biogeography of the southern South american
RT freshwater 'crabs' Aegla (decapoda: Anomura: Aeglidae) using multiple
RT heuristic tree search approaches.";
RL Syst. Biol. 53:767-780(2004).
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- COFACTOR: Copper A (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AY595769; AAT08405.1; -; Genomic DNA.
CC GO; GO:0019866; C:inner membrane; IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005739; C:mitochondrion; IEA.
CC GO; GO:0005507; F:copper ion binding; IEA.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro; IPR011759; COX2_TM.
CC InterPro; IPR002429; Cyt_c_ox_2.
CC Pfam; PF00116; COX2; 1.
CC PRINTS; PF02790; COX2; 1.
CC PRODOM; PD000131; Copper_CUA; 1.
CC PROSITE; PS50857; COX2_CUA; 1.
CC PROSITE; PS50999; COX2_TM; 1.
CC Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
CC Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON TER 189 189
SQ SEQUENCE 189 AA; 21789 MW; 4C3084AAABCF1D43 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEPDA 8
Db 101 FLQLEPDS 108

RESULT 41
Q6PLV6_9EUCA
ID Q6PLV6_9EUCA PRELIMINARY; PRT; 189 AA.
AC Q6PLV6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Aegla platensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC Galatheoidea; Aeglidae; Aegla.
OC NCBI_TaxID=273811;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15545254; DOI=10.1080/10635150490522331;
RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RA "Molecular systematics and biogeography of the southern South american
RT freshwater 'crabs' Aegla (decapoda: Anomura: Aeglidae) using multiple
RT heuristic tree search approaches.";
RL Syst. Biol. 53:767-780(2004).
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- COFACTOR: Copper A (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AY595768; AAT08404.1; -; Genomic DNA.
CC GO; GO:0019866; C:inner membrane; IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005739; C:mitochondrion; IEA.
CC GO; GO:0005507; F:copper ion binding; IEA.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro; IPR011759; COX2_TM.
CC InterPro; IPR002429; Cyt_c_ox_2.
CC Pfam; PF00116; COX2; 1.
CC PRINTS; PF02790; COX2; 1.
CC PRODOM; PD000131; Copper_CUA; 1.
CC PROSITE; PS50857; COX2_CUA; 1.
CC PROSITE; PS50999; COX2_TM; 1.
CC Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
CC Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON TER 189 189
SQ SEQUENCE 189 AA; 21763 MW; CCAE70D0887731A9 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEPDA 8
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ID O6PLW1_9EUCA PRELIMINARY; PRT; 189 AA.
AC O6PLW1_9EUCA PRELIMINARY; PRT; 189 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Aegla leptochela.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC Galatheoidea; Aeglidae; Aegla.
OX NCBI_TaxID=273841;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15545254; DOI=10.1080/10635150490522331;
RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RT "Molecular systematics and biogeography of the southern South American
RT freshwater 'crabs' Aegla (Decapoda: Anomura: Aeglidae) using multiple
RT heuristic tree search approaches.";
RL Syst. Biol. 53:767-780(2004).
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferrocycytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AY595763; AAT08399.1; -; Genomic DNA.
CC EMBL; AY595762; AAT08398.1; -; Genomic DNA.
CC GO; GO:0019866; C:inner membrane; IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005739; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005507; F:copper ion binding; IEA.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transports; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transports; IEA.
CC InterPro; IPR001505; Copper_CuA.
CC InterPro; IPR002429; Cyt_c_ox_2.
CC Pfam; PF02790; COX2_TW; 1.
CC PRINTS; PR01166; CYCOXIDASEII.
CC PROSITE; PS50857; COX2_CUA; 1.
CC PROSITE; PS50999; COX2_TW; 1.
CC Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
CC Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 189
FT NON_TER 189
SQ SEQUENCE 189 AA; 21680 MW; AC72186E83BBA049 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8
Db 101 FLQLEFDS 108

RESULT 45
Q6PLW3_9EUCA
ID O6PLW3_9EUCA PRELIMINARY; PRT; 189 AA.
AC O6PLW3_9EUCA PRELIMINARY; PRT; 189 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)

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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Aegla cavernicola.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC Galatheoidea; Aeglidae; Aegla.
OX NCBI_TaxID=273840;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15545254; DOI=10.1080/10635150490522331;
RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;
RT "Molecular systematics and biogeography of the southern South American
RT freshwater 'crabs' Aegla (Decapoda: Anomura: Aeglidae) using multiple
RT heuristic tree search approaches.";
RL Syst. Biol. 53:767-780(2004).
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1 (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferrocycytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC EMBL; AY595761; AAT08397.1; -; Genomic DNA.
CC EMBL; AY595760; AAT08396.1; -; Genomic DNA.
CC GO; GO:0019866; C:inner membrane; IEA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0005739; C:mitochondrion; IEA.
CC GO; GO:0005507; F:copper ion binding; IEA.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transports; IEA.
CC InterPro; IPR001505; Copper_CuA.
CC InterPro; IPR001759; COX2_TW.
CC Pfam; PF00116; COX2; 1.
CC PRINTS; PR01166; CYCOXIDASEII.
CC PROSITE; PS50857; COX2_CUA; 1.
CC PROSITE; PS50999; COX2_TW; 1.
CC Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;
CC Oxidoreductase; Respiratory chain; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 189
FT NON_TER 189
SQ SEQUENCE 189 AA; 21787 MW; 4A8F4F0A26CE540A CRC64;

Query Match 84.1%; Score 37; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8
Db 101 FLQLEFDS 108

RESULT 46
Q6PLW5_9EUCA
ID O6PLW5_9EUCA PRELIMINARY; PRT; 189 AA.
AC O6PLW5_9EUCA PRELIMINARY; PRT; 189 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).

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GN Name=COII;  
OS Aegla prado.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aeglidae; Aegla.  
OX NCBI\_TaxID=273839;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RP PubMed=15545254; DOI=10.1080/10635150490522331;  
RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
RA "Molecular systematics and biogeography of the southern South american  
RT freshwater 'crabs' Aegla (Decapoda; Anomura; Aeglidae) using multiple  
RT heuristic tree search approaches.";  
RL Syst. Biol. 53:767-780 (2004).  
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1 (By  
CC similarity).  
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -1- COFACTOR: Copper A (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
CC EMBL: AY595759; AA08395.1; -; Genomic DNA.  
CC GO: 0019866; C:inner membrane; IEA.  
CC EMBL: AY595758; AA08394.1; -; Genomic DNA.  
CC GO: 0019866; C:inner membrane; IEA.  
CC GO: 0005739; C:mitochondrial electron transport chain; IEA.  
CC GO: 0005507; F:copper ion binding; IEA.  
CC GO: 0004129; F:cytochrome-c oxidase activity; IEA.  
CC GO: 0006118; P:electron transport; IEA.  
CC GO: 0006810; P:transport; IEA.  
CC InterPro: IPR001505; Copper\_CuA.  
CC InterPro: IPR011759; COX2\_TM.  
CC Pfam: PF00116; COX2; 1.  
CC PRINTS: PR01166; CYCOXIDASEII.  
CC PRODOM: PD000131; Copper\_CuA; 1.  
CC PROSITE: PS50857; COX2\_CUA; 1.  
CC PROSITE: PS50999; COX2\_TM; 1.  
KW Copper; Electron transport; Inner membrane; Membrane; Mitochondrion;  
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.  
FT NON\_TER 1  
FT NON\_TER 189  
SQ SEQUENCE 189 AA; 21721 MW; 5921596114B3F65P CRC64;  
Query Match 84.1%; Score 37; DB 2; Length 189;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FLOLEPDA 8  
Db 101 FLOLEPDS 108  
RESULT 47  
Q6PLW7\_9EUC PRELIMINARY; PRT; 189 AA.  
ID Q6PLW7\_9EUC  
AC Q6PLW7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN Name=COII;  
OS Aegla uruguayana.  
OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Galatheoidea; Aeglidae; Aegla.  
OX NCBI\_TaxID=177212;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RP PubMed=15545254; DOI=10.1080/10635150490522331;  
RX Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
RA "Molecular systematics and biogeography of the southern South american  
RT freshwater 'crabs' Aegla (Decapoda; Anomura; Aeglidae) using multiple  
RT heuristic tree search approaches.";  
RL Syst. Biol. 53:767-780 (2004).  
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1 (By  
CC similarity).  
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -1- COFACTOR: Copper A (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
CC EMBL: AY595757; AA08393.1; -; Genomic DNA.  
CC GO: 0019866; C:inner membrane; IEA.  
CC GO: 0016021; C:integral to membrane; IEA.  
CC GO: 0005746; C:mitochondrial electron transport chain; IEA.  
CC GO: 0005739; C:mitochondrion; IEA.  
CC GO: 0005507; F:copper ion binding; IEA.  
CC GO: 0004129; F:cytochrome-c oxidase activity; IEA.  
CC GO: 0016491; F:oxidoreductase activity; IEA.  
CC GO: 0006118; P:electron transport; IEA.  
CC GO: 0006810; P:transport; IEA.  
CC InterPro: IPR001505; Copper\_CuA.  
CC InterPro: IPR011759; COX2\_TM.  
CC Pfam: PF00116; COX2; 1.  
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CC PRODOM: PD000131; Copper\_CuA; 1.  
CC PROSITE: PS50857; COX2\_CUA; 1.  
CC PROSITE: PS50999; COX2\_TM; 1.  
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
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GN Name=COII;  
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OC Galatheoidea; Aeglidae; Aegla.

RX NCBI\_TaxID=274478;  
 RN [1] NUCLEOTIDE SEQUENCE.  
 RP PubMed=15545254; DOI=10.1080/10635150490522331;  
 RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
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 CC A center to the bimetallic center of the catalytic subunit 1 (By  
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 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
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 DR GO; GO:0005507; F:copper ion binding; IEA.  
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 DR GO; GO:0006118; P:electron transport; IEA.  
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 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
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 GN Name=COII;  
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RA Perez-Losada M., Bond-Buckup G., Jara C.G., Crandall K.A.;  
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 DR EMBL; AY595754; AAT08390.1; -; Genomic DNA.  
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 DR GO; GO:0016021; C:integral to membrane; IEA.  
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 OG Mitochondrion.  
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 OC Galatheoidea; Aegliidae; Aegla.  
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DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.

DR GO; GO:0005739; C:mitochondrion; IEA.

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DR GO; GO:0006118; P:electron transport; IEA.

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KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.

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Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFDA 8

Db 101 FLQLEFDS 108

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Job time : 114.6 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

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(without alignments)  
29.527 Million cell updates/sec

Title: US-09-870-216C-5

Perfect score: 44

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Scoring table: BLOSUM62

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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- 4: /cgn2\_6/ptodata/1/iaa/PCITUS\_COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	32	72.7	596	2	US-09-949-016-9814
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6	32	72.7	633	2	US-09-919-060-13
7	32	72.7	2289	2	US-09-051-019-2
8	31	70.5	210	1	US-07-667-276A-2
9	31	70.5	287	2	US-09-543-681A-7259
10	31	70.5	379	2	US-09-270-767-32891
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12	31	70.5	524	2	US-09-252-991A-17710
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25	30	68.2	582	2	US-09-516-314-21
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29	68.2	1648	2	US-09-515-806-4	Sequence 4, Appli
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38	65.9	141	2	US-09-513-999C-7895	Sequence 7895, Ap
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110	27	61.4	13	2	US-09-140-149-14	Sequence 14, Appl	183	27	61.4	720	2	US-09-634-258B-322	Sequence 322, App
111	27	61.4	13	2	US-09-615-917-14	Sequence 14, Appl	184	27	61.4	758	2	US-09-487-558B-224	Sequence 224, App
112	27	61.4	28	2	US-09-007-905-17	Sequence 17, Appl	185	27	61.4	775	2	US-09-949-016-8799	Sequence 8799, Ap
113	27	61.4	28	2	US-09-232-074-17	Sequence 17, Appl	186	27	61.4	784	2	US-09-982-308B-23	Sequence 23, Appl
114	27	61.4	103	2	US-09-543-681A-7951	Sequence 7951, Ap	187	27	61.4	795	2	US-09-198-452A-314	Sequence 314, App
115	27	61.4	111	2	US-09-270-767-32551	Sequence 32351, A	188	27	61.4	795	2	US-09-438-185A-302	Sequence 302, App
116	27	61.4	111	2	US-09-270-767-47568	Sequence 47568, A	189	27	61.4	797	2	US-09-417-197-141	Sequence 141, App
117	27	61.4	128	2	US-09-149-476-539	Sequence 539, App	190	27	61.4	797	2	US-09-417-197-143	Sequence 143, App
118	27	61.4	143	2	US-09-270-767-46435	Sequence 46435, A	191	27	61.4	797	2	US-09-248-796A-16517	Sequence 16517, A
119	27	61.4	150	2	US-09-198-452A-919	Sequence 919, App	192	27	61.4	805	2	US-09-513-783A-178	Sequence 178, App
120	27	61.4	161	2	US-09-538-092-756	Sequence 756, App	193	27	61.4	805	2	US-10-100-957A-178	Sequence 178, App
121	27	61.4	162	2	US-09-902-540-10362	Sequence 10362, A	194	27	61.4	1002	2	US-09-252-931A-19662	Sequence 19662, A
122	27	61.4	164	2	US-09-252-991A-31507	Sequence 31507, A	195	27	61.4	1068	2	US-08-390-874C-11	Sequence 11, Appl
123	27	61.4	177	2	US-09-543-681A-5313	Sequence 5313, Ap	196	27	61.4	1068	2	US-09-265-772-11	Sequence 11, Appl
124	27	61.4	200	2	US-09-248-796A-15414	Sequence 15414, A	197	27	61.4	1068	1	US-08-162-081B-37	Sequence 37, Appl
125	27	61.4	219	2	US-09-540-236-2633	Sequence 2633, Ap	198	27	61.4	1069	1	US-08-162-081B-37	Sequence 37, Appl
126	27	61.4	222	2	US-09-248-796A-26182	Sequence 26182, A	199	27	61.4	1069	2	US-08-780-872-37	Sequence 37, Appl
127	27	61.4	231	2	US-09-270-767-57449	Sequence 57449, A	200	27	61.4	1069	2	US-09-085-957-37	Sequence 37, Appl
128	27	61.4	237	1	US-08-576-626A-56	Sequence 56, Appl	201	27	61.4	1080	1	US-08-162-081B-36	Sequence 36, Appl
129	27	61.4	237	2	US-09-303-518D-162	Sequence 162, App	202	27	61.4	1080	1	US-08-780-872-36	Sequence 36, Appl
130	27	61.4	246	2	US-09-710-279-3150	Sequence 3150, Ap	203	27	61.4	1207	2	US-09-085-957-36	Sequence 36, Appl
131	27	61.4	256	2	US-09-134-001C-5471	Sequence 5471, Ap	204	27	61.4	1207	2	US-09-328-352-6766	Sequence 6766, Ap
132	27	61.4	293	2	US-09-583-110-3012	Sequence 3012, Ap	205	27	61.4	1218	2	US-09-477-962-100	Sequence 100, App
133	27	61.4	297	2	US-09-107-433-3745	Sequence 3745, Ap	206	27	61.4	1272	1	US-09-543-681A-5732	Sequence 5732, Ap
134	27	61.4	306	2	US-09-270-767-34506	Sequence 34506, A	207	27	61.4	1289	1	US-08-542-003-2	Sequence 2, Appl1
135	27	61.4	306	2	US-09-270-767-34506	Sequence 34506, A	208	27	61.4	1289	1	US-08-322-760A-2	Sequence 2, Appl1
136	27	61.4	308	2	US-09-583-110-4369	Sequence 4369, Ap	209	27	61.4	1289	2	US-09-236-949-2	Sequence 2, Appl1
137	27	61.4	311	2	US-09-248-796A-15828	Sequence 15828, A	210	27	61.4	1799	2	US-09-134-000C-5178	Sequence 5178, Ap
138	27	61.4	317	2	US-09-107-433-4532	Sequence 4532, Ap	211	27	61.4	2544	1	US-08-576-626A-32	Sequence 32, Appl
139	27	61.4	336	2	US-09-489-039A-9200	Sequence 9200, Ap	212	27	61.4	3460	2	US-09-334-220-1	Sequence 1, Appl1
140	27	61.4	345	2	US-09-248-796A-20158	Sequence 20158, A	213	27	61.4	3461	2	US-09-334-220-2	Sequence 2, Appl1
141	27	61.4	358	2	US-09-252-991A-19207	Sequence 19207, A	214	26.5	60.2	245	2	US-09-107-532A-4448	Sequence 4448, Ap
142	27	61.4	358	2	US-09-487-558B-148	Sequence 148, App	215	26	59.1	9	2	US-09-935-430-107	Sequence 107, App
143	27	61.4	389	2	US-09-902-540-12102	Sequence 12102, A	216	26	59.1	9	2	US-09-935-430-223	Sequence 223, App
144	27	61.4	392	2	US-09-248-796A-16393	Sequence 16393, A	217	26	59.1	10	2	US-09-935-430-251	Sequence 251, App
145	27	61.4	416	2	US-09-252-991A-23400	Sequence 23400, A	218	26	59.1	10	2	US-09-935-430-367	Sequence 367, App
146	27	61.4	425	2	US-09-252-991A-33074	Sequence 33074, A	219	26	59.1	10	2	US-09-935-430-403	Sequence 403, App
147	27	61.4	431	1	US-08-190-802A-37	Sequence 37, Appl	220	26	59.1	13	2	US-08-672-213-69	Sequence 69, Appl
148	27	61.4	431	2	US-08-477-346-37	Sequence 37, Appl	221	26	59.1	15	2	US-09-647-372B-70	Sequence 70, Appl
149	27	61.4	431	2	US-08-473-089-37	Sequence 37, Appl	222	26	59.1	22	1	US-08-019-073-9	Sequence 9, Appl1
150	27	61.4	431	2	US-08-487-072A-37	Sequence 37, Appl	223	26	59.1	22	4	PCT-US94-01768-9	Sequence 9, Appl1
151	27	61.4	431	2	US-09-538-092-1267	Sequence 1267, Ap	224	26	59.1	43	2	US-08-924-330A-15	Sequence 15, Appl
152	27	61.4	451	2	US-09-248-796A-19022	Sequence 19022, A	225	26	59.1	43	2	US-09-138-721-15	Sequence 15, Appl
153	27	61.4	453	2	US-09-252-991A-31268	Sequence 31268, A	226	26	59.1	47	2	US-09-270-767-40060	Sequence 40060, A
154	27	61.4	455	2	US-09-221-235-5	Sequence 5, Appl1	227	26	59.1	47	2	US-09-270-767-55276	Sequence 55276, A
155	27	61.4	455	2	US-09-221-928-5	Sequence 5, Appl1	228	26	59.1	52	2	US-09-270-767-38960	Sequence 38960, A
156	27	61.4	455	2	US-09-221-527-5	Sequence 5, Appl1	229	26	59.1	52	2	US-09-270-767-54177	Sequence 54177, A
157	27	61.4	455	2	US-09-221-236-5	Sequence 5, Appl1	230	26	59.1	62	2	US-09-248-796A-24773	Sequence 24773, A
158	27	61.4	455	2	US-09-221-416-5	Sequence 5, Appl1	231	26	59.1	62	2	US-09-248-796A-21079	Sequence 21079, A
159	27	61.4	455	2	US-09-221-245-5	Sequence 5, Appl1	232	26	59.1	76	2	US-09-489-039A-11887	Sequence 11887, A
160	27	61.4	455	2	US-09-163-115-5	Sequence 5, Appl1	233	26	59.1	80	2	US-09-489-039A-12850	Sequence 12850, A
161	27	61.4	455	2	US-09-221-528-5	Sequence 5, Appl1	234	26	59.1	82	2	US-09-902-540-11302	Sequence 11302, A
162	27	61.4	455	2	US-09-593-553-5	Sequence 5, Appl1	235	26	59.1	84	2	US-09-252-991A-27473	Sequence 27473, A
163	27	61.4	455	2	US-09-221-237-5	Sequence 5, Appl1	236	26	59.1	95	2	US-09-902-540-13262	Sequence 13262, A
164	27	61.4	455	2	US-09-399-588-2	Sequence 2, Appl1	237	26	59.1	99	2	US-09-513-999C-7597	Sequence 7597, Ap
165	27	61.4	455	2	US-09-757-982-5	Sequence 5, Appl1	238	26	59.1	108	2	US-09-270-767-40129	Sequence 40129, A
166	27	61.4	457	2	US-10-029-180-24	Sequence 24, Appl	239	26	59.1	108	2	US-09-270-767-55345	Sequence 55345, A
167	27	61.4	460	2	US-09-252-991A-20638	Sequence 20638, A	240	26	59.1	1126	2	US-09-710-279-1174	Sequence 1174, Ap
168	27	61.4	464	2	US-09-949-016-10463	Sequence 10463, A	241	26	59.1	126	2	US-10-314-739A-14	Sequence 14, Appl
169	27	61.4	482	2	US-09-252-991A-28368	Sequence 28368, A	242	26	59.1	131	2	US-09-540-236-2454	Sequence 2454, Ap
170	27	61.4	498	2	US-09-248-796A-26681	Sequence 26681, A	243	26	59.1	132	2	US-09-252-991A-21795	Sequence 21795, A
171	27	61.4	507	2	US-09-248-796A-26681	Sequence 26681, A	244	26	59.1	133	2	US-09-107-532A-6809	Sequence 6809, Ap
172	27	61.4	529	2	US-09-080-044-2	Sequence 2, Appl1	245	26	59.1	135	1	US-08-771-602D-41	Sequence 41, Appl
173	27	61.4	529	2	US-09-531-857A-2	Sequence 2, Appl1	246	26	59.1	146	2	US-09-861-451A-48	Sequence 48, Appl

247	26	59.1	153	2	US-09-621-976-5081	Sequence 5081, Ap	320	26	59.1	407	1	US-08-997-040-2	Sequence 2, Appli
248	26	59.1	161	2	US-09-489-039A-9832	Sequence 9832, Ap	321	26	59.1	407	1	US-09-203-237-2	Sequence 2, Appli
249	26	59.1	164	2	US-09-248-796A-16291	Sequence 16291, A	322	26	59.1	408	1	US-08-924-847A-2	Sequence 2, Appli
250	26	59.1	166	2	US-09-270-767-39721	Sequence 39721, A	323	26	59.1	408	2	US-09-120-052-2	Sequence 2, Appli
251	26	59.1	166	2	US-09-270-767-54938	Sequence 54938, A	324	26	59.1	412	2	US-09-949-016-11689	Sequence 11689, A
252	26	59.1	173	2	US-09-543-681A-7869	Sequence 7869, Ap	325	26	59.1	415	2	US-09-935-430-659	Sequence 659, App
253	26	59.1	178	2	US-09-134-001C-4767	Sequence 4767, Ap	326	26	59.1	420	2	US-09-252-991A-19117	Sequence 19117, A
254	26	59.1	180	2	US-09-489-039A-99331	Sequence 9331, Ap	327	26	59.1	421	2	US-09-583-110-2907	Sequence 2907, Ap
255	26	59.1	186	2	US-09-328-352-6333	Sequence 6333, Ap	328	26	59.1	423	2	US-09-605-703B-3324	Sequence 324, App
256	26	59.1	206	2	US-09-902-540-12815	Sequence 12815, A	329	26	59.1	423	2	US-09-507-703B-3324	Sequence 324, App
257	26	59.1	229	2	US-09-893-737-318	Sequence 318, App	330	26	59.1	430	2	US-08-311-731A-153	Sequence 153, App
258	26	59.1	230	2	US-09-248-796A-14298	Sequence 14298, A	331	26	59.1	431	2	US-09-252-991A-24878	Sequence 24878, A
259	26	59.1	246	2	US-09-270-767-35514	Sequence 35514, A	332	26	59.1	439	2	US-08-311-731A-48	Sequence 48, Appl
260	26	59.1	246	2	US-09-270-767-50731	Sequence 50731, A	333	26	59.1	440	2	US-09-964-956-29	Sequence 29, Appl
261	26	59.1	248	2	US-09-107-532A-4169	Sequence 4169, Ap	334	26	59.1	442	2	US-09-328-352-6777	Sequence 6777, Ap
262	26	59.1	252	2	US-09-949-016-11499	Sequence 11499, A	335	26	59.1	448	2	US-09-107-433-4124	Sequence 4124, Ap
263	26	59.1	259	2	US-09-248-796A-21344	Sequence 21344, A	336	26	59.1	448	2	US-09-583-110-3196	Sequence 3196, Ap
264	26	59.1	262	2	US-09-134-000C-3905	Sequence 3905, Ap	337	26	59.1	452	2	US-09-489-039A-11615	Sequence 11615, A
265	26	59.1	272	2	US-09-270-767-46229	Sequence 46229, A	338	26	59.1	465	2	US-09-270-767-37268	Sequence 37268, A
266	26	59.1	271	2	US-09-248-796A-14697	Sequence 14697, A	339	26	59.1	465	2	US-09-328-352-6777	Sequence 6777, Ap
267	26	59.1	273	2	US-09-107-433-4284	Sequence 4284, Ap	340	26	59.1	473	2	US-09-540-236-3656	Sequence 3656, Ap
268	26	59.1	274	2	US-09-248-796A-17825	Sequence 17825, A	341	26	59.1	474	2	US-09-252-991A-23759	Sequence 23759, A
269	26	59.1	275	2	US-09-252-991A-19818	Sequence 19818, A	342	26	59.1	474	2	US-09-248-796A-20952	Sequence 20952, A
270	26	59.1	275	2	US-09-583-110-3006	Sequence 3006, Ap	343	26	59.1	476	2	US-09-978-309A-77	Sequence 77, Appl
271	26	59.1	275	2	US-10-104-047-3627	Sequence 3627, Ap	344	26	59.1	477	2	US-08-772-270A-13	Sequence 13, Appl
272	26	59.1	288	2	US-09-100-804-15	Sequence 15, Appl	345	26	59.1	477	2	US-08-704-711A-20	Sequence 20, Appl
273	26	59.1	291	2	US-09-248-796A-20587	Sequence 20587, A	346	26	59.1	477	2	US-08-448-489-15	Sequence 15, Appl
274	26	59.1	296	2	US-09-284-926-5	Sequence 5, Appli	347	26	59.1	477	2	US-08-281-313-1	Sequence 9, Appli
275	26	59.1	300	2	US-09-284-926-4	Sequence 4, Appli	348	26	59.1	477	2	US-09-521-220-20	Sequence 20, Appl
276	26	59.1	301	2	US-09-270-767-42595	Sequence 42595, A	349	26	59.1	477	2	US-09-391-104-21	Sequence 21, Appl
277	26	59.1	317	2	US-09-107-532A-6311	Sequence 6311, Ap	350	26	59.1	477	2	US-09-689-730-15	Sequence 15, Appl
278	26	59.1	328	2	US-09-848-294-3	Sequence 3, Appli	351	26	59.1	477	2	US-09-949-002-342	Sequence 342, App
279	26	59.1	338	2	US-09-328-352-4723	Sequence 4723, Ap	352	26	59.1	479	2	US-10-141-634-2	Sequence 2, Appli
280	26	59.1	341	2	US-09-270-767-38191	Sequence 38191, A	353	26	59.1	482	2	US-09-949-002-538	Sequence 538, App
281	26	59.1	341	2	US-09-270-767-53408	Sequence 53408, A	354	26	59.1	490	2	US-09-902-540-16820	Sequence 16820, A
282	26	59.1	342	1	US-08-446-345-39	Sequence 39, Appl	355	26	59.1	502	2	US-09-949-016-5992	Sequence 5992, Ap
283	26	59.1	349	2	US-09-032-523-3	Sequence 3, Appli	356	26	59.1	503	2	US-09-107-433-5099	Sequence 5099, Ap
284	26	59.1	349	2	US-09-802-633-3	Sequence 3, Appli	357	26	59.1	504	2	US-09-252-991A-22291	Sequence 22291, A
285	26	59.1	354	2	US-09-949-016-7936	Sequence 7936, Ap	358	26	59.1	506	2	US-09-540-236-2360	Sequence 2360, Ap
286	26	59.1	356	2	US-09-489-039A-12757	Sequence 12757, A	359	26	59.1	507	2	US-09-949-016-7091	Sequence 7091, Ap
287	26	59.1	369	2	US-09-252-991A-16744	Sequence 16744, A	360	26	59.1	522	2	US-09-107-532A-3678	Sequence 3678, Ap
288	26	59.1	380	2	US-09-825-414-40	Sequence 40, Appl	361	26	59.1	530	2	US-09-248-796A-15830	Sequence 15830, A
289	26	59.1	380	2	US-09-825-414-42	Sequence 42, Appl	362	26	59.1	534	2	US-09-538-092-673	Sequence 673, App
290	26	59.1	380	2	US-09-825-414-44	Sequence 44, Appl	363	26	59.1	534	2	US-09-487-558B-124	Sequence 124, App
291	26	59.1	380	2	US-09-825-414-46	Sequence 46, Appl	364	26	59.1	538	2	US-09-328-352-5741	Sequence 5741, Ap
292	26	59.1	380	2	US-09-825-414-48	Sequence 48, Appl	365	26	59.1	541	2	US-09-252-991A-24521	Sequence 24521, A
293	26	59.1	380	2	US-09-825-414-50	Sequence 50, Appl	366	26	59.1	550	1	US-08-143-219-25	Sequence 25, Appl
294	26	59.1	380	2	US-09-825-414-52	Sequence 52, Appl	367	26	59.1	551	1	US-08-436-771-9	Sequence 9, Appli
295	26	59.1	382	2	US-09-893-737-36	Sequence 36, Appl	368	26	59.1	551	1	US-08-434-998-9	Sequence 9, Appli
296	26	59.1	392	2	US-09-252-991A-30852	Sequence 30852, A	369	26	59.1	551	1	US-08-487-797-9	Sequence 9, Appli
297	26	59.1	396	1	US-08-208-007A-13	Sequence 13, Appl	370	26	59.1	551	1	US-09-949-016-6268	Sequence 6268, Ap
298	26	59.1	396	1	US-08-926-253-2	Sequence 2, Appli	371	26	59.1	551	4	PCT-US95-02058-9	Sequence 9, Appli
299	26	59.1	386	1	US-08-838-219B-9	Sequence 9, Appli	372	26	59.1	562	2	US-09-712-363-254	Sequence 254, App
300	26	59.1	396	2	US-09-120-074-2	Sequence 2, Appli	373	26	59.1	570	2	US-09-068-960-13	Sequence 13, Appl
301	26	59.1	396	2	US-09-233-336A-9	Sequence 9, Appli	374	26	59.1	587	2	US-08-899-578-2	Sequence 2, Appli
302	26	59.1	396	2	US-09-233-752A-9	Sequence 9, Appli	375	26	59.1	591	2	US-09-949-016-11452	Sequence 11452, A
303	26	59.1	396	2	US-09-032-523-9	Sequence 9, Appli	376	26	59.1	630	2	US-09-328-352-7722	Sequence 7722, Ap
304	26	59.1	396	2	US-09-402-036-9	Sequence 9, Appli	377	26	59.1	655	2	US-09-248-796A-14308	Sequence 14308, A
305	26	59.1	396	2	US-08-915-095A-13	Sequence 13, Appl	378	26	59.1	679	2	US-09-252-991A-28325	Sequence 28325, A
306	26	59.1	396	2	US-08-798-096-13	Sequence 13, Appl	379	26	59.1	695	2	US-09-738-946-10	Sequence 10, Appl
307	26	59.1	396	2	US-08-798-095A-13	Sequence 13, Appl	380	26	59.1	713	1	US-08-987-466-3	Sequence 3, Appli
308	26	59.1	396	2	US-09-904-226-9	Sequence 9, Appli	381	26	59.1	713	1	US-08-974-565C-5	Sequence 5, Appli
309	26	59.1	396	2	US-09-953-956-13	Sequence 13, Appl	382	26	59.1	713	2	US-09-255-748-5	Sequence 5, Appli
310	26	59.1	396	2	US-08-553-125A-13	Sequence 13, Appl	383	26	59.1	713	2	US-09-240-359-3	Sequence 3, Appli
311	26	59.1	396	2	US-09-802-633-9	Sequence 9, Appli	384	26	59.1	713	2	US-09-802-741-3	Sequence 3, Appli
312	26	59.1	396	2	US-09-215-450-22	Sequence 22, Appl	385	26	59.1	723	2	US-09-252-991A-18896	Sequence 3, Appli
313	26	59.1	396	2	US-10-114-464-13	Sequence 13, Appl	386	26	59.1	734	2	US-09-328-352-4412	Sequence 2, Appli
314	26	59.1	397	2	US-09-949-016-9464	Sequence 9464, Ap	387	26	59.1	748	1	US-08-920-234-2	Sequence 2, Appli
315	26	59.1	401	2	US-09-270-767-37119	Sequence 37119, A	388	26	59.1	748	1	US-08-937-931-4	Sequence 4, Appli
316	26	59.1	401	2	US-09-270-767-52336	Sequence 52336, A	389	26	59.1	748	2	US-09-285-502-4	Sequence 4, Appli
317	26	59.1	402	2	US-09-134-001C-4138	Sequence 4138, Ap	390	26	59.1	748	2	US-09-030-335-9	Sequence 9, Appli
318	26	59.1	406	2	US-09-215-450-26	Sequence 26, Appl	391	26	59.1	748	2	US-09-709-126-4	Sequence 4, Appli
319	26	59.1	407	1	US-08-487-823B-2	Sequence 2, Appli	392	26	59.1	748	2	US-09-871-385A-4	Sequence 4, Appli

393	26	59.1	755	2	US-09-949-016-7755	Sequence 7755, Ap	466	25.5	58.0	68	1	US-08-057-971-76	Sequence 76, Appl
394	26	59.1	761	2	US-09-949-016-10631	Sequence 10631, A	467	25.5	58.0	68	1	US-08-235-515A-21	Sequence 21, Appl
395	26	59.1	768	4	PCT-US93-03076-3	Sequence 3, Appli	468	25.5	58.0	68	2	US-09-331-793-23	Sequence 23, Appl
396	26	59.1	778	4	PCT-US93-03076-4	Sequence 4, Appli	469	25.5	58.0	70	1	US-07-791-213D-3	Sequence 3, Appli
397	26	59.1	782	2	US-09-769-787-75	Sequence 75, Appl	470	25.5	58.0	70	1	US-07-791-213D-3	Sequence 3, Appli
398	26	59.1	798	2	US-09-935-430-658	Sequence 658, App	471	25.5	58.0	70	1	US-07-791-213D-18	Sequence 18, Appl
399	26	59.1	798	2	US-09-964-956-28	Sequence 28, Appl	472	25.5	58.0	70	1	US-07-791-213D-19	Sequence 19, Appl
400	26	59.1	799	2	US-09-030-335-4	Sequence 4, Appli	473	25.5	58.0	70	1	US-07-972-387-75	Sequence 75, Appl
401	26	59.1	805	2	US-09-344-624-19	Sequence 19, Appl	474	25.5	58.0	70	1	US-08-431-412-75	Sequence 75, Appl
402	26	59.1	805	2	US-09-949-016-6713	Sequence 6713, Ap	475	25.5	58.0	70	1	US-08-057-971-75	Sequence 75, Appl
403	26	59.1	837	2	US-09-964-956-5	Sequence 5, Appli	476	25.5	58.0	70	1	US-08-293-150A-3	Sequence 3, Appli
404	26	59.1	841	2	US-09-935-430-657	Sequence 657, App	477	25.5	58.0	70	1	US-08-293-150A-5	Sequence 5, Appli
405	26	59.1	841	2	US-09-964-956-2	Sequence 2, Appli	478	25.5	58.0	70	1	US-08-293-150A-18	Sequence 18, Appl
406	26	59.1	874	2	US-10-163-214-13	Sequence 13, Appl	479	25.5	58.0	70	1	US-08-293-150A-19	Sequence 19, Appl
407	26	59.1	901	2	US-09-949-016-7207	Sequence 7207, Ap	480	25.5	58.0	70	1	US-08-235-515A-25	Sequence 25, Appl
408	26	59.1	913	2	US-09-848-294-2	Sequence 2, Appli	481	25.5	58.0	72	1	US-07-791-213D-83	Sequence 83, Appl
409	26	59.1	922	2	US-09-303-518D-882	Sequence 882, App	482	25.5	58.0	72	1	US-07-791-213D-100	Sequence 100, App
410	26	59.1	931	2	US-09-252-991A-22550	Sequence 22550, A	483	25.5	58.0	72	1	US-08-293-150A-83	Sequence 83, Appl
411	26	59.1	1006	2	US-09-949-016-8421	Sequence 8421, Ap	484	25.5	58.0	72	1	US-08-293-150A-100	Sequence 100, App
412	26	59.1	1006	2	US-09-949-016-8530	Sequence 8530, Ap	485	25.5	58.0	75	1	US-07-791-213D-96	Sequence 96, Appl
413	26	59.1	1051	2	US-09-252-991A-19145	Sequence 19145, A	486	25.5	58.0	75	1	US-08-293-150A-96	Sequence 96, Appl
414	26	59.1	1167	2	US-09-803-671B-2	Sequence 2, Appli	487	25.5	58.0	83	6	5220013-22	Patent No. 5220013
415	26	59.1	1167	2	US-10-274-409-2	Sequence 2, Appli	488	25.5	58.0	87	1	US-07-791-213D-86	Sequence 86, Appl
416	26	59.1	1380	2	US-09-328-352-8132	Sequence 8132, Ap	489	25.5	58.0	87	1	US-08-293-150A-86	Sequence 86, Appl
417	26	59.1	1513	4	PCT-US93-03076-2	Sequence 2, Appli	490	25.5	58.0	89	1	US-07-972-387-10	Sequence 10, Appl
418	26	59.1	1824	1	US-08-680-327-3	Sequence 3, Appli	491	25.5	58.0	89	1	US-08-431-412-10	Sequence 10, Appl
419	26	59.1	1824	2	US-09-228-246-2	Sequence 2, Appli	492	25.5	58.0	89	1	US-08-057-971-10	Sequence 10, Appl
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421	26	59.1	4551	2	US-09-320-878-1	Sequence 1, Appli	494	25.5	58.0	91	1	US-07-791-213D-89	Sequence 89, Appl
422	26	59.1	4551	2	US-09-141-908-2	Sequence 2, Appli	495	25.5	58.0	91	1	US-07-791-213D-103	Sequence 103, App
423	26	59.1	4551	2	US-09-657-440-1	Sequence 1, Appli	496	25.5	58.0	91	1	US-07-791-213D-106	Sequence 106, App
424	26	59.1	4551	2	US-09-793-708-1	Sequence 1, Appli	497	25.5	58.0	91	1	US-07-972-387-2	Sequence 2, Appli
425	26	59.1	4613	2	US-09-105-537-31	Sequence 31, Appli	498	25.5	58.0	91	1	US-08-431-412-2	Sequence 2, Appli
426	26	59.1	11877	2	US-09-105-537-6	Sequence 6, Appli	499	25.5	58.0	91	1	US-08-057-971-2	Sequence 2, Appli
427	25.5	58.0	15	1	US-08-148-160-2	Sequence 2, Appli	500	25.5	58.0	91	1	US-08-293-150A-76	Sequence 76, Appl
428	25.5	58.0	51	1	US-07-791-213D-1	Sequence 1, Appli	501	25.5	58.0	91	1	US-08-293-150A-89	Sequence 89, Appl
429	25.5	58.0	51	1	US-07-791-213D-2	Sequence 2, Appli	502	25.5	58.0	91	1	US-08-293-150A-103	Sequence 103, App
430	25.5	58.0	51	1	US-07-791-213D-7	Sequence 7, Appli	503	25.5	58.0	91	1	US-08-293-150A-106	Sequence 106, App
431	25.5	58.0	51	1	US-07-791-213D-17	Sequence 17, Appl	504	25.5	58.0	101	1	US-08-235-515A-29	Sequence 29, Appl
432	25.5	58.0	51	1	US-07-972-387-67	Sequence 67, Appl	505	25.5	58.0	122	1	US-08-422-333-12	Sequence 12, Appl
433	25.5	58.0	51	1	US-08-431-412-67	Sequence 67, Appl	506	25.5	58.0	122	6	5187153-20	Patent No. 5187153
434	25.5	58.0	51	1	US-08-057-971-67	Sequence 67, Appl	507	25.5	58.0	122	6	5220013-23	Patent No. 5220013
435	25.5	58.0	51	1	US-08-293-150A-1	Sequence 1, Appli	508	25.5	58.0	122	6	523482-22	Patent No. 523482
436	25.5	58.0	51	1	US-08-293-150A-2	Sequence 2, Appli	509	25.5	58.0	122	6	5466783-23	Patent No. 5466783
437	25.5	58.0	51	1	US-08-293-150A-7	Sequence 7, Appli	510	25.5	58.0	127	6	5466783-24	Patent No. 5466783
438	25.5	58.0	51	1	US-08-293-150A-17	Sequence 17, Appl	511	25.5	58.0	143	1	US-08-422-333-10	Sequence 10, Appl
439	25.5	58.0	51	2	US-09-101-272G-19	Sequence 19, Appl	512	25.5	58.0	143	2	US-09-101-272G-2	Sequence 2, Appli
440	25.5	58.0	54	1	US-07-791-213D-16	Sequence 16, Appl	513	25.5	58.0	143	6	5223482-20	Patent No. 5223482
441	25.5	58.0	54	1	US-08-293-150A-16	Sequence 16, Appl	514	25.5	58.0	144	6	5187153-18	Patent No. 5187153
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443	25.5	58.0	58	1	US-07-700-528-11	Sequence 11, Appl	516	25.5	58.0	147	2	US-09-331-793-24	Sequence 24, Appl
444	25.5	58.0	58	1	US-08-384-489-11	Sequence 11, Appl	517	25.5	58.0	194	2	US-09-101-272G-80	Sequence 80, Appl
445	25.5	58.0	58	1	US-08-358-160-3	Sequence 3, Appli	518	25.5	58.0	201	2	US-09-101-272G-96	Sequence 96, Appl
446	25.5	58.0	58	1	US-08-358-160-75	Sequence 75, Appl	519	25.5	58.0	208	2	US-09-101-272G-98	Sequence 98, Appl
447	25.5	58.0	58	1	US-08-463-155A-39	Sequence 39, Appl	520	25.5	58.0	229	2	US-09-758-759-67	Sequence 67, Appl
448	25.5	58.0	58	1	US-08-463-432B-39	Sequence 39, Appl	521	25.5	58.0	352	2	US-09-491-479-2	Sequence 2, Appli
449	25.5	58.0	58	1	US-08-676-125A-47	Sequence 47, Appl	522	25.5	58.0	352	2	US-09-514-450-5	Sequence 5, Appli
450	25.5	58.0	58	1	US-08-206-310A-39	Sequence 39, Appl	523	25	56.8	16	2	US-09-233-086-8	Sequence 8, Appli
451	25.5	58.0	58	1	US-08-398-010A-39	Sequence 39, Appl	524	25	56.8	18	2	US-09-140-149-5	Sequence 5, Appli
452	25.5	58.0	58	1	US-08-398-628A-39	Sequence 39, Appl	525	25	56.8	18	2	US-09-615-917-5	Sequence 5, Appli
453	25.5	58.0	58	1	US-08-399-115A-39	Sequence 39, Appl	526	25	56.8	22	1	US-08-019-073-11	Sequence 11, Appl
454	25.5	58.0	58	1	US-09-136-012A-47	Sequence 47, Appl	527	25	56.8	22	4	PCT-US94-01768-11	Sequence 11, Appl
455	25.5	58.0	58	2	US-08-676-124-78	Sequence 78, Appl	528	25	56.8	36	2	US-09-902-540-10471	Sequence 10471, A
456	25.5	58.0	58	2	US-09-414-878-78	Sequence 78, Appl	529	25	56.8	43	2	US-08-580-031A-21	Sequence 21, Appl
457	25.5	58.0	58	2	US-09-240-136-78	Sequence 78, Appl	530	25	56.8	58	2	US-09-621-976-4785	Sequence 4785, Ap
458	25.5	58.0	58	2	US-09-638-770A-78	Sequence 78, Appl	531	25	56.8	63	2	US-09-489-039A-7913	Sequence 7913, Ap
459	25.5	58.0	58	4	US-10-167-351-78	Sequence 78, Appl	532	25	56.8	66	2	US-09-328-352-7435	Sequence 7435, Ap
460	25.5	58.0	58	4	PCT-US92-03132-11	Sequence 11, Appl	533	25	56.8	67	2	US-08-311-731A-221	Sequence 221, App
461	25.5	58.0	65	1	US-08-358-160-152	Sequence 152, App	534	25	56.8	69	2	US-09-248-796A-19724	Sequence 19724, A
462	25.5	58.0	66	1	US-07-791-213D-8	Sequence 8, Appli	535	25	56.8	69	2	US-09-248-796A-26255	Sequence 26255, A
463	25.5	58.0	66	1	US-08-293-150A-8	Sequence 8, Appli	536	25	56.8	73	2	US-10-002-344A-163	Sequence 163, App
464	25.5	58.0	68	1	US-07-972-387-76	Sequence 76, Appl	537	25	56.8	77	2	US-09-270-767-33840	Sequence 33840, A
465	25.5	58.0	68	1	US-08-431-412-76	Sequence 76, Appl	538	25	56.8	77	2	US-09-270-767-49057	Sequence 49057, A

539	25	56.8	79	2	US-09-252-991A-27472	Sequence 27472, A	612	25	56.8	228	2	US-09-990-444-135	Sequence 135, App
540	25	56.8	81	2	US-09-107-532A-4387	Sequence 4387, Ap	613	25	56.8	228	2	US-09-997-133-135	Sequence 135, App
541	25	56.8	88	2	US-09-270-767-59127	Sequence 59127, A	614	25	56.8	228	2	US-09-992-598-135	Sequence 135, App
542	25	56.8	88	2	US-09-248-796A-26638	Sequence 26638, A	615	25	56.8	244	2	US-09-270-767-61941	Sequence 61941, A
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546	25	56.8	89	2	US-09-902-540-10409	Sequence 10409, A	619	25	56.8	252	2	US-09-270-767-33297	Sequence 33297, A
547	25	56.8	94	2	US-09-248-796A-21110	Sequence 21110, A	620	25	56.8	253	2	US-09-902-540-14262	Sequence 14262, A
548	25	56.8	95	2	US-09-270-767-43734	Sequence 43734, A	621	25	56.8	258	2	US-09-248-796A-14789	Sequence 14789, A
549	25	56.8	97	2	US-09-248-796A-25871	Sequence 25871, A	622	25	56.8	263	2	US-09-328-352-4853	Sequence 4853, Ap
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551	25	56.8	106	2	US-09-248-796A-22079	Sequence 22079, A	624	25	56.8	265	2	US-09-504-357-6	Sequence 6, Appli
552	25	56.8	108	6	5284931-5	Patent No. 5284931	625	25	56.8	266	2	US-09-583-110-4232	Sequence 4232, Ap
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555	25	56.8	110	2	US-09-270-767-53896	Sequence 53896, A	628	25	56.8	270	2	US-09-323-872A-38	Sequence 38, Appl
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557	25	56.8	119	2	US-09-902-540-12746	Sequence 12746, A	630	25	56.8	272	2	US-09-270-767-46368	Sequence 46368, A
558	25	56.8	121	2	US-09-134-000C-3573	Sequence 3573, Ap	631	25	56.8	273	2	US-09-538-092-542	Sequence 542, App
559	25	56.8	124	2	US-09-270-767-33010	Sequence 33010, A	632	25	56.8	275	2	US-09-540-236-2926	Sequence 2926, Ap
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562	25	56.8	126	2	US-09-673-395A-562	Sequence 562, App	635	25	56.8	279	2	US-09-489-039A-11400	Sequence 11400, A
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564	25	56.8	136	2	US-09-328-352-8127	Sequence 8127, Ap	637	25	56.8	282	2	US-09-328-352-8059	Sequence 8059, Ap
565	25	56.8	144	2	US-09-543-681A-6045	Sequence 6045, Ap	638	25	56.8	282	2	US-09-489-039A-12241	Sequence 12241, A
566	25	56.8	146	2	US-09-252-991A-25884	Sequence 25884, A	639	25	56.8	283	2	US-09-045-632-27	Sequence 27, Appl
567	25	56.8	151	2	US-09-248-796A-23537	Sequence 23537, A	640	25	56.8	283	2	US-09-270-767-43846	Sequence 43846, A
568	25	56.8	152	2	US-09-248-796A-27566	Sequence 27566, A	641	25	56.8	282	2	US-09-502-540-16595	Sequence 16595, A
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573	25	56.8	163	2	US-10-015-389A-158	Sequence 158, App	646	25	56.8	304	2	US-09-328-352-5720	Sequence 5720, Ap
574	25	56.8	163	2	US-10-006-768A-158	Sequence 158, App	647	25	56.8	304	2	US-09-489-039A-11906	Sequence 11906, A
575	25	56.8	163	2	US-10-015-671A-158	Sequence 158, App	648	25	56.8	305	2	US-09-645-337A-8	Sequence 8, Appli
576	25	56.8	163	2	US-10-015-393A-158	Sequence 158, App	649	25	56.8	307	2	US-09-583-110-3427	Sequence 3427, Ap
577	25	56.8	163	2	US-10-011-833A-158	Sequence 158, App	650	25	56.8	311	2	US-09-107-532A-4543	Sequence 4543, Ap
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581	25	56.8	167	2	US-09-053-197A-21	Sequence 21, Appl	654	25	56.8	317	2	US-09-107-433-4862	Sequence 4862, Ap
582	25	56.8	167	2	US-09-085-761A-21	Sequence 21, Appl	655	25	56.8	318	6	5242798-5	Patent No. 5242798
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584	25	56.8	170	2	US-09-732-210-542	Sequence 542, App	657	25	56.8	326	2	US-09-710-279-254	Sequence 254, App
585	25	56.8	181	2	US-09-902-540-16651	Sequence 16651, A	658	25	56.8	328	2	US-09-513-597A-2	Sequence 2, Appli
586	25	56.8	183	2	US-09-122-443-11	Sequence 11, Appl	659	25	56.8	329	2	US-09-248-796A-15679	Sequence 15679, A
587	25	56.8	183	2	US-09-558-089-11	Sequence 11, Appl	660	25	56.8	335	2	US-09-252-991A-30954	Sequence 30954, A
588	25	56.8	183	2	US-09-558-087-11	Sequence 11, Appl	661	25	56.8	335	2	US-09-513-597A-19	Sequence 19, Appl
589	25	56.8	183	2	US-09-252-991A-19710	Sequence 19710, A	662	25	56.8	337	2	US-09-134-001C-3799	Sequence 3799, Ap
590	25	56.8	183	2	US-09-558-474-11	Sequence 11, Appl	663	25	56.8	337	2	US-09-902-540-15173	Sequence 15173, A
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592	25	56.8	184	2	US-09-558-089-13	Sequence 13, Appl	665	25	56.8	339	2	US-09-252-991A-23085	Sequence 23085, A
593	25	56.8	184	2	US-09-558-087-13	Sequence 13, Appl	666	25	56.8	345	1	US-08-134-570-14	Sequence 14, Appl
594	25	56.8	184	2	US-09-558-474-13	Sequence 13, Appl	667	25	56.8	351	2	US-09-902-540-13214	Sequence 13214, A
595	25	56.8	185	2	US-09-045-632-26	Sequence 26, Appl	668	25	56.8	354	1	US-08-447-702-5	Sequence 5, Appli
596	25	56.8	192	2	US-09-270-767-38246	Sequence 38246, A	669	25	56.8	354	1	US-08-465-615-5	Sequence 5, Appli
597	25	56.8	192	2	US-09-270-767-53463	Sequence 53463, A	670	25	56.8	355	2	US-09-442-349A-107	Sequence 107, App
598	25	56.8	200	2	US-09-562-737-110	Sequence 110, App	671	25	56.8	358	2	US-09-270-767-45720	Sequence 45720, A
599	25	56.8	206	2	US-09-830-230A-294	Sequence 294, App	672	25	56.8	358	2	US-09-949-016-11528	Sequence 11528, A
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602	25	56.8	211	2	US-09-248-796A-18107	Sequence 18107, A	675	25	56.8	362	1	US-08-290-731C-15	Sequence 15, Appl
603	25	56.8	213	2	US-09-508-710-10	Sequence 10, Appl	676	25	56.8	362	2	US-09-442-349A-109	Sequence 109, App
604	25	56.8	215	2	US-09-248-796A-16631	Sequence 16631, A	677	25	56.8	364	2	US-09-583-110-3364	Sequence 3364, App
605	25	56.8	216	1	US-08-840-683-9	Sequence 9, Appli	678	25	56.8	365	2	US-09-248-796A-20907	Sequence 20907, A
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607	25	56.8	216	2	US-09-384-301-9	Sequence 9, Appli	680	25	56.8	369	2	US-09-107-433-3236	Sequence 3236, Ap
608	25	56.8	222	2	US-10-101-464A-720	Sequence 720, App	681	25	56.8	373	2	US-09-252-991A-31094	Sequence 31094, A
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610	25	56.8	223	2	US-09-134-000C-4867	Sequence 4867, Ap	683	25	56.8	374	2	US-09-442-349A-2	Sequence 2, Appli
611	25	56.8	228	2	US-09-991-181-135	Sequence 135, App	684	25	56.8	374	2	US-09-442-349A-5	Sequence 5, Appli

685	25	56.8	374	2	US-09-442-349A-6	Sequence 6, Appli	758	25	56.8	501	2	US-09-903-540-16762	Sequence 16762, A
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687	25	56.8	374	2	US-09-442-349A-20	Sequence 20, Appl	760	25	56.8	502	2	US-09-328-352-5891	Sequence 5891, Ap
688	25	56.8	374	2	US-09-442-349A-21	Sequence 21, Appl	761	25	56.8	502	2	US-09-107-532A-4747	Sequence 4747, Ap
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690	25	56.8	375	2	US-08-872-979-3	Sequence 3, Appli	763	25	56.8	503	2	US-09-583-447A-2	Sequence 2, Appli
691	25	56.8	376	2	US-09-041-718-2	Sequence 2, Appli	764	25	56.8	504	2	US-09-045-632-19	Sequence 19, Appl
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693	25	56.8	379	2	US-09-328-352-8215	Sequence 8215, Ap	766	25	56.8	507	2	US-09-107-532A-4386	Sequence 4386, Ap
694	25	56.8	387	2	US-09-248-796A-17976	Sequence 17976, A	767	25	56.8	508	2	US-09-949-016-7092	Sequence 7092, Ap
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697	25	56.8	399	2	US-09-543-681A-6125	Sequence 6125, Ap	770	25	56.8	525	2	US-09-328-857A-3	Sequence 3, Appli
698	25	56.8	399	2	US-09-513-597A-1	Sequence 1, Appli	771	25	56.8	528	2	US-09-248-796A-15397	Sequence 15397, A
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703	25	56.8	405	2	US-09-902-540-15722	Sequence 15722, A	776	25	56.8	532	2	US-08-329-892B-33	Sequence 33, Appl
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706	25	56.8	413	2	US-09-248-796A-23092	Sequence 23092, A	779	25	56.8	545	2	US-10-020-445A-254	Sequence 254, App
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708	25	56.8	417	2	US-09-605-703B-2300	Sequence 2300, Ap	781	25	56.8	554	2	US-09-949-016-11161	Sequence 11161, A
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712	25	56.8	424	1	US-08-879-337-5	Sequence 5, Appli	785	25	56.8	570	2	US-09-368-408-7	Sequence 7, Appli
713	25	56.8	426	2	US-09-252-991A-31959	Sequence 31959, A	786	25	56.8	570	2	US-09-489-039A-7328	Sequence 7328, Ap
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715	25	56.8	430	2	US-09-107-532A-5107	Sequence 5107, Ap	788	25	56.8	579	2	US-09-792-024-97	Sequence 97, Appl
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717	25	56.8	434	2	US-09-433-241A-14	Sequence 14, Appl	790	25	56.8	583	2	US-09-598-419-333	Sequence 353, App
718	25	56.8	434	2	US-09-540-236-3040	Sequence 3040, Ap	791	25	56.8	584	1	US-08-426-819A-36	Sequence 36, Appl
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721	25	56.8	438	2	US-09-061-154-2	Sequence 2, Appli	794	25	56.8	585	1	US-08-455-355-2	Sequence 2, Appli
722	25	56.8	441	2	US-09-061-154-4	Sequence 4, Appli	795	25	56.8	585	2	US-09-367-513-2	Sequence 2, Appli
723	25	56.8	441	2	US-09-061-154-4	Sequence 4, Appli	796	25	56.8	585	2	US-10-407-339-2	Sequence 2, Appli
724	25	56.8	444	2	US-09-328-352-7914	Sequence 7914, Ap	797	25	56.8	589	2	US-09-643-657-14	Sequence 14, Appl
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726	25	56.8	442	1	US-08-693-457-4	Sequence 4, Appli	799	25	56.8	599	2	US-09-045-632-28	Sequence 28, Appl
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735	25	56.8	455	2	US-09-328-352-5160	Sequence 5160, Ap	808	25	56.8	619	2	US-09-543-681A-5503	Sequence 5503, Ap
736	25	56.8	455	2	US-09-248-796A-16155	Sequence 16155, A	809	25	56.8	619	2	US-09-489-039A-12704	Sequence 12704, A
737	25	56.8	456	2	US-09-134-000C-5697	Sequence 5697, Ap	810	25	56.8	622	1	US-08-426-819A-35	Sequence 35, Appl
738	25	56.8	456	2	US-09-270-767-60481	Sequence 60481, A	811	25	56.8	622	2	US-09-513-597A-21	Sequence 21, Appl
739	25	56.8	456	2	US-10-017-754-1925	Sequence 1925, Ap	812	25	56.8	622	2	US-09-949-016-6660	Sequence 6660, Ap
740	25	56.8	456	2	US-09-991-181-248	Sequence 248, App	813	25	56.8	624	2	US-09-525-305-49	Sequence 49, Appl
741	25	56.8	456	2	US-09-990-444-248	Sequence 248, App	814	25	56.8	626	2	US-09-949-016-6213	Sequence 6213, Ap
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747	25	56.8	468	2	US-09-489-039A-14323	Sequence 14323, A	820	25	56.8	631	2	US-09-720-317A-29	Sequence 29, Appl
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749	25	56.8	470	2	US-09-107-532A-5780	Sequence 5780, Ap	822	25	56.8	642	2	US-09-045-632-35	Sequence 35, Appl
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753	25	56.8	484	2	US-09-543-681A-4699	Sequence 4699, Ap	826	25	56.8	656	1	US-08-533-669A-6	Sequence 6, Appli
754	25	56.8	498	2	US-08-657-749D-23	Sequence 23, Appl	827	25	56.8	656	2	US-09-183-861-6	Sequence 6, Appli
755	25	56.8	499	2	US-09-252-991A-31820	Sequence 31820, A	828	25	56.8	656	2	US-09-022-765-6	Sequence 6, Appli
756	25	56.8	499	2	US-09-540-236-3217	Sequence 3217, Ap	829	25	56.8	656	2	US-09-551-974A-6	Sequence 6, Appli
757	25	56.8	501	1	US-08-408-095-31	Sequence 31, Appl	830	25	56.8	656	2	US-09-565-501A-6	Sequence 6, Appli



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832	25	56.8	656	2	US-09-874-923-6	Sequence 6, Appli	905	25	56.8	1021	2	US-09-252-991A-27405	Sequence 27405, A
833	25	56.8	656	2	US-08-798-841-6	Sequence 6, Appli	906	25	56.8	1038	2	US-09-538-092-487	Sequence 487, App
834	25	56.8	659	2	US-09-949-016-7616	Sequence 7616, Ap	907	25	56.8	1040	2	US-09-564-805-238	Sequence 238, App
835	25	56.8	659	2	US-09-949-016-7617	Sequence 7617, Ap	908	25	56.8	1048	2	US-09-356-952-5	Sequence 5, Appli
836	25	56.8	660	2	US-09-248-796A-14578	Sequence 14578, A	909	25	56.8	1050	2	US-09-045-632-49	Sequence 49, Appli
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838	25	56.8	662	2	US-10-098-808-3	Sequence 3, Appli	911	25	56.8	1060	2	US-09-248-796A-16624	Sequence 16624, A
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841	25	56.8	667	2	US-09-902-540-15678	Sequence 15678, A	914	25	56.8	1112	2	US-09-045-632-2	Sequence 2, Appli
842	25	56.8	674	2	US-08-961-083-200	Sequence 200, App	915	25	56.8	1112	2	US-09-045-632-3	Sequence 3, Appli
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845	25	56.8	674	2	US-09-765-272A-200	Sequence 200, App	918	25	56.8	1137	2	US-09-949-002-542	Sequence 542, App
846	25	56.8	680	2	US-09-270-767-43944	Sequence 43944, A	919	25	56.8	1171	2	US-09-949-016-10019	Sequence 10019, A
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849	25	56.8	701	2	US-09-183-861-16	Sequence 16, Appli	922	25	56.8	1198	2	US-09-949-016-6109	Sequence 6109, Ap
850	25	56.8	701	2	US-09-022-765-16	Sequence 16, Appli	923	25	56.8	1225	2	US-09-949-016-9468	Sequence 9468, Ap
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852	25	56.8	701	2	US-09-565-501A-16	Sequence 16, Appli	925	25	56.8	1247	1	US-08-323-460A-10	Sequence 10, Appli
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854	25	56.8	701	2	US-09-874-923-16	Sequence 16, Appli	927	25	56.8	1247	2	US-08-461-145C-10	Sequence 10, Appli
855	25	56.8	701	2	US-08-798-841-16	Sequence 16, Appli	928	25	56.8	1286	2	US-09-170-496D-291	Sequence 291, App
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860	25	56.8	704	2	US-09-551-974A-17	Sequence 17, Appli	933	25	56.8	1377	2	US-09-171-164-467	Sequence 467, App
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862	25	56.8	704	2	US-09-639-206A-17	Sequence 17, Appli	935	25	56.8	1419	2	US-10-197-220-173	Sequence 173, App
863	25	56.8	704	2	US-09-874-923-17	Sequence 17, Appli	936	25	56.8	1427	2	US-09-551-974A-97	Sequence 97, Appli
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868	25	56.8	720	2	US-09-990-444-231	Sequence 231, App	941	25	56.8	1469	2	US-09-262-537-58	Sequence 58, Appli
869	25	56.8	720	2	US-09-997-333-231	Sequence 231, App	942	25	56.8	1471	2	US-08-811-519-1	Sequence 1, Appli
870	25	56.8	726	2	US-09-992-598-231	Sequence 231, App	943	25	56.8	1481	2	US-09-231-899-70	Sequence 70, Appli
871	25	56.8	726	2	US-09-352-991A-26767	Sequence 26767, A	944	25	56.8	1500	2	US-09-323-472A-2	Sequence 2, Appli
872	25	56.8	743	2	US-09-248-796A-15523	Sequence 15523, A	945	25	56.8	1500	2	US-09-323-472A-4	Sequence 4, Appli
873	25	56.8	753	2	US-09-538-092-31	Sequence 31, Appli	946	25	56.8	1500	2	US-09-323-472A-12	Sequence 12, Appli
874	25	56.8	792	2	US-09-994-192-2	Sequence 2, Appli	947	25	56.8	1500	2	US-09-323-472A-14	Sequence 14, Appli
875	25	56.8	797	2	US-09-994-192-4	Sequence 4, Appli	948	25	56.8	1500	2	US-09-585-077C-2	Sequence 2, Appli
876	25	56.8	818	2	US-09-045-632-25	Sequence 25, Appli	949	25	56.8	1500	2	US-09-585-077C-4	Sequence 4, Appli
877	25	56.8	821	2	US-09-556-877-195	Sequence 195, App	950	25	56.8	1500	2	US-09-585-077C-12	Sequence 12, Appli
878	25	56.8	821	2	US-09-620-412C-195	Sequence 195, App	951	25	56.8	1500	2	US-09-585-077C-14	Sequence 14, Appli
879	25	56.8	821	2	US-09-598-419-195	Sequence 195, App	952	25	56.8	1500	2	US-09-538-092-1051	Sequence 1051, Ap
880	25	56.8	831	2	US-09-269-861A-8	Sequence 8, Appli	953	25	56.8	1554	2	US-09-252-991A-26814	Sequence 26814, A
881	25	56.8	831	2	US-09-949-002-328	Sequence 328, App	954	25	56.8	1597	2	US-09-423-890-13	Sequence 13, Appli
882	25	56.8	861	2	US-09-045-632-34	Sequence 34, Appli	955	25	56.8	1597	2	US-08-628-829-14	Sequence 14, Appli
883	25	56.8	862	2	US-09-949-002-427	Sequence 427, App	956	25	56.8	1602	2	US-09-269-874A-7	Sequence 7, Appli
884	25	56.8	884	2	US-09-538-092-172	Sequence 172, App	957	25	56.8	1621	2	US-09-269-874A-5	Sequence 5, Appli
885	25	56.8	890	1	US-08-472-934-8	Sequence 8, Appli	958	25	56.8	1639	2	US-09-269-874A-3	Sequence 3, Appli
886	25	56.8	890	1	US-08-323-460A-8	Sequence 8, Appli	959	25	56.8	1641	2	US-09-551-974A-96	Sequence 96, Appli
887	25	56.8	890	1	US-08-461-145C-8	Sequence 8, Appli	960	25	56.8	1641	2	US-09-565-501A-96	Sequence 96, Appli
888	25	56.8	890	2	US-08-461-145C-8	Sequence 8, Appli	961	25	56.8	1641	2	US-09-639-206A-96	Sequence 96, Appli
889	25	56.8	890	2	US-08-628-829-12	Sequence 12, Appli	962	25	56.8	1641	2	US-09-874-923-96	Sequence 96, Appli
890	25	56.8	892	2	US-09-538-092-678	Sequence 678, App	963	25	56.8	1645	2	US-09-976-594-769	Sequence 769, App
891	25	56.8	909	2	US-10-163-214-2	Sequence 2, Appli	964	25	56.8	1753	2	US-09-248-796A-19154	Sequence 19154, A
892	25	56.8	918	2	US-09-045-632-21	Sequence 21, Appli	965	25	56.8	1776	2	US-09-556-877-179	Sequence 179, App
893	25	56.8	923	2	US-09-949-016-8986	Sequence 8986, Ap	966	25	56.8	1776	2	US-09-620-412C-179	Sequence 179, App
894	25	56.8	948	1	US-08-698-551-14	Sequence 14, Appli	967	25	56.8	1776	2	US-09-598-419-179	Sequence 179, App
895	25	56.8	948	1	US-08-602-228-14	Sequence 14, Appli	968	25	56.8	1803	2	US-09-902-540-15978	Sequence 15978, A
896	25	56.8	948	1	US-08-533-901B-14	Sequence 14, Appli	969	25	56.8	1867	2	US-09-824-574-5	Sequence 5, Appli
897	25	56.8	948	1	US-08-839-032A-14	Sequence 14, Appli	970	25	56.8	1884	2	US-09-538-092-1329	Sequence 1329, Ap
898	25	56.8	948	1	US-08-839-031A-14	Sequence 14, Appli	971	25	56.8	1927	2	US-10-152-886-63	Sequence 63, Appli
899	25	56.8	948	2	US-09-185-258C-14	Sequence 14, Appli	972	25	56.8	2214	2	US-09-902-540-15988	Sequence 15988, A
900	25	56.8	948	4	PCT-US95-1272A-14	Sequence 14, Appli	973	25	56.8	2233	1	US-08-569-853-1	Sequence 1, Appli
901	25	56.8	956	2	US-09-902-540-10395	Sequence 10395, A	974	25	56.8	2233	1	US-08-569-853-2	Sequence 2, Appli
902	25	56.8	961	2	US-09-045-632-33	Sequence 33, Appli	975	25	56.8	2233	1	US-08-987-439-1	Sequence 1, Appli
903	25	56.8	990	2	US-09-248-796A-20230	Sequence 20230, A	976	25	56.8	2471	2	US-09-112-450-4	Sequence 4, Appli

977 25 56.8 2471 2 US-09-419-291A-4 Sequence 4, Appli  
978 25 56.8 2471 2 US-10-116-048-4 Sequence 4, Appli  
979 25 56.8 2516 4 PCT-US94-00198-3 Sequence 10280, A  
980 25 56.8 2938 2 US-09-949-016-10280 Sequence 3, Appli  
981 25 56.8 2942 2 US-09-902-540-9733 Sequence 9733, Ap  
982 25 56.8 3056 1 US-08-508-836A-8 Sequence 8, Appli  
983 25 56.8 3056 1 US-08-629-001A-3 Sequence 3, Appli  
984 25 56.8 3056 1 US-08-874-266-2 Sequence 2, Appli  
985 25 56.8 3056 2 US-08-642-274D-3 Sequence 3, Appli  
986 25 56.8 3056 2 US-08-952-127-3 Sequence 3, Appli  
987 25 56.8 3056 2 US-08-952-014C-3 Sequence 3, Appli  
988 25 56.8 3056 2 US-09-360-416-2 Sequence 2, Appli  
989 25 56.8 3056 2 US-08-984-090-2 Sequence 2, Appli  
990 25 56.8 3056 2 US-10-351-733-1 Sequence 1, Appli  
991 25 56.8 3056 2 US-10-175-225-2 Sequence 2, Appli  
992 25 56.8 3057 2 US-09-360-416-3 Sequence 3, Appli  
993 25 56.8 3066 2 US-10-175-225-3 Sequence 12, Appli  
994 25 56.8 3066 2 US-08-952-127-12 Sequence 172, App  
995 25 56.8 3092 2 US-09-487-558B-172 Sequence 84, Appli  
996 25 56.8 4654 2 US-08-476-515A-84 Sequence 84, Appli  
997 25 56.8 4655 2 US-08-652-877-84 Sequence 86, Appli  
998 25 56.8 4655 2 US-08-652-877-86 Sequence 86, Appli  
999 25 56.8 4655 2 US-08-652-877-88 Sequence 88, Appli  
1000 25 56.8 4655 2 US-08-652-877-90 Sequence 90, Appli

ALIGNMENTS

RESULT 1  
US-09-248-796A-18548  
; Sequence 18548, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18548  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-18548

Query Match 75.0%; Score 33; DB 2; Length 420;  
Best Local Similarity 85.7%; Pred. No. 93;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFPAV 9  
Db 339 QLEFPAI 345

RESULT 2  
US-09-252-991A-27064  
; Sequence 27064, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18

105 ; PRIOR APPLICATION NUMBER: US 60/094,190  
106 ; PRIOR FILING DATE: 1998-07-27  
107 ; NUMBER OF SEQ ID NOS: 33142  
108 ; SEQ ID NO 27064  
109 ; LENGTH: 419  
110 ; TYPE: PRT  
111 ; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27064

Query Match 72.7%; Score 32; DB 2; Length 419;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEFPAV 9  
Db 226 LQLEFPAI 233

RESULT 3  
US-09-270-767-43156  
; Sequence 43156, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43156  
; LENGTH: 523  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-43156

Query Match 72.7%; Score 32; DB 2; Length 523;  
Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFPA 8  
Db 477 FLQLEFPA 484

RESULT 4  
US-09-949-016-9814  
; Sequence 9814, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9814  
; LENGTH: 596  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9814

Query Match 72.7%; Score 32; DB 2; Length 596;

Best Local Similarity 85.7%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0;

Qy 1 FLOLEPD 7  
Db 352 FLQLKFD 358

RESULT 5  
US-09-949-016-6008  
; Sequence 6008, Application US/09949016  
; Patent No. 8812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6008  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6008

Query Match 72.7%; Score 32; DB 2; Length 599;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0;

Qy 1 FLOLEPD 7  
Db 355 FLQLKFD 361

RESULT 6  
US-09-919-060-13  
; Sequence 13, Application US/09919060  
; Patent No. 6638744  
; GENERAL INFORMATION:  
; APPLICANT: Wisniewski, Nancy  
; APPLICANT: Brandt, Kevin S.  
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES  
; FILE REFERENCE: AD-1  
; CURRENT APPLICATION NUMBER: US/09/919,060  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: 60/224,486  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 633  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-919-060-13

Query Match 72.7%; Score 32; DB 2; Length 633;  
Best Local Similarity 85.7%; Pred. No. 2.2e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0;

Qy 1 FLOLEPD 7  
Db 389 FLQLKFD 395

RESULT 7

US-09-051-019-2  
; Sequence 2, Application US/09051019  
; Patent No. 6103229  
; GENERAL INFORMATION:  
; APPLICANT: KAHMANN, Regine and QUADBECK-SEEGER, Claudia  
; TITLE OF INVENTION: Regulatory gene from Ustilago maydis  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Keil & Weinkauff  
; STREET: 1101 Connecticut Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage  
; COMPUTER: IBM AT-compatible, Pentium processor  
; OPERATING SYSTEM: Windows 98  
; SOFTWARE: WordPerfect version 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/051,019  
; FILING DATE: 31-MAR-1998  
; CLASSIFICATION:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2289 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-051-019-2

Query Match 72.7%; Score 32; DB 2; Length 2289;  
Best Local Similarity 66.7%; Pred. No. 8.1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 1;

Qy 1 FLOLEPD 9  
Db 1510 FLPLEWD 1518

RESULT 8  
US-07-667-276A-2  
; Sequence 2, Application US/07667276A  
; Patent No. 5470971  
; GENERAL INFORMATION:  
; APPLICANT: Kondo, Keiji  
; APPLICANT: Inouye, Masayori  
; TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING  
; THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND  
; APPLICATIONS  
; TITLE OF INVENTION: APPLICATIONS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Weiser & Associates  
; STREET: 230 S. Fifteenth Street, Suite 500  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/667,276A  
; FILING DATE: 11-MAR-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weiser, Gerard J.  
; REGISTRATION NUMBER: 19,763  
; REFERENCE/DOCKET NUMBER: 377.5351P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-875-8383  
; TELEFAX: 215-875-8394

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 210 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-07-667-276A-2

Query Match          70.5%; Score 31; DB 1; Length 210;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLEFDV 9
      ||::|||:
Db      78 FSELDFDAI 86

RESULT 9
US-09-543-681A-7259
; Sequence 7259, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7259
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7259

Query Match          70.5%; Score 31; DB 2; Length 287;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 QLEFDV 9
      ||::|||:
Db      139 QVEFDV 145

RESULT 10
US-09-270-767-32891
; Sequence 32891, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32891
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32891

Query Match          70.5%; Score 31; DB 2; Length 379;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLEFDV 9
      ||::|||:
Db      360 FLSMQYDAV 368

RESULT 11
US-09-270-767-48108
; Sequence 48108, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48108
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48108

Query Match          70.5%; Score 31; DB 2; Length 379;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLEFDV 9
      ||::|||:
Db      360 FLSMQYDAV 368

RESULT 12
US-09-252-991A-17710
; Sequence 17710, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17710
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17710

Query Match          70.5%; Score 31; DB 2; Length 524;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLEFDV 9
      ||::|||:
Db      245 FLQVEVDAL 253

RESULT 13
US-09-489-039A-12742
; Sequence 12742, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12742
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; LENGTH: 803
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12742

Query Match          70.5%; Score 31; DB 2; Length 803;
Best Local Similarity 77.8%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLOLEFDVAV 9
Db 577 FLHLLFDVAV 585

RESULT 14
US-09-621-976-6999
; Sequence 6999, Application US/09621976
; Patent No. 8639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.V.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GNSSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6999
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6999

Query Match          68.2%; Score 30; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEFD 7
Db 25 LQLEFD 30

RESULT 15
US-09-303-518D-160
; Sequence 160, Application US/09303518D
; Patent No. 8914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Maignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIRO160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 160
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-160

Query Match          68.2%; Score 30; DB 2; Length 237;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QLEFDVAV 9
Db 142 QLEFEAV 148

RESULT 16
US-09-584-568C-6
; Sequence 6, Application US/09584568C
; Patent No. 6506657
; GENERAL INFORMATION:
; APPLICANT: Gluckmann, Maria, Alexandra et al.
; TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USBS THEREFOR
; FILE REFERENCE: MNI-140
; CURRENT APPLICATION NUMBER: US/09/584,568C
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/193,954
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-584-568C-6

Query Match          68.2%; Score 30; DB 2; Length 299;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLEFDVAV 9
Db 266 FPQVQFDVAV 274

RESULT 17
US-09-194-146-6
; Sequence 6, Application US/09194146
; Patent No. 6458557
; GENERAL INFORMATION:
; APPLICANT: Miller, Brian
; APPLICANT: Diaz-Torres, Maria
; TITLE OF INVENTION: Gram-Positive Microorganism Formate Pathway
; FILE REFERENCE: GC395-US
; CURRENT APPLICATION NUMBER: US/09/194,146
; CURRENT FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: GB 9724627.6
; PRIOR FILING DATE: 1997-11-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Bacillus
US-09-194-146-6

Query Match          68.2%; Score 30; DB 2; Length 300;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLEFD 7
Db 63 FLRIEFD 69

RESULT 18
US-09-248-796A-17292
; Sequence 17292, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
```

; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 17292  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-17292

Query Match 68.2%; Score 30; DB 2; Length 333;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLEF 6  
|||:||||  
DB 129 FLOLEF 134

RESULT 19  
US-09-134-001C-3403  
; Sequence 3403, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3403  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3403

Query Match 68.2%; Score 30; DB 2; Length 370;  
Best Local Similarity 75.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEPDAV 9  
|||:||||  
DB 5 LQLEPDAV 12

RESULT 20  
US-09-710-279-696  
; Sequence 696, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 696  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-696

Query Match 68.2%; Score 30; DB 2; Length 370;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEPDAV 9  
|||:||||  
DB 5 LQLEPDAV 12

RESULT 21  
US-09-710-279-1328  
; Sequence 1328, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1328  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-1328

Query Match 68.2%; Score 30; DB 2; Length 370;  
Best Local Similarity 75.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEPDAV 9  
|||:||||  
DB 5 LQLEPDAV 12

RESULT 22  
US-09-602-777A-130  
; Sequence 130, Application US/09602777A  
; Patent No. 6831165  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION  
; FILE REFERENCE: BGI-128CP  
; CURRENT APPLICATION NUMBER: US/09/602,777A  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932125.6  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932126.4  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932127.2  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932128.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932129.9  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: DE 19932226.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932920.6  
; PRIOR FILING DATE: 1999-07-14

; PRIOR APPLICATION NUMBER: DE 19932922.2  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932924.9  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932928.1  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932930.3  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932933.8  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932935.4  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932973.7  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933002.6  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933003.4  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933005.0  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933006.9  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19941378.9  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941390.8  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941391.6  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19942088.2  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 442  
; SEQ ID NO 130  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-602-777A-130

Query Match 68.2%; Score 30; DB 2; Length 472;  
Best Local Similarity 85.7%; Pred. No. 4.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
Db 140 FQOLEFD 146

RESULT 23  
US-09-602-777A-132  
; Sequence 132, Application US/09602777A  
; Patent No. 6831165  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; FILE REFERENCE: INVOLVED IN HOMEOSTASIS AND ADAPTATION  
; FILE REFERENCE: BGI-128CP  
; CURRENT APPLICATION NUMBER: US/09/602,777A  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: DE 19931636.8  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932125.6  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932126.4  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932127.2  
; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: DE 19932128.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932129.9  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: DE 19932226.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932920.6  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932922.2  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932924.9  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932928.1  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932930.3  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932933.8  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932935.4  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932973.7  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933002.6  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933003.4  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933005.0  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933006.9  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19941378.9  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941390.8  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941391.6  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19942088.2  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 442  
; SEQ ID NO 132  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-602-777A-132

Query Match 68.2%; Score 30; DB 2; Length 472;  
Best Local Similarity 85.7%; Pred. No. 4.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
Db 140 FQOLEFD 146

RESULT 24  
US-09-515-806-3  
; Sequence 3, Application US/09515806  
; Patent No. 6864078  
; GENERAL INFORMATION:  
; APPLICANT: COOK, WILLIAM J.  
; APPLICANT: KAPPELLER-LIBERMANN, ROSANA  
; TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR  
; FILE REFERENCE: 38155-20002.00  
; CURRENT APPLICATION NUMBER: US/09/515,806  
; CURRENT FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 548  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-09-515-806-3

Query Match 68.2%; Score 30; DB 2; Length 548;  
Best Local Similarity 75.0%; Pred. No. 4.8e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLEFDA 8  
|||:|:  
Db 486 FLSLEWDA 493

## RESULT 25

US-09-516-914-21  
; Sequence 21, Application US/09516914  
; Patent No. 633401  
; GENERAL INFORMATION:  
; APPLICANT: Breinig, Sabine  
; TITLE OF INVENTION: Phenol-induced Proteins of Thauera aromatica  
; FILE REFERENCE: BC1006 US NA  
; CURRENT APPLICATION NUMBER: US/09/516,914  
; EARLIER FILING DATE: 2000-03-01  
; EARLIER FILING DATE: 60/122,952  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 21  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Thauera aromatica  
US-09-516-914-21

Query Match 68.2%; Score 30; DB 2; Length 582;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLEFD 7  
|||||  
Db 109 LQLEFD 114

## RESULT 26

US-09-976-594-793  
; Sequence 793, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 793  
; LENGTH: 1176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6673549 1806212CD1  
US-09-976-594-793

Query Match 68.2%; Score 30; DB 2; Length 1176;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLEFD 7  
|||||  
Db 1010 LQLEFD 1015

## RESULT 27

US-09-949-016-6255  
; Sequence 6255, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6255  
; LENGTH: 1634  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6255

Query Match 68.2%; Score 30; DB 2; Length 1634;  
Best Local Similarity 62.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLEFD 9  
|||:|:  
Db 30 LQMEYDAL 37

## RESULT 28

US-09-515-806-2  
; Sequence 2, Application US/09515806  
; Patent No. 6864078  
; GENERAL INFORMATION:  
; APPLICANT: COOK, WILLIAM J.  
; TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR  
; FILE REFERENCE: 38155-20002.00  
; CURRENT APPLICATION NUMBER: US/09/515,806  
; CURRENT FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1643  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-515-806-2

Query Match 68.2%; Score 30; DB 2; Length 1643;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLEFDA 8  
|||:|:  
Db 1587 FLSLEWDA 1594

## RESULT 29

US-09-515-806-4  
; Sequence 4, Application US/09515806  
; Patent No. 6864078  
; GENERAL INFORMATION:  
; APPLICANT: COOK, WILLIAM J.  
; TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR  
; FILE REFERENCE: 38155-20002.00  
; CURRENT APPLICATION NUMBER: US/09/515,806



```
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1648
; TYPE: PRT
; ORGANISM: Murine Species
US-09-515-806-4

Query Match      68.2%; Score 30; DB 2; Length 1648;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLOLEFDA 8
DB      1586 FLSLEWDA 1593

RESULT 30
US-09-949-016-11387
; Sequence 11387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11387
; LENGTH: 1650
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11387

Query Match      68.2%; Score 30; DB 2; Length 1650;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 LQLEFDV 9
DB      46 LQMEYDAL 53

RESULT 31
US-09-513-999C-7337
; Sequence 7337, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7337
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-513-999C-7337

Query Match      65.9%; Score 29; DB 2; Length 57;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLOLEFDA 8
DB      32 FLNLEMDA 39

RESULT 32
US-09-902-540-10858
; Sequence 10858, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10858
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10858

Query Match      65.9%; Score 29; DB 2; Length 122;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LQLEFDA 8
DB      35 LQIDFDA 41

RESULT 33
US-09-302-769-29
; Sequence 29, Application US/09302769
; Patent No. 6323317
; GENERAL INFORMATION:
; APPLICANT: HILTON, Douglas J
; APPLICANT: ALEXANDER, Warren S
; APPLICANT: VINEY, Elizabeth M
; APPLICANT: WILLSON, Tracey A
; APPLICANT: RICHARDSON, Rachael T
; APPLICANT: STARR, Robyn
; APPLICANT: NICHOLSON, Sandra E
; APPLICANT: METCALF, Donald
; APPLICANT: NICOLA, Nicolas
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
; FILE REFERENCE: 10976Z
; CURRENT APPLICATION NUMBER: US/09/302,769
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 08/962,560
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mouse
US-09-302-769-29

Query Match      65.9%; Score 29; DB 2; Length 130;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 FLQLRFD 7
Db      120 FLQLDFE 126

RESULT 34
US-08-962-560C-29
; Sequence 29, Application US/08962560C
; Patent No. 6905842
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Alexander, Warren S.
; APPLICANT: Viney, Elizabeth M.
; APPLICANT: Wilson, Tracy A.
; APPLICANT: Richardson, Rachel
; APPLICANT: Starr, Robyn
; APPLICANT: Nicholson, Sandra E.
; APPLICANT: Metcalf, Donald
; APPLICANT: Nicola, Nicos A.
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
; FILE REFERENCE: Davies Collison Cave
; CURRENT APPLICATION NUMBER: US/08/962,560C
; CURRENT FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-962-560C-29

Query Match      65.9%; Score 29; DB 2; Length 130;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLRFD 7
Db      120 FLQLDFE 126

RESULT 35
US-09-270-767-60072
; Sequence 60072, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60072
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-60072

Query Match      65.9%; Score 29; DB 2; Length 134;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LQLEFDV 9
Db      87 LQLELDSV 94

RESULT 36
US-09-621-976-6981
; Sequence 6981, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6981
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6981

Query Match      65.9%; Score 29; DB 2; Length 141;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LQLEFDV 9
Db      79 LQMEFKAV 86

RESULT 37
US-09-621-976-6982
; Sequence 6982, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6982
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6982

Query Match      65.9%; Score 29; DB 2; Length 141;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LQLEFDV 9
Db      79 LQMEFKAV 86

RESULT 38
US-09-513-999C-7895
; Sequence 7895, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7895
; LENGTH: 141
; TYPE: PRT

```

; ORGANISM: Homo sapiens  
US-09-513-999C-7895

Query Match 65.9%; Score 29; DB 2; Length 141;  
Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLEFDV 9  
||:||||  
Db 79 LQMEFKV 86

## RESULT 39

US-09-502-540-16742  
; Sequence 16742, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 16742

; LENGTH: 163

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-502-540-16742

## Query Match

Best Local Similarity 85.7%; Score 29; DB 2; Length 163;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLOLEFD 7  
|||:||||  
Db 19 FLOHEFD 25

## RESULT 40

US-09-153-447-21

; Sequence 21, Application US/09153447

; Patent No. 6610838

; GENERAL INFORMATION:

; APPLICANT: BERGSTROM, Sven

; TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA

; FILE REFERENCE: 454312-3130.1

; CURRENT APPLICATION NUMBER: US/09/153,447

; CURRENT FILING DATE: 1998-09-15

; EARLIER APPLICATION NUMBER: 60/059,036

; EARLIER FILING DATE: 1997-09-10

; EARLIER APPLICATION NUMBER: 1041/97

; EARLIER FILING DATE: 1997-09-10

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 178

; TYPE: PRT

; ORGANISM: Borrelia afzelii

US-09-153-447-21

## Query Match

Best Local Similarity 77.8%; Score 29; DB 2; Length 178;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLOLEFDV 9  
|||:||||  
Db 72 FLILGFDV 80

## RESULT 41

US-09-489-039A-9443

; Sequence 9443, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 9443

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-9443

## Query Match

Best Local Similarity 65.9%; Score 29; DB 2; Length 185;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLOLEFDA 8  
||:||||  
Db 170 FMQLQLDA 177

## RESULT 42

US-09-328-352-7485

; Sequence 7485, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 7485

; LENGTH: 212

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-7485

## Query Match

Best Local Similarity 65.9%; Score 29; DB 2; Length 212;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLOLEFDV 9  
|||:||||  
Db 88 FLQLSPFAI 96

## RESULT 43

US-08-622-352A-3

; Sequence 3, Application US/08622352A

; Patent No. 5824546

; GENERAL INFORMATION:

; APPLICANT: Bishai, William R.

; APPLICANT: DeMaio, James

; TITLE OF INVENTION: REGULATION OF A SIGMA FACTOR

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillabury Madison & Sutro, L.L.P.

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

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, ZIP: 20005-3918
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, COMPUTER READABLE FORM:
,
, MEDIUM TYPE: Floppy disk
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, COMPUTER: IBM PC compatible-
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, OPERATING SYSTEM: PC-DOS/MS-DOS
,
, SOFTWARE: Word Perfect
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, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/08/622,352A
,
, FILING DATE: 27-MAR-1996
,
, CLASSIFICATION: 435
,
, INFORMATION FOR SEQ ID NO: 3:
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, SEQUENCE CHARACTERISTICS:
,
, LENGTH: 242 amino acids
,
, TYPE: amino acid
,
, TOPOLOGY: linear
,
, MOLECULE TYPE: protein
,
, HYPOTHETICAL: NO
,
, ANTI-SENSE: NO
,
, ORIGINAL SOURCE:
,
, ORGANISM: Mycobacterium tuberculosis
,
, US-08-622-352A-3

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Query Match 65.9%; Score 29; DB 1; Length 242;  
Best Local Similarity 66.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLEF DAV 9  
Db 139 FEDLDF DAV 147

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RESULT 44
US-08-826-390-3
; Sequence 3, Application US/08826390
; Patent No. 6004764
; GENERAL INFORMATION:
; APPLICANT: Bishai, William R.
; APPLICANT: Young, Douglas B.
; APPLICANT: Zhang, Ying
; APPLICANT: Demato, James
; TITLE OF INVENTION: Stationary
; TITLE OF INVENTION: Sigma Factor
; TITLE OF INVENTION: Regulation
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pillsbury Madison
; STREET: 1100 New York Avenue,
; CITY: Washington
; STATE: DC
; COUNTRY: USA

```

; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Mycobacterium tuberculosis  
 US-08-826-390-3

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Query Match      65.9%; Score 29; DB 2; Length 242;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 FLQLEFDV 9  
| : |||  
Db 139 FEDLDFDV 147

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RESULT 45
US-09-902-540-11549
; Sequence 11549, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11549
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11549

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Query Match      65.9%; Score 29; DB 2; Length 257;
Best Local Similarity 77.8%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	1	FLQLEFDV	9
Db	200	FLVDEFDV	208

```

RESULT 46
US-09-540-236-3467
; Sequence 3467, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3467
; LENGTH: 316
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3467

```

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Query Match      65.9%; Score 29; DB 2; Length 316;
Best Local Similarity 75.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 FLQLEFDA 8  
|||  
Db 223 FLPAEFDA 230

RESULT 47

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US-09-270-767-44624
; Sequence 44624, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44624
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44624

Query Match          65.9%; Score 29; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LQLEFDV 9
      ||||| |
Db      342 LQLEDSV 349

RESULT 48
US-09-252-991A-19612
; Sequence 19612, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19612
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19612

Query Match          65.9%; Score 29; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLOLEFDV 9
      ||||| |
Db      247 FLDLQVDV 255

RESULT 49
US-09-107-532A-6186
; Sequence 6186, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

US-09-107-532A-7248
; Sequence 7248, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6186:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...467
SEQUENCE DESCRIPTION: SEQ ID NO: 6186:
US-09-107-532A-6186

Query Match          65.9%; Score 29; DB 2; Length 467;
Best Local Similarity 55.8%; Pred. No. 6.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLOLEFDV 9
      ||||| |
Db      304 FIQVAFV 312

RESULT 50
US-09-107-532A-7248
; Sequence 7248, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
```

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;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ariniello, Pamela Deneke
;   REGISTRATION NUMBER: 40,489
;   REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7248:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 512 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;     ORGANISM: Enterococcus faecium
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...512
;   SEQUENCE DESCRIPTION: SEQ ID NO: 7248:
US-09-107-532A-7248

Query Match      65.9%; Score 29; DB 2; Length 512;
Best Local Similarity 62.5%; Pred. No. 7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLEFDA 8
      ||||| :|:
Db      48 FLQLSYDS 55

Search completed: May 9, 2006, 02:28:15
Job time : 34.2 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 02:25:44 ; Search time 80.8 Seconds  
(without alignments)  
46.540 Million cell updates/sec

Title: US-09-870-216C-5  
Perfect score: 44  
Sequence: 1 FLQLEFPAV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:\*

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- 2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	35	79.5	219	4	US-10-425-115-212999
5	35	79.5	282	5	US-10-501-282-592
6	35	79.5	285	5	US-10-501-282-594
7	35	79.5	461	4	US-10-425-115-213000
8	35	79.5	654	4	US-10-369-493-9433
9	35	79.5	680	4	US-10-369-493-17753
10	35	79.5	1612	6	US-11-037-143-6099
11	34	77.3	156	4	US-10-437-963-198066
12	33	75.0	125	4	US-10-424-599-274136
13	33	75.0	374	5	US-10-741-849-7038
14	33	75.0	388	4	US-10-369-493-12756
15	32	72.7	225	4	US-10-282-122A-49767
16	32	72.7	274	4	US-10-282-122A-51999
17	32	72.7	414	4	US-10-260-937-5
18	32	72.7	414	4	US-10-260-937-49
19	32	72.7	414	4	US-10-260-937-59
20	32	72.7	440	5	US-10-663-377-4
21	32	72.7	489	5	US-10-690-880-41
22	32	72.7	537	5	US-10-663-377-6
23	32	72.7	551	4	US-10-382-248-8
24	32	72.7	551	4	US-10-741-853A-2
25	32	72.7	562	4	US-10-741-601-515
26	32	72.7	562	5	US-10-961-139-24
27	32	72.7	574	5	US-10-663-377-2
28	32	72.7	580	4	US-10-260-937-34
29	32	72.7	594	5	US-10-663-377-8
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33	32	72.7	599	4	US-10-382-248-6
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36	32	72.7	599	5	US-10-663-377-10
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38	32	72.7	600	4	US-10-260-937-48
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47	32	72.7	632	4	US-10-260-937-60
48	32	72.7	633	3	US-09-919-060-13
49	32	72.7	633	4	US-10-260-937-2
50	32	72.7	633	4	US-10-679-140-13
51	32	72.7	641	4	US-10-369-493-8814
52	32	72.7	756	4	US-10-369-493-17121
53	31	70.5	141	4	US-10-437-963-160478
54	31	70.5	167	4	US-10-437-963-194355
55	31	70.5	188	4	US-10-308-460-4
56	31	70.5	190	4	US-10-308-460-2
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58	31	70.5	195	4	US-10-276-774-2688
59	31	70.5	212	4	US-10-437-963-194570
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61	31	70.5	384	5	US-10-732-923-7682
62	31	70.5	390	4	US-10-282-122A-54337
63	31	70.5	608	6	US-11-097-143-29904
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86	30	68.2	326	4	US-10-128-714-8529
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95	30	68.2	472	5	US-10-721-922A-200
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285	28	63.6	100	3	US-09-852-797-61	Sequence 61, Appl	358	28	63.6	599	4	US-10-467-721-6	Sequence 6, Appli
286	28	63.6	100	4	US-10-058-993-61	Sequence 61, Appl	359	28	63.6	601	4	US-10-437-963-113065	Sequence 113065,
287	28	63.6	100	5	US-10-951-993-61	Sequence 61, Appl	360	28	63.6	602	4	US-10-121-235-19	Sequence 19, Appl
288	28	63.6	101	5	US-10-926-683-1557	Sequence 1557, Ap	361	28	63.6	602	4	US-10-260-708-78	Sequence 78, Appl
289	28	63.6	106	3	US-09-978-360A-551	Sequence 551, App	362	28	63.6	622	4	US-10-467-721-4	Sequence 4, Appli
290	28	63.6	106	3	US-09-978-360A-701	Sequence 701, App	363	28	63.6	635	4	US-10-732-923-3162	Sequence 3162, Ap
291	28	63.6	106	4	US-10-319-763-95	Sequence 95, Appl	364	28	63.6	645	5	US-10-080-334-164	Sequence 164, App
292	28	63.6	106	4	US-10-319-763-189	Sequence 189, App	365	28	63.6	688	4	US-10-369-493-6056	Sequence 6056, Ap
293	28	63.6	108	4	US-10-424-599-267045	Sequence 267045,	366	28	63.6	690	4	US-10-369-493-6056	Sequence 6056, Ap
294	28	63.6	110	4	US-10-437-963-177290	Sequence 177290,	367	28	63.6	703	4	US-10-282-122A-63529	Sequence 63529, A
295	28	63.6	113	4	US-10-425-115-202774	Sequence 202774,	368	28	63.6	737	4	US-10-620-669-18	Sequence 18, Appl
296	28	63.6	115	4	US-10-425-115-199178	Sequence 199178,	369	28	63.6	759	4	US-10-424-599-168898	Sequence 168898,
297	28	63.6	117	4	US-10-437-963-129245	Sequence 129245,	370	28	63.6	845	4	US-10-369-493-6337	Sequence 6337, Ap
298	28	63.6	118	4	US-10-425-115-202776	Sequence 202776,	371	28	63.6	870	5	US-10-739-930-5748	Sequence 5748, Ap
299	28	63.6	120	4	US-10-424-599-230297	Sequence 230297,	372	28	63.6	903	3	US-09-758-007-1	Sequence 1, Appli
300	28	63.6	131	4	US-10-424-599-200536	Sequence 200536,	373	28	63.6	1067	4	US-10-369-493-6334	Sequence 6334, Ap
301	28	63.6	133	4	US-10-389-566-1767	Sequence 1767, Ap	374	28	63.6	1078	4	US-10-437-963-197679	Sequence 197679,
302	28	63.6	133	4	US-10-425-115-287207	Sequence 287207,	375	28	63.6	1080	5	US-10-437-963-171732	Sequence 171732,
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304	28	63.6	143	5	US-10-501-282-1498	Sequence 1498, Ap	377	28	63.6	1081	5	US-10-810-486-45	Sequence 45, Appl
305	28	63.6	153	4	US-10-767-701-42407	Sequence 42407, A	378	28	63.6	1084	4	US-10-437-963-173751	Sequence 173751,
306	28	63.6	154	4	US-10-282-122A-52521	Sequence 52521, A	379	28	63.6	1241	5	US-10-930-723A-18	Sequence 18, Appl
307	28	63.6	161	4	US-10-425-115-366560	Sequence 366560,	380	28	63.6	1241	5	US-10-927-951A-18	Sequence 18, Appl
308	28	63.6	163	4	US-10-437-963-133314	Sequence 133314,	381	28	63.6	1254	5	US-10-732-923-12302	Sequence 12302, A
309	28	63.6	166	5	US-10-972-024-249	Sequence 249, App	382	28	63.6	1308	4	US-10-425-115-305699	Sequence 305699,
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313	28	63.6	204	4	US-10-156-761-11551	Sequence 11551, A	386	28	63.6	1414	4	US-10-437-963-145033	Sequence 145033,
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315	28	63.6	212	5	US-10-450-763-30477	Sequence 30477, A	388	28	63.6	1650	4	US-10-437-963-121155	Sequence 121155,
316	28	63.6	222	4	US-10-437-963-186893	Sequence 186893,	389	28	63.6	1735	5	US-10-937-379-41	Sequence 41, Appl
317	28	63.6	239	4	US-10-437-963-195898	Sequence 195898,	390	28	63.6	1803	4	US-10-437-963-145035	Sequence 145035,
318	28	63.6	259	4	US-10-369-493-13858	Sequence 13858, A	391	28	63.6	1803	4	US-10-437-963-145036	Sequence 145036,
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394	28	63.6	2066	4	US-10-203-295-39	Sequence 39, Appl	467	27	61.4	225	4	US-10-425-115-237220	Sequence 237220,
395	28	63.6	2202	4	US-10-437-963-192900	Sequence 192900,	468	27	61.4	227	5	US-10-732-923-16462	Sequence 16462, A
396	28	63.6	3133	4	US-10-369-493-18917	Sequence 18917, A	469	27	61.4	227	5	US-10-732-923-16505	Sequence 16505, A
397	28	63.6	3352	4	US-10-156-763-7961	Sequence 7961, Ap	470	27	61.4	228	5	US-10-732-923-16495	Sequence 16495, A
398	28	63.6	5936	4	US-10-378-083-20	Sequence 20, Appl	471	27	61.4	228	5	US-10-732-923-16496	Sequence 16496, A
399	28	63.6	6641	4	US-10-282-122A-70580	Sequence 70580, A	472	27	61.4	229	3	US-09-924-358-2	Sequence 2, Appli
400	28	63.6	10303	4	US-10-661-809-23	Sequence 23, Appl	473	27	61.4	229	4	US-10-410-764-2	Sequence 2, Appli
401	28	63.6	10303	4	US-10-724-972A-4098	Sequence 4098, Ap	474	27	61.4	231	5	US-10-732-923-16470	Sequence 16470, A
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403	27.5	62.5	259	4	US-10-032-585-7601	Sequence 7601, Ap	476	27	61.4	241	4	US-10-156-761-12445	Sequence 12445, A
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410	27	61.4	63	4	US-10-437-963-161385	Sequence 161385, A	483	27	61.4	260	4	US-10-314-669-131	Sequence 131, App
411	27	61.4	69	4	US-10-424-599-208047	Sequence 208047, A	484	27	61.4	260	4	US-10-669-861-131	Sequence 131, App
412	27	61.4	69	4	US-10-425-115-201262	Sequence 201262, A	485	27	61.4	260	5	US-10-732-923-13427	Sequence 73, Appl
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417	27	61.4	84	4	US-10-767-701-61649	Sequence 61649, A	490	27	61.4	280	5	US-10-501-282-3552	Sequence 3552, Ap
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427	27	61.4	105	4	US-10-424-599-229670	Sequence 229670, A	500	27	61.4	300	4	US-10-241-742-358	Sequence 358, App
428	27	61.4	106	4	US-10-437-963-120096	Sequence 120096, A	501	27	61.4	300	4	US-10-440-523-358	Sequence 358, App
429	27	61.4	106	5	US-10-450-763-41034	Sequence 41034, A	502	27	61.4	300	4	US-10-440-503-358	Sequence 358, App
430	27	61.4	109	4	US-10-437-963-133530	Sequence 133530, A	503	27	61.4	300	4	US-10-461-925-358	Sequence 358, App
431	27	61.4	112	4	US-10-032-201B-87	Sequence 87, Appl	504	27	61.4	301	5	US-10-732-923-19326	Sequence 19326, A
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434	27	61.4	116	4	US-10-437-963-109412	Sequence 109412, A	507	27	61.4	305	5	US-10-732-923-2743	Sequence 2743, Ap
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436	27	61.4	123	4	US-10-424-599-255519	Sequence 255519, A	509	27	61.4	306	4	US-10-282-122A-74233	Sequence 74233, A
437	27	61.4	123	4	US-10-437-963-179548	Sequence 179548, A	510	27	61.4	306	5	US-10-472-928-4640	Sequence 4640, Ap
438	27	61.4	123	4	US-10-437-963-179660	Sequence 179660, A	511	27	61.4	310	3	US-09-734-569-148	Sequence 148, App
439	27	61.4	128	3	US-09-809-391-539	Sequence 539, App	512	27	61.4	311	4	US-10-282-122A-77779	Sequence 77779, A
440	27	61.4	128	3	US-09-882-171-539	Sequence 539, App	513	27	61.4	312	4	US-10-664-421-137	Sequence 137, App
441	27	61.4	128	4	US-10-164-861-539	Sequence 539, App	514	27	61.4	312	5	US-10-941-635-139	Sequence 139, App
442	27	61.4	128	4	US-10-424-599-179007	Sequence 179007, A	515	27	61.4	315	4	US-10-432-737-10	Sequence 10, Appl
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445	27	61.4	150	4	US-10-289-762-919	Sequence 919, App	518	27	61.4	317	5	US-10-617-320-4532	Sequence 4532, Ap
446	27	61.4	157	4	US-10-425-114-42939	Sequence 42939, A	519	27	61.4	329	4	US-10-437-963-162367	Sequence 162367,
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448	27	61.4	162	3	US-09-724-569-16	Sequence 16, Appl	521	27	61.4	332	4	US-10-295-403-40	Sequence 40, Appl
449	27	61.4	166	4	US-10-424-599-211636	Sequence 211636, A	522	27	61.4	332	4	US-10-225-066A-620	Sequence 620, App
450	27	61.4	166	4	US-10-424-599-225129	Sequence 225129, A	523	27	61.4	332	4	US-10-374-780A-2506	Sequence 2506, App
451	27	61.4	166	4	US-10-437-963-179770	Sequence 179770, A	524	27	61.4	332	4	US-10-412-699B-678	Sequence 678, App
452	27	61.4	168	3	US-09-815-242-11353	Sequence 11353, A	525	27	61.4	332	5	US-10-739-930-6505	Sequence 6505, Ap
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454	27	61.4	168	4	US-10-425-114-72400	Sequence 72400, A	527	27	61.4	334	4	US-10-425-114-61097	Sequence 61097, A
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457	27	61.4	182	4	US-10-437-963-190475	Sequence 190475, A	530	27	61.4	336	4	US-10-425-115-232345	Sequence 232345,
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459	27	61.4	188	3	US-09-764-864-1115	Sequence 1115, Ap	532	27	61.4	339	5	US-10-732-923-422	Sequence 422, App
460	27	61.4	188	4	US-10-425-115-285169	Sequence 285169, A	533	27	61.4	341	3	US-09-948-649-2	Sequence 2, Appli
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462	27	61.4	192	5	US-10-450-763-54765	Sequence 54765, A	535	27	61.4	341	3	US-10-425-114-54064	Sequence 54064, A
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543	27	61.4	358	5	US-10-732-923-7402	Sequence 7402, App	616	27	61.4	583	3	US-09-815-242-13458	Sequence 13458, A
544	27	61.4	367	4	US-10-282-122A-67402	Sequence 67402, A	617	27	61.4	583	3	US-10-282-122A-74149	Sequence 74149, A
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546	27	61.4	369	4	US-10-424-599-225126	Sequence 225126, A	619	27	61.4	583	5	US-10-472-928-3804	Sequence 3804, App
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552	27	61.4	378	4	US-10-669-861-6	Sequence 6, Appli	625	27	61.4	630	4	US-10-400-053-15	Sequence 15, Appl
553	27	61.4	378	4	US-10-669-861-18	Sequence 18, Appl	626	27	61.4	630	4	US-10-400-053-24	Sequence 24, Appl
554	27	61.4	378	4	US-10-669-861-20	Sequence 20, Appl	627	27	61.4	636	4	US-10-381-779-28	Sequence 28, Appl
555	27	61.4	382	4	US-10-314-669-4	Sequence 4, Appli	628	27	61.4	641	4	US-10-369-493-15592	Sequence 15592, A
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557	27	61.4	382	4	US-10-669-861-8	Sequence 8, Appli	630	27	61.4	642	5	US-10-830-828-48	Sequence 48, Appl
558	27	61.4	387	4	US-10-767-701-45920	Sequence 45920, A	631	27	61.4	654	4	US-10-400-053-14	Sequence 14, Appl
559	27	61.4	389	5	US-10-450-763-46120	Sequence 46120, A	632	27	61.4	664	4	US-10-325-881-70	Sequence 70, Appl
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561	27	61.4	392	4	US-10-302-267-200	Sequence 200, App	634	27	61.4	685	4	US-10-029-180-82	Sequence 82, Appl
562	27	61.4	392	4	US-10-412-699B-936	Sequence 936, App	635	27	61.4	685	5	US-10-952-045-82	Sequence 82, Appl
563	27	61.4	393	4	US-10-156-761-8531	Sequence 8531, App	636	27	61.4	688	4	US-10-254-074-2	Sequence 2, Appli
564	27	61.4	402	5	US-10-501-282-4342	Sequence 4342, App	637	27	61.4	690	3	US-09-768-877-18	Sequence 18, Appl
565	27	61.4	405	4	US-10-425-114-48686	Sequence 48686, A	638	27	61.4	690	4	US-10-116-519-13	Sequence 13, Appl
566	27	61.4	406	4	US-10-425-114-48693	Sequence 48693, A	639	27	61.4	690	4	US-10-390-585-7	Sequence 7, Appli
567	27	61.4	410	4	US-10-108-260A-4330	Sequence 4330, App	640	27	61.4	697	4	US-10-767-701-47198	Sequence 47198, A
568	27	61.4	410	4	US-10-669-861-4	Sequence 4, Appli	641	27	61.4	700	4	US-10-259-165-266	Sequence 266, App
569	27	61.4	416	6	US-11-097-143-16062	Sequence 16062, A	642	27	61.4	705	3	US-09-907-907A-42	Sequence 42, Appl
570	27	61.4	416	4	US-10-425-114-39622	Sequence 39622, A	643	27	61.4	705	3	US-09-907-907A-44	Sequence 44, Appl
571	27	61.4	423	5	US-10-770-600-20	Sequence 20, Appl	644	27	61.4	713	4	US-10-282-122A-56812	Sequence 56812, A
572	27	61.4	426	4	US-10-156-761-9768	Sequence 9768, App	645	27	61.4	729	4	US-10-282-122A-53156	Sequence 53156, A
573	27	61.4	436	4	US-10-437-963-189519	Sequence 189519, A	646	27	61.4	729	4	US-10-408-765A-2957	Sequence 2957, App
574	27	61.4	437	4	US-10-425-114-72308	Sequence 72308, A	647	27	61.4	731	5	US-10-491-467-34	Sequence 34, Appl
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577	27	61.4	438	4	US-10-260-877-64	Sequence 64, Appl	650	27	61.4	738	4	US-10-221-172-200	Sequence 200, App
578	27	61.4	446	4	US-10-032-585-7872	Sequence 7872, App	651	27	61.4	742	4	US-10-437-963-145589	Sequence 145589, A
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587	27	61.4	457	4	US-10-029-180-24	Sequence 24, Appl	660	27	61.4	784	4	US-10-145-014-23	Sequence 23, Appl
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589	27	61.4	466	4	US-10-138-473-38	Sequence 38, Appl	662	27	61.4	784	4	US-10-456-947-46	Sequence 46, Appl
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591	27	61.4	468	5	US-10-450-763-55654	Sequence 55654, A	664	27	61.4	784	4	US-10-732-798A-4	Sequence 4, Appli
592	27	61.4	473	4	US-10-296-115-837	Sequence 837, App	665	27	61.4	784	5	US-10-741-600-1390	Sequence 1390, App
593	27	61.4	485	4	US-10-369-493-20557	Sequence 20557, A	666	27	61.4	784	5	US-10-741-600-1391	Sequence 1391, App
594	27	61.4	492	4	US-10-282-122A-57922	Sequence 57922, A	667	27	61.4	784	5	US-10-975-909-4	Sequence 4, Appli
595	27	61.4	493	4	US-10-424-599-170309	Sequence 170309, A	668	27	61.4	784	5	US-10-756-149-4847	Sequence 4847, App
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597	27	61.4	512	4	US-10-369-493-8347	Sequence 8347, App	670	27	61.4	795	4	US-10-289-762-314	Sequence 314, App
598	27	61.4	515	4	US-10-425-114-54007	Sequence 54007, A	671	27	61.4	797	4	US-10-072-036-141	Sequence 141, App
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685	27	61.4	885	4	US-10-240-154-6	Sequence 6, Appli	758	59.1	43	4	US-10-016-349A-147	Sequence 147, App
686	27	61.4	885	4	US-10-307-817-602	Sequence 602, App	759	59.1	44	4	US-10-425-115-307165	Sequence 307165,
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729	27	61.4	4345	6	US-11-097-143-26043	Sequence 26043, A	802	59.1	106	4	US-10-424-599-227068	Sequence 227068,
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733	27	61.4	4899	6	US-11-097-143-40200	Sequence 3945, Ap	806	59.1	113	3	US-09-764-868-1179	Sequence 1179, Ap
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738	26	59.1	9	4	US-10-277-292-223	Sequence 107, App	811	59.1	119	4	US-10-767-701-56701	Sequence 56701, A
739	26	59.1	9	4	US-10-280-340-107	Sequence 223, App	812	59.1	123	4	US-10-424-599-256797	Sequence 256797,
740	26	59.1	9	4	US-10-280-340-223	Sequence 107, App	813	59.1	123	4	US-10-767-701-45139	Sequence 45139, A
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743	26	59.1	10	3	US-09-935-430-251	Sequence 223, App	816	59.1	128	5	US-10-450-763-30703	Sequence 30703, A
744	26	59.1	10	3	US-09-935-430-367	Sequence 251, App	817	59.1	129	4	US-10-424-599-159107	Sequence 159107,
745	26	59.1	10	3	US-09-935-430-403	Sequence 367, App	818	59.1	130	4	US-10-109-048-992	Sequence 992, App
746	26	59.1	10	4	US-10-277-292-21	Sequence 403, App	819	59.1	131	5	US-10-220-335-576	Sequence 576, App
747	26	59.1	10	4	US-10-277-292-367	Sequence 251, App	820	59.1	135	4	US-10-425-115-249974	Sequence 249974,
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852	26	59.1	174	4	US-10-425-115-339287	Sequence 339287, A	925	26	59.1	289	4	US-10-282-122A-75442	Sequence 75442, A
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854	26	59.1	176	4	US-10-424-599-156922	Sequence 156922, A	927	26	59.1	299	4	US-10-767-701-44989	Sequence 44989, A
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989 26 59.1 366 4 US-10-767-701-40873 Sequence 40873, A  
990 26 59.1 367 4 US-10-369-493-3459 Sequence 3459, Ap  
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996 26 59.1 377 4 US-10-424-599-166102 Sequence 166102, A  
997 26 59.1 380 3 US-09-825-414-40 Sequence 40, Appl  
998 26 59.1 380 3 US-09-825-414-42 Sequence 42, Appl  
999 26 59.1 380 3 US-09-825-414-44 Sequence 44, Appl  
1000 26 59.1 380 3 US-09-825-414-46 Sequence 46, Appl

## ALIGNMENTS

RESULT 1  
US-09-870-216C-5  
; Sequence 5, Application US/09870216C  
; Publication No. US20040138135A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Nicolette  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER  
; FILE REFERENCE: 68126881210100  
; CURRENT APPLICATION NUMBER: US/09/870,216C  
; CURRENT FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: 60/209,391  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 60/226,256  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/257,008  
; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-870-216C-5

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 FQLEFDV 9  
RESULT 2  
US-10-017-327-5  
; Sequence 5, Application US/10017327  
; Publication No. US20020155471A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Nicolette  
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND  
; FILE REFERENCE: METHODS FOR USING SAME  
; CURRENT APPLICATION NUMBER: US/10/017,327  
; CURRENT FILING DATE: 2001-12-06

; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; LENGTH: 9  
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; ORGANISM: Homo sapiens  
US-10-017-327-5  
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
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Db 1 FQLEFDV 9  
RESULT 3  
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; Sequence 79, Application US/10828924  
; Publication No. US20050003401A1  
; GENERAL INFORMATION:  
; APPLICANT: STRATAGENE  
; TITLE OF INVENTION: PFU REPLICATION ACCESSORY FACTORS AND METHODS OF USE  
; FILE REFERENCE: 04121.0161-00000  
; CURRENT APPLICATION NUMBER: US/10/828,924  
; CURRENT FILING DATE: 2004-04-20  
; PRIOR APPLICATION NUMBER: 60/146,580  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 79  
; LENGTH: 1278  
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; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Helicase 7  
US-10-828-924-79  
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US-10-425-115-212999  
; Sequence 212999, Application US/10425115  
; Publication No. US2004021472A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 212999  
; LENGTH: 219  
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; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_125856C.1.pep  
US-10-425-115-212999  
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Best Local Similarity 77.8%; Pred. No. 61;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
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Db 72 FLQLEIDSV 80

RESULT 5

US-10-501-282-592

; Sequence 592, Application US/10501282

; Publication No. US20050203280A1

; GENERAL INFORMATION:

; APPLICANT: MCMICHAEL, JOHN CALHOUN

; APPLICANT: ZAGURSKY, ROBERT JOHN

; APPLICANT: RUSSELL, DAVID PARRISH

; APPLICANT: FLETCHER, LEAH DIANE

; TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING

; TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF

; FILE REFERENCE: AM100780 L2

; CURRENT APPLICATION NUMBER: US/10/501,282

; PRIOR FILING DATE: 2004-07-09

; PRIOR APPLICATION NUMBER: 60/333,777

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: 60/426,742

; PRIOR FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: PCT/US02/36123

; PRIOR FILING DATE: 2002-11-25

; NUMBER OF SEQ ID NOS: 6653

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 592

; LENGTH: 282

; TYPE: PRT

; ORGANISM: Alloioococcus otitidis

US-10-501-282-592

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Best Local Similarity 77.8%; Pred. No. 79;

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Db 184 FLQLEIDSV 192

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US-10-501-282-594

; Sequence 594, Application US/10501282

; Publication No. US20050203280A1

; GENERAL INFORMATION:

; APPLICANT: MCMICHAEL, JOHN CALHOUN

; APPLICANT: ZAGURSKY, ROBERT JOHN

; APPLICANT: RUSSELL, DAVID PARRISH

; APPLICANT: FLETCHER, LEAH DIANE

; TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING

; TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF

; FILE REFERENCE: AM100780 L2

; CURRENT APPLICATION NUMBER: US/10/501,282

; PRIOR FILING DATE: 2004-07-09

; PRIOR APPLICATION NUMBER: 60/333,777

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: 60/426,742

; PRIOR FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: PCT/US02/36123

; PRIOR FILING DATE: 2002-11-25

; NUMBER OF SEQ ID NOS: 6653

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 594

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Alloioococcus otitidis

US-10-501-282-594

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Best Local Similarity 77.8%; Pred. No. 80;

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Db 187 FLQLEIDSV 195

RESULT 7

US-10-425-115-213000

; Sequence 213000, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 213000

; LENGTH: 461

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(461)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_125857C.1.pep

US-10-425-115-213000

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Best Local Similarity 77.8%; Pred. No. 1.3e+02;

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QY 1 FLQLEFDV 9  
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Db 72 FLQLEIDSV 80

RESULT 8

US-10-369-493-9433

; Sequence 9433, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 9433

; LENGTH: 654

; TYPE: PRT

; ORGANISM: Xylella fastidiosa

US-10-369-493-9433

Query Match 79.5%; Score 35; DB 4; Length 654;

Best Local Similarity 77.8%; Pred. No. 1.9e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9

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US-10-369-493-17753
; Sequence 17753, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
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; LENGTH: 680
; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-369-493-17753

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Best Local Similarity 77.8%; Pred. No. 2e+02;
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; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
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; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
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US-11-097-143-6099
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||:||||:
Db          254 YLELEFDAL 262

RESULT 11
US-10-437-963-198066
; Sequence 198066, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198066
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_93763C.1.pap
US-10-437-963-198066

Query Match          77.3%; Score 34; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFDVA 9
||||:||||
Db          78 QLEFDVA 84

RESULT 12
US-10-424-599-274136
; Sequence 274136, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274136
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(125)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89567C.1.pap
US-10-424-599-274136
```



Query Match 75.0%; Score 33; DB 4; Length 125;  
Best Local Similarity 77.8%; Pred. No. 86;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLEFDV 9  
Db 77 FLQLPFDV 85

## RESULT 13

US-10-741-849-7038  
; Sequence 7038, Application US/10741849  
; Publication No. US20050019931A1  
; GENERAL INFORMATION:  
; APPLICANT: Roemer, Terry  
; APPLICANT: Jiang, Bo  
; APPLICANT: Boone, Charles  
; APPLICANT: Bussey, Howard  
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of  
; FILE REFERENCE: 10182-023-999  
; CURRENT FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: US/10/741,849  
; CURRENT FILING DATE: 2003-12-19  
; PRIOR FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 8000  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7038  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-10-741-849-7038

Query Match 75.0%; Score 33; DB 5; Length 374;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QLEFDV 9  
Db 293 QLEFDV 299

## RESULT 14

US-10-369-493-12756  
; Sequence 12756, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 12756  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: Aspergillus nidulans  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(388)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-12756

Query Match 75.0%; Score 33; DB 4; Length 388;  
Best Local Similarity 87.5%; Pred. No. 2.8e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLEFDV 9  
Db 54 LQLNFDV 61

## RESULT 15

US-10-282-122A-49767  
; Sequence 49767, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 49767  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: Burkholderia fungorum  
US-10-282-122A-49767

Query Match 72.7%; Score 32; DB 4; Length 225;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLEFDV 9  
Db 111 YLKLFDV 119

## RESULT 16

US-10-282-122A-51999  
; Sequence 51999, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl

```
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51999
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51999

Query Match          72.7%; Score 32; DB 4; Length 274;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1  FLQLDFDAV 9
      |||:|:|:
Db      205  FLKLDFDGI 213

RESULT 17
US-10-260-937-5
; Sequence 5, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 5
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-260-937-5

Query Match          72.7%; Score 32; DB 4; Length 414;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  FLQLDFD 7
      |||:|:|
Db      170  FLQLKFD 176

RESULT 18
US-10-260-937-49
; Sequence 49, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-260-937-49

Query Match          72.7%; Score 32; DB 4; Length 414;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  FLQLDFD 7
      |||:|:|
Db      170  FLQLKFD 176

RESULT 19
US-10-260-937-59
; Sequence 59, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
```

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 59

; LENGTH: 414

; TYPE: PRT

; ORGANISM: Canis familiaris

US-10-260-937-59

Query Match 72.7%; Score 32; DB 4; Length 414;  
Best Local Similarity 85.7%; Pred. No. 4.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLEPD 7

||||:|

Db 170 FLQLKFD 176

RESULT 20

US-10-663-377-4

; Sequence 4, Application US/10663377

; Publication No. US20050233429A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Yanbin

; APPLICANT: Woodward, David F.

; TITLE OF INVENTION: HUMAN COX-1 ALTERNATIVELY SPLICED

; FILE REFERENCE: 66872-028 (AR5746)

; CURRENT APPLICATION NUMBER: US/10/663,377

; CURRENT FILING DATE: 2003-09-15

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 440

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-663-377-4

Query Match 72.7%; Score 32; DB 5; Length 440;  
Best Local Similarity 85.7%; Pred. No. 5.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLEPD 7

||||:|

Db 196 FLQLKFD 202

RESULT 21

US-10-690-880-41

; Sequence 41, Application US/10690880

; Publication No. US20050014165A1

; GENERAL INFORMATION:

; APPLICANT: LEE, NANCY M

; APPLICANT: CHEN, LING C

; TITLE OF INVENTION: BIOMARKER PANEL FOR COLORECTAL CANCER

; FILE REFERENCE: CPMC-01000US1

; CURRENT APPLICATION NUMBER: US/10/690,880

; CURRENT FILING DATE: 2003-10-22

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 41

; LENGTH: 489

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-690-880-41

Query Match 72.7%; Score 32; DB 5; Length 489;  
Best Local Similarity 85.7%; Pred. No. 5.7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLEPD 7

||||:|

Db 246 FLQLKFD 252

RESULT 22

US-10-663-377-6

; Sequence 6, Application US/10663377

; Publication No. US20050233429A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Yanbin

; APPLICANT: Woodward, David F.

; TITLE OF INVENTION: HUMAN COX-1 ALTERNATIVELY SPLICED

; FILE REFERENCE: 66872-028 (AR5746)

; CURRENT APPLICATION NUMBER: US/10/663,377

; CURRENT FILING DATE: 2003-09-15

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 537

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-663-377-6

Query Match 72.7%; Score 32; DB 5; Length 537;  
Best Local Similarity 85.7%; Pred. No. 6.3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLEPD 7

||||:|

Db 330 FLQLKFD 336

RESULT 23

US-10-382-248-8

; Sequence 8, Application US/10382248

; Publication No. US20040058347A1

; GENERAL INFORMATION:

; APPLICANT: Alsbrook, et al.

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-568C

; CURRENT APPLICATION NUMBER: US/10/382,248

; CURRENT FILING DATE: 2003-03-05

; PRIOR APPLICATION NUMBER: 60/366,928

; PRIOR FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: 60/361,974

; PRIOR FILING DATE: 2002-03-06

; PRIOR APPLICATION NUMBER: 60/365,477

; PRIOR FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 60/401,661

; PRIOR FILING DATE: 2002-08-06

; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: CuraseqList version 0.1

; SEQ ID NO 8

; LENGTH: 551

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-382-248-8

Query Match 72.7%; Score 32; DB 4; Length 551;  
Best Local Similarity 85.7%; Pred. No. 6.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLEPD 7

||||:|

Db 307 FLQLKFD 313

RESULT 24

US-10-741-853A-2

; Sequence 2, Application US/10741853A

; Publication No. US20040203030A1

; GENERAL INFORMATION:

; APPLICANT: Garrett-Engle, Philip, W

; TITLE OF INVENTION: Alternatively Spliced Isoform of Human COX1

; FILE REFERENCE: RS0206

; CURRENT APPLICATION NUMBER: US/10/741,853A

```
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US 60/435,478
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-853A-2

Query Match          72.7%; Score 32; DB 4; Length 551;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 307 FLQLKFD 313

RESULT 25
US-10-741-601-515
; Sequence 515, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 515
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-515

Query Match          72.7%; Score 32; DB 4; Length 562;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 355 FLQLKFD 361

RESULT 26
US-10-961-139-24
; Sequence 24, Application US/10961139
; Publication No. US20050153313A1
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Glatt, Karen
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Xu, Yong Yao
; APPLICANT: Zhao, Xumei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND PROTEINS FOR
; TITLE OF INVENTION: THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: MRI-065
; CURRENT APPLICATION NUMBER: US/10/961,139
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: 60/509,171
; PRIOR FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 24
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-961-139-24

Query Match          72.7%; Score 32; DB 5; Length 562;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 355 FLQLKFD 361

RESULT 27
US-10-663-377-2
; Sequence 2, Application US/10663377
; Publication No. US20050233429A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Yanbin
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: HUMAN COX-1 ALTERNATIVELY SPLICED
; TITLE OF INVENTION: VARIANTS AND METHODS OF USING SAME
; FILE REFERENCE: 66872-028 (AR5746)
; CURRENT APPLICATION NUMBER: US/10/663,377
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-663-377-2

Query Match          72.7%; Score 32; DB 5; Length 574;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 330 FLQLKFD 336

RESULT 28
US-10-260-937-34
; Sequence 34, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-260-937-34
```

```
Query Match      72.7%; Score 32; DB 4; Length 580;
Best Local Similarity 85.7%; Pred. No. 6.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFD 7
Db 344 FLQLKFD 350

RESULT 29
US-10-663-377-8
; Sequence 8, Application US/10663377
; Publication No. US20050233429A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Yanbin
; TITLE OF INVENTION: HUMAN COX-1 ALTERNATIVELY SPLICED
; FILE REFERENCE: 66872-028 (AR5746)
; CURRENT APPLICATION NUMBER: US/10/663,377
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-663-377-8

Query Match      72.7%; Score 32; DB 5; Length 594;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFD 7
Db 350 FLQLKFD 356

RESULT 30
US-09-953-067A-3
; Sequence 3, Application US/09953067A
; Publication No. US20030082141A1
; GENERAL INFORMATION:
; APPLICANT: O'CONNOR, J. Patrick
; TITLE OF INVENTION: COX-2 FUNCTION AND WOUND HEALING
; FILE REFERENCE: 267/043
; CURRENT APPLICATION NUMBER: US/09/953,067A
; CURRENT FILING DATE: 2001-09-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-067A-3

Query Match      72.7%; Score 32; DB 3; Length 599;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFD 7
Db 355 FLQLKFD 361

RESULT 31
US-10-097-340-264
; Sequence 264, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
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; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-264

Query Match      72.7%; Score 32; DB 4; Length 599;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLEFD 7
Db 355 FLQLKFD 361

RESULT 32
US-10-260-937-47
; Sequence 47, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
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; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-937-47

Query Match          72.7%; Score 32; DB 4; Length 599;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 355 FLQLKFD 361

RESULT 33
US-10-382-248-6
; Sequence 6, Application US/10382248
; Publication No. US20040058347A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-568C
; CURRENT APPLICATION NUMBER: US/10/382,248
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/361,974
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 60/365,477
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/401,661
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-382-248-6

Query Match          72.7%; Score 32; DB 4; Length 599;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 355 FLQLKFD 361

RESULT 34
US-10-741-601-514
; Sequence 514, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 514
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-514

Query Match          72.7%; Score 32; DB 4; Length 599;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 355 FLQLKFD 361

RESULT 35
US-10-961-139-22
; Sequence 22, Application US/10961139
; Publication No. US20050153313A1
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Glatt, Karen
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Xu, Yong Yao
; APPLICANT: Zhao, Xumei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND PROTEINS FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-065
; CURRENT APPLICATION NUMBER: US/10/961,139
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: 60/509,171
; PRIOR FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-961-139-22

Query Match          72.7%; Score 32; DB 5; Length 599;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 355 FLQLKFD 361

RESULT 36
US-10-663-377-10
; Sequence 10, Application US/10663377
; Publication No. US20050233429A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Yanbin
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: HUMAN COX-1 ALTERNATIVELY SPLICED VARIANTS AND METHODS OF USING SAME
; FILE REFERENCE: 66872-028 (ARS746)
; CURRENT APPLICATION NUMBER: US/10/663,377
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-663-377-10

Query Match          72.7%; Score 32; DB 5; Length 599;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
Db 355 FLQLKFD 361
```

```
RESULT 37
US-11-050-926-264
; Sequence 264, Application US/11050926
; Publication No. US20050214831A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HORRSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/11/050,926
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-926-264

Query Match      72.7%; Score 32; DB 6; Length 599;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  FLQLEFD 7
Db      355  FLQLKFD 361

RESULT 38
US-10-260-937-48
; Sequence 48, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; PRIOR FILING DATE: 2001-09-28
; SEQ ID NO 264
```

```
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-260-937-48

Query Match      72.7%; Score 32; DB 4; Length 600;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  FLQLEFD 7
Db      356  FLQLKFD 362

RESULT 39
US-09-953-067A-7
; Sequence 7, Application US/09953067A
; Publication No. US20030082141A1
; GENERAL INFORMATION:
; APPLICANT: O'CONNOR, J. Patrick
; TITLE OF INVENTION: COX-2 FUNCTION AND WOUND HEALING
; FILE REFERENCE: 267/043
; CURRENT APPLICATION NUMBER: US/09/953,067A
; CURRENT FILING DATE: 2001-09-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-953-067A-7

Query Match      72.7%; Score 32; DB 3; Length 602;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  FLQLEFD 7
Db      358  FLQLKFD 364

RESULT 40
US-10-260-937-51
; Sequence 51, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
```

```
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-260-937-51

Query Match          72.7%; Score 32; DB 4; Length 602;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
   |||:|
Db 358 FLQLKFD 364

RESULT 41
US-10-260-937-52
; Sequence 52, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-260-937-52

Query Match          72.7%; Score 32; DB 4; Length 602;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
   |||:|
Db 358 FLQLKFD 364

RESULT 42
US-10-260-937-58
; Sequence 58, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 58
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-260-937-58

Query Match          72.7%; Score 32; DB 4; Length 603;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
   |||:|
Db 359 FLQLKFD 365

RESULT 43
US-10-260-937-50
; Sequence 50, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-260-937-50

Query Match          72.7%; Score 32; DB 4; Length 606;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7
   |||:|
Db 362 FLQLKFD 368

RESULT 44
US-10-260-937-15
; Sequence 15, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
```



; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 629  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-260-937-15

Query Match 72.7%; Score 32; DB 4; Length 629;  
Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKFD 7  
|||:|  
Db 385 FLQLKFD 391

## RESULT 45

US-10-783-297A-9  
; Sequence 9, Application US/10783297A  
; Publication No. US20040235017A1  
; GENERAL INFORMATION:

; APPLICANT: Johnson & Johnson Pharmaceutical Research and development  
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-3 AND USES THEREOF  
; FILE REFERENCE: PRD-2041  
; CURRENT APPLICATION NUMBER: US/10/783,297A  
; CURRENT FILING DATE: 2004-02-20  
; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 9  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-783-297A-9

Query Match 72.7%; Score 32; DB 5; Length 630;  
Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKFD 7  
|||:|  
Db 386 FLQLKFD 392

## RESULT 46

US-10-783-297A-11  
; Sequence 11, Application US/10783297A  
; Publication No. US20040235017A1  
; GENERAL INFORMATION:

; APPLICANT: Johnson & Johnson Pharmaceutical Research and development  
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-3 AND USES THEREOF  
; FILE REFERENCE: PRD-2041  
; CURRENT APPLICATION NUMBER: US/10/783,297A  
; CURRENT FILING DATE: 2004-02-20  
; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-783-297A-11

Query Match 72.7%; Score 32; DB 5; Length 630;  
Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKFD 7  
|||:|  
Db 386 FLQLKFD 392

## RESULT 47

US-10-260-937-60  
; Sequence 60, Application US/10260937

; Publication No. US20030220306A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Daniel  
; APPLICANT: Chandrasekharan, N. Vishvanath  
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND  
; TITLE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: 07913-007001  
; CURRENT APPLICATION NUMBER: US/10/260,937  
; CURRENT FILING DATE: 2002-09-28  
; PRIOR APPLICATION NUMBER: US 60/326,133  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/373,225  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/373,661  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/411,575  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60  
; LENGTH: 632  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus sequence  
US-10-260-937-60

Query Match 72.7%; Score 32; DB 4; Length 632;

Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKFD 7  
|||:|  
Db 389 FLQLKFD 395

## RESULT 48

US-09-919-060-13  
; Sequence 13, Application US/09919060  
; Patent No. US20020064845A1  
; GENERAL INFORMATION:

; APPLICANT: Wisniewski, Nancy  
; APPLICANT: Brandt, Kevin S.  
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES  
; FILE REFERENCE: AD-1  
; CURRENT APPLICATION NUMBER: US/09/919,060  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: 60/224,486  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 633  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-919-060-13

Query Match 72.7%; Score 32; DB 3; Length 633;

Best Local Similarity 85.7%; Pred. No. 7.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLKFD 7  
|||:|  
Db 389 FLQLKFD 395

## RESULT 49

US-10-260-937-2  
; Sequence 2, Application US/10260937  
; Publication No. US20030220306A1  
; GENERAL INFORMATION:

; APPLICANT: Simmons, Daniel  
; APPLICANT: Chandrasekharan, N. Vishvanath

; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND  
; TITLE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: 07913-007001  
; CURRENT APPLICATION NUMBER: US/10/260,937  
; CURRENT FILING DATE: 2002-09-28  
; PRIOR APPLICATION NUMBER: US 60/326,133  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/373,225  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/373,661  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/411,575  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 89  
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US-10-260-937-2

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; Publication No. US20040091986A1  
; GENERAL INFORMATION:  
; APPLICANT: Wisniewski, Nancy  
; APPLICANT: Brandt, Kevin S.  
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES  
; FILE REFERENCE: AD-1  
; CURRENT APPLICATION NUMBER: US/10/679,140  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US/09/919,060  
; PRIOR FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: 60/224,486  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 25  
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Title: US-09-870-216C-5

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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8	30	68.2	370	11	US-11-188-298-13429
9	30	68.2	370	11	US-11-188-298-14941
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14	29	65.9	130	11	US-11-214-199-29
15	29	65.9	161	9	US-10-821-234-1278
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252	26	59.1	821	9	US-10-453-372-600	Sequence 600, App	325	25	56.8	163	9	US-10-152-370-504	Sequence 504, App
253	26	59.1	835	9	US-10-501-035-216	Sequence 216, App	326	25	56.8	163	11	US-11-290-133-504	Sequence 504, App
254	26	59.1	837	9	US-10-453-372-594	Sequence 594, App	327	25	56.8	166	11	US-11-096-568A-31439	Sequence 31439, A
255	26	59.1	837	9	US-10-877-346-5	Sequence 5, Appli	328	25	56.8	166	11	US-11-096-568A-33934	Sequence 33934, A
256	26	59.1	841	9	US-10-453-372-586	Sequence 586, App	329	25	56.8	168	9	US-10-821-234-1426	Sequence 1426, Ap
257	26	59.1	841	9	US-10-453-372-592	Sequence 592, App	330	25	56.8	176	9	US-10-330-773-525	Sequence 525, App
258	26	59.1	841	9	US-10-453-372-602	Sequence 602, App	331	25	56.8	180	11	US-11-096-568A-3472	Sequence 3472, Ap
259	26	59.1	841	9	US-10-877-346-2	Sequence 2, Appli	332	25	56.8	180	11	US-11-264-096-2116	Sequence 2116, Ap
260	26	59.1	841	9	US-10-989-767A-657	Sequence 657, App	333	25	56.8	189	9	US-10-506-454-557	Sequence 557, App
261	26	59.1	860	11	US-11-188-298-15462	Sequence 15462, A	334	25	56.8	189	11	US-11-096-568A-3496	Sequence 3496, Ap
262	26	59.1	1036	11	US-11-096-568A-28315	Sequence 28315, A	335	25	56.8	189	11	US-11-188-298-1600	Sequence 1600, Ap
263	26	59.1	1070	11	US-11-096-568A-28314	Sequence 28314, A	336	25	56.8	195	11	US-11-188-298-1600	Sequence 16129, A
264	26	59.1	1179	11	US-11-045-004-372	Sequence 372, App	337	25	56.8	197	11	US-11-188-298-16129	Sequence 98, Appl
265	26	59.1	1276	11	US-11-096-568A-28313	Sequence 28313, A	338	25	56.8	207	11	US-11-123-104-98	Sequence 97, Appl
266	26	59.1	1647	11	US-11-052-554A-260	Sequence 260, App	339	25	56.8	208	11	US-11-129-104-97	Sequence 5274, Ap
267	26	59.1	1857	11	US-11-057-058-60	Sequence 60, Appl	340	25	56.8	209	11	US-11-087-099-4451	Sequence 4451, Ap
268	26	59.1	1857	11	US-11-057-058-61	Sequence 61, Appl	341	25	56.8	213	11	US-11-096-568A-20420	Sequence 20420, A
269	26	59.1	1960	11	US-11-069-834-48	Sequence 48, Appl	342	25	56.8	213	11	US-11-188-298-1106	Sequence 1106, Ap
270	26	59.1	2376	11	US-11-188-298-9871	Sequence 9871, Ap	343	25	56.8	217	11	US-11-096-568A-3495	Sequence 3495, Ap
271	26	59.1	5738	8	US-10-505-928-150	Sequence 150, App	344	25	56.8	226	11	US-11-096-568A-25394	Sequence 25394, A
272	25.5	58.0	58	11	US-11-125-639-31	Sequence 31, Appl	345	25	56.8	226	11	US-11-096-568A-27070	Sequence 27070, A
273	25.5	58.0	61	9	US-10-207-797-171	Sequence 171, App	346	25	56.8	227	11	US-11-045-004-1304	Sequence 1304, Ap
274	25.5	58.0	61	9	US-10-207-797-178	Sequence 178, App	347	25	56.8	228	9	US-10-194-487-114	Sequence 114, App
275	25.5	58.0	352	11	US-11-000-463-450	Sequence 450, App	348	25	56.8	228	9	US-10-195-883-114	Sequence 114, App
276	25.5	58.0	352	11	US-11-000-463-922	Sequence 922, App	349	25	56.8	228	9	US-10-195-888-114	Sequence 114, App
277	25.5	58.0	352	11	US-11-177-506-28	Sequence 28, Appl	350	25	56.8	228	9	US-10-195-888-114	Sequence 1226, Ap
278	25.5	58.0	404	11	US-11-172-740-1394	Sequence 1394, Ap	351	25	56.8	233	9	US-10-784-004-1226	Sequence 233, App
279	25.5	58.0	404	11	US-11-172-740-1395	Sequence 1395, Ap	352	25	56.8	250	9	US-10-330-773-233	Sequence 1036, Ap
280	25.5	58.0	404	11	US-11-172-740-1398	Sequence 1398, Ap	353	25	56.8	255	11	US-11-264-096-1036	Sequence 11597, Ap
281	25.5	58.0	404	11	US-11-188-298-8401	Sequence 8401, Ap	354	25	56.8	258	11	US-11-087-099-11597	Sequence 16924, A
282	25.5	58.0	404	11	US-11-188-298-9931	Sequence 9931, Ap	355	25	56.8	259	11	US-11-188-298-15924	Sequence 20419, A
283	25.5	58.0	406	11	US-11-172-740-1396	Sequence 1396, Ap	356	25	56.8	263	11	US-11-096-568A-20419	Sequence 7906, Ap
284	25.5	58.0	406	11	US-11-188-298-10590	Sequence 10590, A	357	25	56.8	265	9	US-10-467-657-7906	Sequence 668, App
285	25	56.8	18	11	US-11-033-039-1297	Sequence 1297, Ap	358	25	56.8	283	11	US-11-264-096-668	Sequence 669, App
286	25	56.8	18	11	US-11-033-039-1305	Sequence 1305, Ap	359	25	56.8	283	11	US-11-264-096-669	Sequence 22255, A
287	25	56.8	44	11	US-11-004-399-263	Sequence 263, App	360	25	56.8	291	9	US-11-096-568A-22255	Sequence 165, App
288	25	56.8	44	11	US-11-004-399-594	Sequence 594, App	361	25	56.8	297	9	US-10-511-989-165	Sequence 6771, Ap
289	25	56.8	44	11	US-11-004-399-4012	Sequence 4012, Ap	362	25	56.8	297	11	US-11-079-463-6771	Sequence 5, Appli
290	25	56.8	88	11	US-11-135-855-32	Sequence 32, Appl	363	25	56.8	299	11	US-11-040-215-5	Sequence 5, Appli
291	25	56.8	93	11	US-11-087-099-4873	Sequence 4873, Ap	364	25	56.8	302	9	US-10-330-773-235	Sequence 235, App
292	25	56.8	93	11	US-11-087-099-11728	Sequence 11728, A	365	25	56.8	303	9	US-10-517-939-214	Sequence 214, App
293	25	56.8	93	11	US-11-087-099-13114	Sequence 12114, A	366	25	56.8	303	11	US-11-087-099-3483	Sequence 3483, Ap
294	25	56.8	93	11	US-11-096-568A-15378	Sequence 15378, A	367	25	56.8	304	11	US-11-087-099-6526	Sequence 6526, Ap
295	25	56.8	95	11	US-11-096-568A-31441	Sequence 31441, A	368	25	56.8	304	11	US-11-087-099-8537	Sequence 8637, Ap
296	25	56.8	95	11	US-11-096-568A-33936	Sequence 33936, A	369	25	56.8	305	11	US-11-079-463-6837	Sequence 22254, A
297	25	56.8	97	9	US-10-485-788A-682	Sequence 682, App	370	25	56.8	306	11	US-11-096-568A-22254	Sequence 4, Appli
298	25	56.8	97	11	US-11-053-076-50	Sequence 50, Appl	371	25	56.8	307	11	US-11-040-215-4	Sequence 22, Appli
299	25	56.8	110	11	US-11-072-512-2974	Sequence 2974, Ap	372	25	56.8	307	11	US-11-040-240-4	Sequence 4, Appli
300	25	56.8	120	11	US-11-098-686-11261	Sequence 11261, A	373	25	56.8	319	9	US-10-467-657-640	Sequence 640, App
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303	25	56.8	128	9	US-11-096-568A-15377	Sequence 15377, A	376	25	56.8	323	9	US-10-506-454-447	Sequence 447, App
304	25	56.8	128	9	US-10-506-454-1393	Sequence 1393, Ap	377	25	56.8	325	9	US-11-188-298-18472	Sequence 18472, A
305	25	56.8	128	11	US-11-045-004-148	Sequence 148, App	378	25	56.8	325	11	US-10-793-626-254	Sequence 254, App
306	25	56.8	133	11	US-11-098-686-11145	Sequence 11145, A	379	25	56.8	326	11	US-11-096-568A-11596	Sequence 11596, A
307	25	56.8	134	11	US-11-096-568A-31440	Sequence 31440, A	380	25	56.8	326	11	US-11-087-099-6481	Sequence 6481, Ap
308	25	56.8	134	11	US-11-096-568A-33935	Sequence 33935, A	381	25	56.8	331	11	US-11-096-568A-11595	Sequence 11595, A
309	25	56.8	135	9	US-10-330-773-528	Sequence 528, App	382	25	56.8	331	11	US-11-098-686-10781	Sequence 10781, A
310	25	56.8	137	11	US-11-045-004-865	Sequence 865, App	383	25	56.8	332	11	US-11-096-568A-8379	Sequence 8379, Ap
311	25	56.8	137	11	US-11-045-004-1734	Sequence 1734, Ap	384	25	56.8	332	11	US-11-045-004-279	Sequence 279, App
312	25	56.8	139	9	US-10-467-657-5728	Sequence 5728, Ap	385	25	56.8	334	11	US-11-098-686-10126	Sequence 10126, A
313	25	56.8	145	9	US-10-330-773-530	Sequence 530, App	386	25	56.8	338	11	US-11-087-099-4640	Sequence 4640, Ap

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388	25	56.8	340	11	US-11-188-298-13099	Sequence 13099, A	461	25	56.8	491	9	US-10-219-062-34	Sequence 34, Appl
389	25	56.8	343	11	US-11-096-568A-15572	Sequence 15572, A	462	25	56.8	491	9	US-10-219-062-34	Sequence 34, Appl
390	25	56.8	348	11	US-11-096-568A-8378	Sequence 8378, Ap	463	25	56.8	491	9	US-10-233-134-34	Sequence 34, Appl
391	25	56.8	349	11	US-11-087-099-2026	Sequence 2026, Ap	464	25	56.8	495	11	US-11-188-298-6184	Sequence 6184, Ap
392	25	56.8	349	11	US-11-096-568A-5972	Sequence 5972, Ap	465	25	56.8	497	11	US-11-188-298-7036	Sequence 7036, Ap
393	25	56.8	349	11	US-11-096-568A-8377	Sequence 8377, Ap	466	25	56.8	497	11	US-11-188-298-8171	Sequence 8171, Ap
394	25	56.8	349	11	US-11-106-270-22	Sequence 22, Appl	467	25	56.8	497	11	US-11-188-298-13926	Sequence 13926, A
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398	25	56.8	365	11	US-11-096-568A-5971	Sequence 5971, Ap	471	25	56.8	503	9	US-10-878-556A-2	Sequence 2, Appli
399	25	56.8	365	11	US-11-096-568A-11594	Sequence 11594, A	472	25	56.8	504	11	US-11-232-440-37	Sequence 37, Appl
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401	25	56.8	376	11	US-11-075-185-15	Sequence 15, Appl	474	25	56.8	510	11	US-11-024-259-409	Sequence 409, App
402	25	56.8	378	11	US-11-207-626A-34	Sequence 34, Appl	475	25	56.8	511	11	US-11-188-298-9912	Sequence 9912, Ap
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404	25	56.8	380	11	US-11-096-568A-18516	Sequence 18516, A	477	25	56.8	512	11	US-11-079-463-10078	Sequence 10078, A
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407	25	56.8	387	11	US-11-188-298-7450	Sequence 7450, Ap	480	25	56.8	529	10	US-11-106-014-44	Sequence 44, Appl
408	25	56.8	389	11	US-11-096-568A-5634	Sequence 5634, Ap	481	25	56.8	529	11	US-11-073-457-44	Sequence 44, Appl
409	25	56.8	389	11	US-11-188-298-1562	Sequence 1562, Ap	482	25	56.8	529	11	US-11-073-460-44	Sequence 44, Appl
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411	25	56.8	391	11	US-11-087-099-3440	Sequence 3440, Ap	484	25	56.8	532	11	US-11-188-298-16230	Sequence 16230, A
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413	25	56.8	398	11	US-11-040-240-3	Sequence 3, Appli	486	25	56.8	536	9	US-10-194-487-58	Sequence 58, Appl
414	25	56.8	401	9	US-10-878-556A-179	Sequence 179, App	487	25	56.8	545	9	US-10-195-883-58	Sequence 58, Appl
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418	25	56.8	409	11	US-11-098-686-10130	Sequence 10130, A	491	25	56.8	548	9	US-10-467-657-696	Sequence 696, App
419	25	56.8	410	11	US-11-188-298-3233	Sequence 3233, Ap	492	25	56.8	552	11	US-11-232-406A-4	Sequence 4, Appli
420	25	56.8	413	11	US-11-188-298-3235	Sequence 3235, Ap	493	25	56.8	555	9	US-10-763-712A-30	Sequence 30, Appl
421	25	56.8	413	11	US-11-188-298-15320	Sequence 15320, A	494	25	56.8	559	11	US-11-096-568A-27572	Sequence 27572, A
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423	25	56.8	415	11	US-11-188-298-11955	Sequence 11955, A	496	25	56.8	577	11	US-11-087-099-5216	Sequence 5216, Ap
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429	25	56.8	424	11	US-11-188-298-9036	Sequence 9036, Ap	502	25	56.8	603	11	US-11-188-298-6362	Sequence 6362, A
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432	25	56.8	429	11	US-11-079-463-7406	Sequence 7406, Ap	505	25	56.8	614	11	US-11-072-512-3892	Sequence 3892, Ap
433	25	56.8	433	11	US-11-096-568A-5633	Sequence 5633, Ap	506	25	56.8	620	9	US-10-517-151-2	Sequence 2, Appli
434	25	56.8	438	11	US-11-172-740-2497	Sequence 2497, Ap	507	25	56.8	620	11	US-11-186-284-134	Sequence 134, App
435	25	56.8	439	11	US-11-087-099-2955	Sequence 2955, Ap	508	25	56.8	621	9	US-10-821-234-1376	Sequence 1376, Ap
436	25	56.8	439	11	US-11-172-740-2496	Sequence 2496, Ap	509	25	56.8	621	11	US-11-050-857-986	Sequence 986, App
437	25	56.8	439	11	US-11-188-298-13828	Sequence 13828, Ap	510	25	56.8	622	11	US-11-021-441-35	Sequence 35, Appl
438	25	56.8	440	11	US-11-087-099-10050	Sequence 10050, A	511	25	56.8	622	11	US-11-155-288-17	Sequence 17, Appl
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441	25	56.8	446	11	US-11-096-568A-11065	Sequence 11065, A	514	25	56.8	622	11	US-11-054-281-48	Sequence 48, Appl
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443	25	56.8	454	11	US-11-096-568A-27573	Sequence 27573, A	516	25	56.8	622	11	US-11-054-281-50	Sequence 50, Appl
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445	25	56.8	456	9	US-10-195-883-188	Sequence 188, App	518	25	56.8	626	10	US-11-180-855-1	Sequence 1, Appli
446	25	56.8	456	9	US-10-195-888-188	Sequence 188, App	519	25	56.8	628	11	US-11-040-215-1	Sequence 1, Appli
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448	25	56.8	456	11	US-11-301-554-1925	Sequence 1925, Ap	521	25	56.8	628	11	US-11-054-281-4	Sequence 4, Appli
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450	25	56.8	459	11	US-11-000-463-923	Sequence 923, App	523	25	56.8	628	11	US-11-050-857-225	Sequence 225, App
451	25	56.8	459	11	US-11-045-004-2051	Sequence 2051, Ap	524	25	56.8	630	11	US-11-155-288-18	Sequence 18, Appl
452	25	56.8	472	11	US-11-165-211-6	Sequence 6, Appli	525	25	56.8	630	11	US-11-054-281-47	Sequence 47, Appl
453	25	56.8	472	11	US-11-165-211-7	Sequence 7, Appli	526	25	56.8	662	9	US-10-493-909-80	Sequence 80, Appl
454	25	56.8	472	11	US-11-165-226-6	Sequence 6, Appli	527	25	56.8	677	11	US-11-188-298-6738	Sequence 6738, Ap
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456	25	56.8	478	11	US-11-079-463-8301	Sequence 8301, Ap	529	25	56.8	711	11	US-11-087-100-18	Sequence 18, Appl
457	25	56.8	481	11	US-11-188-298-12607	Sequence 12607, A	530	25	56.8	711	11	US-11-087-084-18	Sequence 18, Appl
458	25	56.8	482	11	US-11-045-004-2627	Sequence 2627, Ap	531	25	56.8	711	11	US-11-087-085-18	Sequence 18, Appl
459	25	56.8	488	9	US-10-995-561-860	Sequence 860, App	532	25	56.8	720	9	US-10-063-703-38	Sequence 38, Appl
			491	9	US-10-218-784-34	Sequence 34, Appl							

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535	25	56.8	720	9	US-10-195-888-170	Sequence 170, App	608	24	54.5	103	9	US-10-485-788A-739	Sequence 739, App
536	25	56.8	720	9	US-10-195-889-170	Sequence 170, App	609	24	54.5	103	11	US-11-053-076-109	Sequence 109, App
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541	25	56.8	735	11	US-11-087-099-9167	Sequence 9167, Ap	614	24	54.5	139	11	US-11-188-298-14140	Sequence 14140, A
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543	25	56.8	758	11	US-11-188-298-21656	Sequence 21656, A	616	24	54.5	155	9	US-10-467-657-5586	Sequence 5586, Ap
544	25	56.8	782	9	US-10-995-561-861	Sequence 861, App	617	24	54.5	156	11	US-11-045-004-2276	Sequence 2276, Ap
545	25	56.8	792	9	US-10-467-657-6026	Sequence 6026, Ap	618	24	54.5	186	9	US-10-506-454-1220	Sequence 1220, Ap
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549	25	56.8	847	9	US-10-995-561-863	Sequence 863, App	622	24	54.5	195	9	US-10-784-004-1054	Sequence 1054, Ap
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554	25	56.8	858	9	US-10-645-441-20	Sequence 20, Appl	627	24	54.5	201	9	US-10-195-888-108	Sequence 108, App
555	25	56.8	858	9	US-10-645-441-23	Sequence 23, Appl	628	24	54.5	201	9	US-10-195-889-108	Sequence 108, App
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592	25	56.8	2910	11	US-11-087-084-2	Sequence 2, Appl1	665	24	54.5	272	11	US-11-096-568A-22609	Sequence 22609, A
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595	25	56.8	3056	9	US-10-995-561-556	Sequence 556, App	668	24	54.5	281	11	US-11-179-977-5	Sequence 5, Appl1
596	25	56.8	7968	11	US-11-143-980-49	Sequence 49, Appl	669	24	54.5	281	11	US-11-096-568A-10188	Sequence 10188, A
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604	24	54.5	93	11	US-11-096-568A-4491	Sequence 4491, Ap	677	24	54.5	296	11	US-11-096-568A-17796	Sequence 17796, A
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681	24	54.5	300	9	US-10-195-888-18	Sequence 18, Appl	754	24	54.5	372	11	US-11-087-099-1983	Sequence 1983, Ap
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691	24	54.5	307	11	US-11-188-298-17520	Sequence 17520, A	764	24	54.5	383	11	US-11-096-568A-11435	Sequence 11435, A
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698	24	54.5	313	11	US-11-188-298-792	Sequence 792, App	771	24	54.5	399	11	US-11-096-568A-6651	Sequence 6651, Ap
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702	24	54.5	319	11	US-11-188-298-20507	Sequence 20507, A	775	24	54.5	408	11	US-11-087-099-2091	Sequence 2091, Ap
703	24	54.5	320	11	US-11-054-281-119	Sequence 119, App	776	24	54.5	410	11	US-11-226-869-495	Sequence 495, App
704	24	54.5	320	11	US-11-188-298-380	Sequence 380, App	777	24	54.5	410	11	US-11-045-004-2269	Sequence 2269, Ap
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709	24	54.5	328	11	US-11-096-568A-25249	Sequence 25249, A	782	24	54.5	417	8	US-10-511-937-2542	Sequence 2542, Ap
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711	24	54.5	330	11	US-11-055-822-202	Sequence 202, App	784	24	54.5	423	11	US-11-184-156-2	Sequence 2, Appli
712	24	54.5	330	11	US-11-239-674-86	Sequence 86, Appl	785	24	54.5	423	11	US-11-096-568A-13117	Sequence 13117, A
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734	24	54.5	352	11	US-11-096-568A-5125	Sequence 5125, Ap	807	24	54.5	446	11	US-11-229-371-92	Sequence 92, Appl
735	24	54.5	353	11	US-11-087-099-6968	Sequence 6968, Ap	808	24	54.5	446	11	US-11-228-923-92	Sequence 92, Appl
736	24	54.5	355	9	US-10-467-657-7628	Sequence 7628, Ap	809	24	54.5	446	11	US-11-228-875-92	Sequence 92, Appl
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738	24	54.5	357	11	US-11-087-099-11008	Sequence 11008, A	811	24	54.5	448	11	US-11-087-099-7022	Sequence 7022, Ap
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742	24	54.5	357	11	US-11-045-004-1742	Sequence 1742, Ap	815	24	54.5	463	11	US-11-087-099-6433	Sequence 6433, Ap
743	24	54.5	362	9	US-10-714-887-38	Sequence 38, Appl	816	24	54.5	463	11	US-11-087-099-8007	Sequence 8007, Ap
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ALIGNMENTS

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; APPLICANT: Lee, Nancy M
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; FILE REFERENCE: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF
; CURRENT APPLICATION NUMBER: US/11/242,111
; PRIOR FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: 60/614,746
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/651,344
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
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; TYPE: PRT
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; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
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; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
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; Sequence 8759, Application US/11079463
; Publication No. US20060073161A1
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; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
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; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
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; Publication No. US2006068386A1  
; GENERAL INFORMATION:  
; APPLICANT: Slesarev, Alexi I  
; APPLICANT: Mezhevaya, Katja V  
; APPLICANT: Polushin, Nikolai N  
; APPLICANT: Shcherbinina, Olga V  
; APPLICANT: Shakhova, Vera V  
; APPLICANT: Malykh, Andrei G  
; APPLICANT: Kozlyavkin, Sergei A  
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile  
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens  
; FILE REFERENCE: FID001  
; CURRENT APPLICATION NUMBER: US/10/506,454  
; CURRENT FILING DATE: 2004-08-31  
; PRIOR APPLICATION NUMBER: PCT/US03/06664  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: 60/361,742  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 1722  
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US-10-506-454-1079

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; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
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; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
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Query Match 68.2%; Score 30; DB 9; Length 370;  
Best Local Similarity 75.0%; Pred. No. 87;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
||:|  
Db 5 LQAQFDV 12

RESULT 8  
US-11-188-298-13429  
; Sequence 13429, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 13429  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus subsp. aureus Mu50  
US-11-188-298-13429

Query Match 68.2%; Score 30; DB 11; Length 370;  
Best Local Similarity 75.0%; Pred. No. 87;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
||:|  
Db 5 LQAQFDV 12

RESULT 9  
US-11-188-298-14941  
; Sequence 14941, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298

```
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14941
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis ATCC 12228
US-11-188-298-14941
```

```
Query Match      68.2%; Score 30; DB 11; Length 370;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 LQLEFDV 9
        ||:||||
DB       5 LQAFDVA 12
```

```
RESULT 10
US-10-454-437-130
; Sequence 130, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 130
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-130
```

```
Query Match      68.2%; Score 30; DB 9; Length 472;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 FQLEFDF 7
        ||:||||
DB       140 FQLEFDF 146
```

```
RESULT 11
US-10-454-437-132
```

```
; Sequence 132, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 132
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-132
```

```
Query Match      68.2%; Score 30; DB 9; Length 472;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 FQLEFDF 7
        ||:||||
DB       140 FQLEFDF 146
```

```
RESULT 12
US-10-506-454-1359
; Sequence 1359, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaeva, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozyavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; METHANOPYRUS KANDLERI AV19 AND MONOPHYLY OF ARCHAEAL METHANOGENS
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
```

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1359  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Methanopyrus kandleri  
US-10-506-454-1359

Query Match 68.2%; Score 30; DB 9; Length 585;  
Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEPDV 9  
|||::|||:  
Db 37 FLKVEFDGM 45

RESULT 13  
US-11-076-164-23  
; Sequence 23, Application US/11076164  
; Publication No. US20050283851A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrahams, Sharon  
; APPLICANT: Ashton, Anthony R  
; APPLICANT: Tanner, Gregory J  
; APPLICANT: Larkin, Philip J  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS INVOLVED IN PROANTHOCYANIDIN SYNTHESIS  
; FILE REFERENCE: 72110  
; CURRENT APPLICATION NUMBER: US/11/076,164  
; CURRENT FILING DATE: 2005-03-09  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Arabidopsis  
US-11-076-164-23

Query Match 65.9%; Score 29; DB 11; Length 31;  
Best Local Similarity 55.6%; Pred. No. 9.2;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEPDV 9  
|||::|||:  
Db 17 FLQVKFTAI 25

RESULT 14  
US-11-214-199-29  
; Sequence 29, Application US/11214199  
; Publication No. US2006003377A1  
; GENERAL INFORMATION:  
; APPLICANT: HILTON, Douglas J  
; APPLICANT: ALEXANDER, Warren S  
; APPLICANT: VINEY, Elizabeth M  
; APPLICANT: WILLSON, Tracey A  
; APPLICANT: RICHARDSON, Rachael T  
; APPLICANT: STARR, Robyn  
; APPLICANT: NICHOLSON, Sandra E  
; APPLICANT: METCALF, Donald  
; APPLICANT: NICOLA, Nicos A  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC PROTEINS COMPRISING A SOCS  
; FILE REFERENCE: 109762A  
; CURRENT APPLICATION NUMBER: US/11/214,199  
; CURRENT FILING DATE: 2005-08-29  
; PRIOR APPLICATION NUMBER: US/09/908,805  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/302,769  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 130

; TYPE: PRT  
; ORGANISM: Mouse  
US-11-214-199-29

Query Match 65.9%; Score 29; DB 11; Length 130;  
Best Local Similarity 71.4%; Pred. No. 45;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
|||::|||:  
Db 120 FLQLDFE 126

RESULT 15  
US-10-821-234-1278  
; Sequence 1278, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pc\_seq\_genes version 1.0  
; SEQ ID NO 1278  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1278

Query Match 65.9%; Score 29; DB 9; Length 161;  
Best Local Similarity 75.0%; Pred. No. 57;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
|||::|||:  
Db 79 LQMEKAV 86

RESULT 16  
US-11-076-164-2  
; Sequence 2, Application US/11076164  
; Publication No. US20050283851A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrahams, Sharon  
; APPLICANT: Ashton, Anthony R  
; APPLICANT: Tanner, Gregory J  
; APPLICANT: Larkin, Philip J  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS INVOLVED IN PROANTHOCYANIDIN SYNTHESIS  
; FILE REFERENCE: 72110  
; CURRENT APPLICATION NUMBER: US/11/076,164  
; CURRENT FILING DATE: 2005-03-09  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Arabidopsis  
US-11-076-164-2

Query Match 65.9%; Score 29; DB 11; Length 209;  
Best Local Similarity 55.6%; Pred. No. 76;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
|||::|||:  
Db 37 FLQVKFTAI 45

```
RESULT 17
US-11-076-164-18
; Sequence 18, Application US/11076164
; Publication No. US20050283851A1
; GENERAL INFORMATION:
; APPLICANT: Abrahams, Sharon
; APPLICANT: Ashton, Anthony R
; APPLICANT: Tanner, Gregory J
; APPLICANT: Larkin, Philip J
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS INVOLVED IN PROANTHOCYANIDIN SYNTHESIS
; FILE REFERENCE: 721110
; CURRENT APPLICATION NUMBER: US/11/076,164
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: A.thaliana
US-11-076-164-18

Query Match      65.9%; Score 29; DB 11; Length 209;
Best Local Similarity 55.6%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 0;

QY      1 FLQLEPDAV 9
Db      37 FLQVKFTAI 45

RESULT 18
US-11-188-298-5285
; Sequence 5285, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 5285
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Campylobacter jejuni subsp. jejuni NCTC 11168
US-11-188-298-5285

Query Match      65.9%; Score 29; DB 11; Length 280;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY      2 LQLEPDAV 9
Db      250 LLELPDKI 257

RESULT 19
US-11-096-568A-30214
; Sequence 30214, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30214
```

```
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(291)
; OTHER INFORMATION: Ceres Seq. ID no. 4950120
US-11-096-568A-30214

Query Match      65.9%; Score 29; DB 11; Length 291;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLEFD 7
Db      118 FVKLEFD 124

RESULT 20
US-11-096-568A-30213
; Sequence 30213, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30213
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(292)
; OTHER INFORMATION: Ceres Seq. ID no. 4950119
US-11-096-568A-30213

Query Match      65.9%; Score 29; DB 11; Length 292;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLEFD 7
Db      119 FVKLEFD 125

RESULT 21
US-11-096-568A-30212
; Sequence 30212, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30212
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(308)
; OTHER INFORMATION: Ceres Seq. ID no. 4950118
US-11-096-568A-30212

Query Match      65.9%; Score 29; DB 11; Length 308;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
```

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLOLEFD 7  
|:|:|:|  
Db 135 FVKLEFD 141

## RESULT 22

US-11-079-463-7003  
; Sequence 7003, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA  
; FILE REFERENCE: PATH00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 7003  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-11-079-463-7003

Query Match 65.9%; Score 29; DB 11; Length 406;

Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLOLEFDA 8  
|:|:|:|  
Db 385 YLDLEYDA 392

## RESULT 23

US-11-096-568A-30753  
; Sequence 30753, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 30753  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(426)  
; OTHER INFORMATION: Ceres Seq. ID no. 4972073  
US-11-096-568A-30753

Query Match 65.9%; Score 29; DB 11; Length 426;

Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLEFPAV 9  
|:|:|:|  
Db 81 LELDFDSV 88

## RESULT 24

US-11-054-168B-6  
; Sequence 6, Application US/11054168B  
; Publication No. US20050273879A1

; GENERAL INFORMATION:  
; APPLICANT: Shi, Jinrui  
; APPLICANT: Sleister, Heidi  
; TITLE OF INVENTION: Phytate Polynucleotides and Methods of  
; FILE REFERENCE: 035718/285984  
; CURRENT APPLICATION NUMBER: US/11/054,168B  
; CURRENT FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: 60/543,079  
; PRIOR FILING DATE: 2004-02-09  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-054-168B-6

Query Match 65.9%; Score 29; DB 11; Length 451;  
Best Local Similarity 77.8%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLOLEFPAV 9  
|:|:|:|  
Db 287 FLOLVSDAV 295

## RESULT 25

US-11-096-568A-30752  
; Sequence 30752, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 30752  
; LENGTH: 520  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(520)  
; OTHER INFORMATION: Ceres Seq. ID no. 4972072  
US-11-096-568A-30752

Query Match 65.9%; Score 29; DB 11; Length 520;  
Best Local Similarity 62.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLEFPAV 9  
|:|:|:|  
Db 175 LELDFDSV 182

## RESULT 26

US-11-096-568A-30751  
; Sequence 30751, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 30751  
; LENGTH: 542  
; TYPE: PRT

ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(542)  
OTHER INFORMATION: Ceres Seq. ID no. 4972071  
US-11-096-568A-30751

Query Match 65.9%; Score 29; DB 11; Length 542;  
Best Local Similarity 62.5%; Pred. No. 2.2e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
Db 197 LELDFDSV 204

RESULT 27  
US-11-182-016-8  
Sequence 8, Application US/11182016  
Publication No. US20060019294A1  
GENERAL INFORMATION:  
APPLICANT: SUGEN, INC.  
TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS  
FILE REFERENCE: 038602/0102  
CURRENT APPLICATION NUMBER: US/11/182,016  
CURRENT FILING DATE: 2005-07-15  
PRIOR APPLICATION NUMBER: US/09/958,359  
PRIOR FILING DATE: 2002-02-05  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 832  
TYPE: PRT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Tks 202  
US-11-182-016-8

Query Match 65.9%; Score 29; DB 11; Length 832;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
Db 391 FLQSELDAL 399

RESULT 28  
US-11-079-463-9378  
Sequence 9378, Application US/11079463  
Publication No. US20060073161A1  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR  
FILE REFERENCE: PATH00-03DIV2  
CURRENT APPLICATION NUMBER: US/11/079,463  
CURRENT FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/128,705  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: US 09/540,209  
PRIOR FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 10444  
SEQ ID NO 9378  
LENGTH: 1081  
TYPE: PRT  
ORGANISM: B. fragilis  
US-11-079-463-9378

Query Match 65.9%; Score 29; DB 11; Length 1081;  
Best Local Similarity 71.4%; Pred. No. 4.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEPDAV 9  
Db 767 EIEFDV 773

RESULT 29  
US-09-978-360A-699  
Sequence 699, Application US/09978360A  
Publication No. US20060009633A9  
GENERAL INFORMATION:  
APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueret, Lydie  
APPLICANT: Jobert, Severin  
APPLICANT: Clusel, Catherine  
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
FILE REFERENCE: 56.US4.CIP  
CURRENT APPLICATION NUMBER: US/09/978,360A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: US 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: US 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: US 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: US 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: US 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: US 60/099,273  
PRIOR FILING DATE: -09-04  
PRIOR APPLICATION NUMBER: US 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: US 09/215,435  
PRIOR FILING DATE: 1998-12-17  
PRIOR APPLICATION NUMBER: PCT/IB98/02122  
PRIOR FILING DATE: 1998-12-17  
PRIOR APPLICATION NUMBER: US 09/247,155  
PRIOR FILING DATE: 1999-02-09  
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 810  
SOFTWARE: Patent.pm  
SEQ ID NO 699  
LENGTH: 72  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -32..-1  
US-09-978-360A-699

Query Match 63.6%; Score 28; DB 7; Length 72;  
Best Local Similarity 55.6%; Pred. No. 38;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLOLEFDV 9  
Db 36 FSQIRYDAV 44

RESULT 30  
US-09-978-360A-551  
Sequence 551, Application US/09978360A  
Publication No. US20060009633A9  
GENERAL INFORMATION:  
APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueret, Lydie  
APPLICANT: Jobert, Severin  
APPLICANT: Clusel, Catherine  
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
FILE REFERENCE: 56.US4.CIP  
CURRENT APPLICATION NUMBER: US/09/978,360A



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; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 551
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -32..-1
US-09-978-360A-551

Query Match 63.6%; Score 28; DB 7; Length 106;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FQLEPDAV 9
Db 36 FSQIRYDAV 44

RESULT 31
US-09-978-360A-701
; Sequence 701, Application US/09978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
```

```
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 701
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -32..-1
US-09-978-360A-701

Query Match 63.6%; Score 28; DB 7; Length 106;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FQLEPDAV 9
Db 36 FSQIRYDAV 44

RESULT 32
US-11-087-099-9107
; Sequence 9107, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9107
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Perilla frutescens var. crispa
US-11-087-099-9107

Query Match 63.6%; Score 28; DB 11; Length 176;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQLEPDA 8
Db 169 FLEBEDA 176

RESULT 33
US-11-188-298-19433
; Sequence 19433, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19433
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Perilla frutescens var. crispa
US-11-188-298-19433

Query Match 63.6%; Score 28; DB 11; Length 176;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 FLOLEFDA 8

||:|||||

Db 169 FLELEEDA 176

RESULT 34

US-11-079-463-5651  
; Sequence 5651, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Brelton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR  
; FILE REFERENCE: PATH00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 5651  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: B. fragilis  
US-11-079-463-5651

Query Match

Best Local Similarity 63.6%; Score 28; DB 11; Length 187;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLOLEFDA 8

||:|||||

Db 35 FQQEFDA 42

RESULT 35

US-11-098-686-11043  
; Sequence 11043, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: US 60/416,395  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11043  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-11043

Query Match

Best Local Similarity 63.6%; Score 28; DB 11; Length 329;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LQLEFDAV 9

|||||

Db 306 LSLEFDKV 313

RESULT 36

US-11-098-686-11320  
; Sequence 11320, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:

; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: US 60/416,395  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11320  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-11320

Query Match 63.6%; Score 28; DB 11; Length 376;

Best Local Similarity 85.7%; Pred. No. 2.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLEFDA 8

|||||

Db 356 LQEFDA 362

RESULT 37

US-10-714-887-176  
; Sequence 176, Application US/10714887  
; Publication No. US20060015972A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: HEARD, Jacqueline  
; APPLICANT: RIECHMANN, Jose Luis  
; APPLICANT: CREELMAN, Robert  
; APPLICANT: RATCLIFFE, Oliver  
; APPLICANT: CANALES, Roger  
; APPLICANT: REPETTI, Peter  
; APPLICANT: KUMIMOTO, Roderick W  
; APPLICANT: GUTTERSON, Neal  
; APPLICANT: REUBER, T. Lynne  
; APPLICANT: PINEDA, Omaira  
; APPLICANT: SHERMAN, Bradley K  
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS  
; FILE REFERENCE: MEI0058-CIP  
; CURRENT APPLICATION NUMBER: US/10/714,887  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 10/412,699  
; PRIOR FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: 09/506,720  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/135,134  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/394,519  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: 09/533,392  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/533,029  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/532,591  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/533,030  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 60/125,814  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/713,994  
; PRIOR FILING DATE: 2000-11-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 430  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 176  
; LENGTH: 387

; TYPE: PRT  
; ORGANISM: Oryza sativa (japonica cultivar-group)  
; FEATURE:  
; OTHER INFORMATION: G3746 polypeptide Orthologous to G3086  
US-10-714-887-176

Query Match 63.6%; Score 28; DB 9; Length 387;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEPDAV 9  
|:|||||  
Db 297 FLQLQPDV 305

## RESULT 38

US-11-087-099-5010  
; Sequence 5010, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 5010  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-087-099-5010

Query Match 63.6%; Score 28; DB 11; Length 388;  
Best Local Similarity 55.6%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEPDAV 9  
|:|||||  
Db 113 FVSTQPDV 121

## RESULT 39

US-11-087-099-6630  
; Sequence 6630, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 6630  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-087-099-6630

Query Match 63.6%; Score 28; DB 11; Length 388;  
Best Local Similarity 55.6%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEPDAV 9  
|:|||||  
Db 113 FVSTQPDV 121

## RESULT 40

US-11-087-099-9369  
; Sequence 9369, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 9369  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-087-099-9369

Query Match 63.6%; Score 28; DB 11; Length 388;  
Best Local Similarity 55.6%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEPDAV 9  
|:|||||  
Db 113 FVSTQPDV 121

## RESULT 41

US-11-188-298-6017  
; Sequence 6017, Application US/11188298  
; Publication No. US2006007552A1  
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 6017  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis V583  
US-11-188-298-6017

Query Match 63.6%; Score 28; DB 11; Length 390;  
Best Local Similarity 55.8%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEPDAV 9  
|:|||||  
Db 93 FIPTDFDAV 101

## RESULT 42

US-10-506-454-355  
; Sequence 355, Application US/10506454  
; Publication No. US20060068386A1  
; GENERAL INFORMATION:

; APPLICANT: Slesarev, Alexi I  
; APPLICANT: Mezhevaya, Katja V  
; APPLICANT: Polushin, Nikolai N  
; APPLICANT: Shcherbinina, Olga V  
; APPLICANT: Shakhova, Vera V  
; APPLICANT: Malykh, Andrei G  
; APPLICANT: Kozyavkin, Sergei A  
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophilic  
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens  
; TITLE OF INVENTION: and Methods of Use Thereof  
; FILE REFERENCE: FID001  
; CURRENT APPLICATION NUMBER: US/10/506,454  
; CURRENT FILING DATE: 2004-08-31  
; PRIOR APPLICATION NUMBER: PCT/US03/06664  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: 60/361,742  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 1722  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 355

1 LENGTH: 410  
1 TYPE: PRT  
1 ORGANISM: Methanopyrus kandleri  
US-10-506-454-355

Query Match 63.6%; Score 28; DB 9; Length 410;  
Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
Db 187 FLRFEFD 193

RESULT 43  
US-11-188-298-10873  
; Sequence 10873, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 10873  
; LENGTH: 493  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(493)  
; OTHER INFORMATION: unsure at all xaa locations  
US-11-188-298-10873

Query Match 63.6%; Score 28; DB 11; Length 493;  
Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFD 7  
Db 213 FLQDEFD 219

RESULT 44  
US-11-188-298-5120  
; Sequence 5120, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 5120  
; LENGTH: 511  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-11-188-298-5120

Query Match 63.6%; Score 28; DB 11; Length 511;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEFDV 9  
Db 375 LKIEFDSI 382

RESULT 45  
US-11-288-720-18  
; Sequence 18, Application US/11288720  
; Publication No. US20060084798A1  
; GENERAL INFORMATION:  
; APPLICANT: Bradfield, Christopher A.  
; APPLICANT: Gu, Yi Zhong  
; APPLICANT: Hogenesch, John B.  
; TITLE OF INVENTION: cDNAs and Proteins Involved in Hypoxia, Circadian and Orphan Signaling Pathways, and Methods of Use  
; FILE REFERENCE: WARF-0044 (P98022)  
; CURRENT APPLICATION NUMBER: US/11/288,720  
; CURRENT FILING DATE: 2005-11-29  
; PRIOR APPLICATION NUMBER: US/09/555,362  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: PCT/US98/25314  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/066,863  
; PRIOR FILING DATE: 1997-11-28  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-288-720-18

Query Match 63.6%; Score 28; DB 11; Length 585;  
Best Local Similarity 71.4%; Pred. No. 3.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLEFDV 9  
Db 545 QLEFDAL 551

RESULT 46  
US-11-143-980-50  
; Sequence 50, Application US/11143980  
; Publication No. US2005027133A1  
; GENERAL INFORMATION:  
; APPLICANT: He, Min  
; APPLICANT: Hucul, John  
; APPLICANT: Haltli, Bradley A.  
; APPLICANT: Wagenaar, Melissa M.  
; APPLICANT: Graziani, Edmund  
; APPLICANT: Summers, Mia  
; APPLICANT: Kulowski, Kerry  
; APPLICANT: Pong, Kevin  
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex Polyketide  
; FILE REFERENCE: AM-101426US  
; CURRENT APPLICATION NUMBER: US/11/143,980  
; CURRENT FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: US 60/664,483  
; PRIOR FILING DATE: 2005-03-23  
; PRIOR APPLICATION NUMBER: US 60/576,895  
; PRIOR FILING DATE: 2004-06-03  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 50  
; LENGTH: 3073  
; TYPE: PRT  
; ORGANISM: Streptomyces sp.  
US-11-143-980-50

Query Match 63.6%; Score 28; DB 11; Length 3073;  
Best Local Similarity 55.6%; Pred. No. 2.5e+03;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEFDV 9  
Db 1 LKIEFDV 9

Db 2973 FVELGFDSV 2981

## RESULT 47

US-10-793-626-2964  
; Sequence 2964, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2964  
; LENGTH: 5024  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (5024)  
; OTHER INFORMATION: variable amino acid  
US-10-793-626-2964

Query Match 63.6%; Score 28; DB 9; Length 5024;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLEPFD 7

Db 4178 LQLEPFD 4183

## RESULT 48

US-11-079-463-10264  
; Sequence 10264, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR  
; FILE REFERENCE: PATH00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 10264  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-11-079-463-10264

Query Match 61.4%; Score 27; DB 11; Length 91;  
Best Local Similarity 44.4%; Pred. No. 82;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLEPDAV 9

Db 53 YFEVEPDAV 61

## RESULT 49

US-11-144-947-539  
; Sequence 539, Application US/11144947

; Publication No. US20060084082A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2C2  
; CURRENT APPLICATION NUMBER: US/11/144,947  
; CURRENT FILING DATE: 2005-06-06  
; PRIOR APPLICATION NUMBER: 09/882,171  
; PRIOR FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/190,068  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 10/164,861  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 539  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (36)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-11-144-947-539

Query Match 61.4%; Score 27; DB 11; Length 128;  
Best Local Similarity 44.4%; Pred. No. 1.2e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLEPDAV 9

Db 61 YIQVEFSAL 69

## RESULT 50

US-11-079-463-5238  
; Sequence 5238, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR  
; FILE REFERENCE: PATH00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 5238  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-11-079-463-5238

Query Match 61.4%; Score 27; DB 11; Length 158;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLQLEPD 7  
|||  
Db 52 FLQFNFD 58

Search completed: May 9, 2006, 02:36:12  
Job time : 19.8 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:05:23 ; Search time 98.4 Seconds  
(without alignments)  
40.187 Million cell updates/sec

Title: US-09-870-216C-7

Perfect score: 50

Sequence: 1 FLWFEIDIV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- A\_Geneseq\_21.\*
- 1: Geneseq1980s.\*
  - 2: Geneseq1990s.\*
  - 3: Geneseq2000s.\*
  - 4: Geneseq2001s.\*
  - 5: Geneseq2002s.\*
  - 6: Geneseq2003as.\*
  - 7: Geneseq2003bs.\*
  - 8: Geneseq2004s.\*
  - 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	5	ABR08363 Synthetic
2	50	100.0	9	7	ABR82215 Human ant
3	50	100.0	352	5	ABR08368 Human can
4	39	78.0	585	7	ABO67351 Klebsiell
5	39	78.0	587	6	AAO30104 Yersinia
6	39	78.0	1717	4	AAB20498 Ostrinia
7	39	78.0	1717	8	ADS76164 European
8	38	76.0	589	6	ABM69298 Phototrab
9	37	74.0	109	9	ADY17237 PRO polyp
10	37	74.0	150	5	ABB49338 Listeria
11	37	74.0	273	5	ABP64842 Human pro
12	37	74.0	528	5	ABB54865 Lactococc
13	37	74.0	529	8	ADS29413 Bacterial
14	37	74.0	587	6	ABM70700 Phototrab
15	36	72.0	269	5	ABB53431 Lactococc
16	36	72.0	280	4	ABG01152 Novel hum
17	36	72.0	373	7	ABO75288 Pseudomon
18	36	72.0	402	8	ADS41622 Bacterial
19	36	72.0	410	4	ABG01159 Novel hum
20	36	72.0	591	6	ABM68497 Phototrab
21	36	72.0	652	6	ABO14689 Novel hum
22	36	72.0	700	6	ABO14690 Novel hum
23	36	72.0	700	7	ADD14125 Human src
24	36	72.0	700	7	ADJ70236 Human hea

25	36	72.0	1097	4	ABG01151	Abg01151 Novel hum
26	36	72.0	1759	8	ADS76158	Ads76158 Black cut
27	35	70.0	217	5	ADI17021	Adi17021 Human NOV
28	35	70.0	232	7	ADC86399	Adc86399 Human GPC
29	35	70.0	307	4	AAG71459	Aag71459 Human olf
30	35	70.0	315	4	AAG72215	Aag72215 Human olf
31	35	70.0	315	5	ABG79345	Abg79345 Human GPC
32	35	70.0	315	5	ADI16656	Adi16656 Human NOV
33	35	70.0	315	6	ABR01643	AbR01643 Human G p
34	35	70.0	315	8	ADN42310	Adn42310 Human nov
35	35	70.0	326	5	ABP95915	Abp95915 Human GPC
36	35	70.0	326	5	AAU95516	Aau95516 Human olf
37	35	70.0	326	7	ADC85959	Adc85959 Human GPC
38	35	70.0	326	7	ADC85993	Adc85993 Human GPC
39	35	70.0	326	8	ADG83292	Adg83292 Human Olf
40	35	70.0	379	8	ADM42835	Adm42835 Rat odour
41	35	70.0	543	8	ADL04719	Adl04719 M. catarr
42	35	70.0	599	3	AAE25149	Aae25149 Eucalyptu
43	35	70.0	720	8	ADY25106	Ady25106 Plant ful
44	35	70.0	816	3	AAE25508	Aae25508 Eucalyptu
45	35	70.0	951	6	ADA33169	Ada33169 Acinetoba
46	34	68.0	37	4	AAE88375	Aae88375 Human imm
47	34	68.0	73	4	AAE89032	Aae89032 Human imm
48	34	68.0	81	8	ADV88683	Adv88683 Streptoco
49	34	68.0	81	8	ADV79936	Adv79936 Streptoco
50	34	68.0	195	3	AAG21340	Aag21340 Arabidops
51	34	68.0	209	3	AAE18245	Aae18245 Plasmodiu
52	34	68.0	215	3	AAG38094	Aag38094 Arabidops
53	34	68.0	215	3	AAG21339	Aag21339 Arabidops
54	34	68.0	215	3	AAG36773	Aag36773 Arabidops
55	34	68.0	215	3	AAE14291	Aae14291 Arabidops
56	34	68.0	254	6	ABM72105	Abm72105 Staphyloc
57	34	68.0	254	8	ADS91297	Ads91297 FenX, SEQ
58	34	68.0	262	7	ABO80272	AbO80272 Pseudomon
59	34	68.0	296	6	ABU26071	Abu26071 Protein e
60	34	68.0	318	3	AAG40072	Aag40072 Arabidops
61	34	68.0	318	3	AAG36772	Aag36772 Arabidops
62	34	68.0	318	3	AAG38093	Aag38093 Arabidops
63	34	68.0	318	3	AAG14290	Aag14290 Arabidops
64	34	68.0	342	3	AAG14289	Aag14289 Arabidops
65	34	68.0	342	3	AAG38092	Aag38092 Arabidops
66	34	68.0	358	3	AAG40071	Aag40071 Arabidops
67	34	68.0	366	3	AAG40070	Aag40070 Arabidops
68	34	68.0	378	3	AAE13573	Aae13573 Streptomy
69	34	68.0	416	6	ABU20792	Abu20792 Protein e
70	34	68.0	422	3	AAG36771	Aag36771 Arabidops
71	34	68.0	422	8	ADN73955	Adn73955 Thale cre
72	34	68.0	422	8	ADT56474	Adt56474 Plant pol
73	34	68.0	534	5	ABE91079	AbE91079 Herbicida
74	34	68.0	651	8	ADQ65671	Adq65671 Novel hum
75	34	68.0	720	8	ADS28846	Ads28846 Bacterial
76	34	68.0	2118	4	ABG23416	Abg23416 Novel hum
77	33	66.0	49	8	ADN33138	Adn33138 Human tra
78	33	66.0	55	4	ABG17988	Abg17988 Novel hum
79	33	66.0	55	8	ABO55227	AbO55227 Human gen
80	33	66.0	67	4	AAU22272	Aau22272 Human car
81	33	66.0	67	7	ADJ07658	Adj07658 Human car
82	33	66.0	67	8	ADJ07658	Adj07658 Human car
83	33	66.0	85	2	AAW32800	Aaw32800 ERT-1 pro
84	33	66.0	85	2	AAW27723	Aaw27723 Amino aci
85	33	66.0	85	4	AAW24177	Aaw24177 Human EST
86	33	66.0	217	5	ADI17024	Adi17024 Human NOV
87	33	66.0	225	3	AAG06368	Aag06368 Arabidops
88	33	66.0	226	3	AAG06367	Aag06367 Arabidops
89	33	66.0	226	8	ADN74753	Adn74753 Thale cre
90	33	66.0	227	2	AAE60569	Aae60569 Human nor
91	33	66.0	232	6	AAU25058	Aau25058 Protein e
92	33	66.0	235	4	AAU57493	Aau57493 Propionib
93	33	66.0	235	6	ABM54012	Abm54012 Propionib
94	33	66.0	239	3	AAG06366	Aag06366 Arabidops
95	33	66.0	256	3	AAG58234	Aag58234 Arabidops
96	33	66.0	269	7	ABG75161	Abg75161 R mellilot
97	33	66.0	270	8	ADS29986	Ads29986 Bacterial

98	33	66.0	284	2	AAW98436	Aaw98436	H. pylori	171	32	64.0	229	3	AAG52872	Arabidops
99	33	66.0	296	6	ABO14635	Abol14635	Novel hum	172	32	64.0	229	4	AU33521	Enterococ
100	33	66.0	296	6	ABG99919	Abg99919	Human nov	173	32	64.0	229	4	AU35020	Enterococ
101	33	66.0	309	2	AAW32798	Aaw32798	Polypepti	174	32	64.0	229	6	ABU14479	Staphyloc
102	33	66.0	309	2	AAW27722	Aaw27722	Anino aci	175	32	64.0	229	6	ABU14479	Staphyloc
103	33	66.0	309	8	ADN05882	Adn05882	Antipsori	176	32	64.0	229	6	ABU24040	Protein e
104	33	66.0	311	4	ABG71801	Abg71801	Human olf	177	32	64.0	229	6	ABU24839	Protein e
105	33	66.0	311	5	ABP61140	Abp61140	Human GPC	178	32	64.0	230	4	AU37459	Staphyloc
106	33	66.0	311	5	AAU95620	Aau95620	Human olf	179	32	64.0	230	4	AU37191	Staphyloc
107	33	66.0	311	7	ADC86219	Adc86219	Human GPC	180	32	64.0	230	6	ABU16463	Protein e
108	33	66.0	311	7	ADC79338	Adc79338	Human G p	181	32	64.0	230	6	ABM72465	Staphyloc
109	33	66.0	338	2	AAV35632	Aay35632	Chlamydia	182	32	64.0	231	5	ABP39249	Staphyloc
110	33	66.0	343	5	ABB90614	Abb90614	Chlamydia	183	32	64.0	231	6	ABU43783	Protein e
111	33	66.0	345	4	AAU24676	Aau24676	Human olf	184	32	64.0	231	6	ABU43157	Protein e
112	33	66.0	345	5	ABP95901	Abp95901	Human GPC	185	32	64.0	231	8	ADU06013	Staphyloc
113	33	66.0	345	5	AAU85296	Aau85296	G-coupled	186	32	64.0	252	9	ABE40743	L. pneumo
114	33	66.0	357	8	ADR43051	Adr43051	IPT-like	187	32	64.0	255	9	ABE37428	L. pneumo
115	33	66.0	363	6	ADA34674	Ada34674	Acinetoba	188	32	64.0	267	8	ABM84469	Human dia
116	33	66.0	416	6	ABO14636	Abol14636	Novel hum	189	32	64.0	279	6	ADA34294	Acinetoba
117	33	66.0	441	6	ABU39056	Abu39056	Protein e	190	32	64.0	284	3	AAG61660	Arabidops
118	33	66.0	516	2	AAU80279	Aar80279	N. crassa	191	32	64.0	284	7	ADD48502	Human Pro
119	33	66.0	601	5	ABB93437	Abb93437	Herbicida	192	32	64.0	284	7	ADD46807	Human Pro
120	33	66.0	602	5	ABU49869	Abu49869	Protein e	193	32	64.0	284	7	ADD46811	Human Pro
121	33	66.0	611	6	ABU49703	Abu49703	Protein e	194	32	64.0	285	9	ADV16952	Human hyd
122	33	66.0	784	4	ABB61207	Abb61207	Drosophil	195	32	64.0	286	7	ADD48605	Human Pro
123	33	66.0	1230	4	AAU70675	Aau70675	Human oto	196	32	64.0	306	8	ADY08615	Plant ful
124	33	66.0	1307	4	AAU70672	Aau70672	Human oto	197	32	64.0	308	8	ADA35806	Acinetoba
125	33	66.0	1992	4	AAU70674	Aau70674	Murine ot	198	32	64.0	314	8	ADX93292	Plant ful
126	33	66.0	1997	4	AAU70676	Aau70676	Brain lon	199	32	64.0	328	4	AAU37649	Streptoco
127	33	66.0	1997	4	AAU70673	Aau70673	Human oto	200	32	64.0	328	5	ABP28638	Streptoco
128	33	66.0	1997	4	AAU70671	Aau70671	Murine ot	201	32	64.0	328	5	ABP28639	Streptoco
129	33	66.0	298	4	AAU70669	Aau70669	Murine co	202	32	64.0	328	6	ABU02873	S. pneumo
130	33	66.0	2371	4	AAU70670	Aau70670	Murine br	203	32	64.0	328	6	ABP81574	Streptoco
131	32	64.0	39	4	AAU14378	Aam14378	Peptide #	204	32	64.0	328	6	ABU45775	Protein e
132	32	64.0	39	4	ABB33326	Abb33326	Peptide #	205	32	64.0	328	6	ABU46600	Protein e
133	32	64.0	39	4	AAU26791	Aam26791	Peptide #	206	32	64.0	328	8	ADK48484	Streptoco
134	32	64.0	39	4	ABB28151	Abb28151	Human pep	207	32	64.0	328	8	ADM92050	S pneumo
135	32	64.0	39	4	ABB18786	Abb18786	Protein #	208	32	64.0	328	8	ADV88992	Streptoco
136	32	64.0	39	4	AAU66505	Aam66505	Human bon	209	32	64.0	328	8	ADV80245	Streptoco
137	32	64.0	39	5	ABG36157	Abg36157	Human pep	210	32	64.0	328	8	ADV82369	Streptoco
138	32	64.0	43	4	AAU14395	Aam14395	Peptide #	211	32	64.0	342	8	ADN25879	Novel S.
139	32	64.0	43	4	ABB33343	Abb33343	Peptide #	212	32	64.0	342	8	ADN25879	Novel S.
140	32	64.0	43	4	AAU26808	Aam26808	Peptide #	213	32	64.0	343	9	AEA58347	Streptoco
141	32	64.0	43	4	ABE28168	Abb28168	Human pep	214	32	64.0	364	7	ADM05927	Human pro
142	32	64.0	43	4	ABE18803	Abb18803	Protein #	215	32	64.0	390	3	AAG19495	Arabidops
143	32	64.0	43	4	AAU66522	Aam66522	Human bon	216	32	64.0	390	3	AAG52871	Arabidops
144	32	64.0	43	4	AAU54129	Aam54129	Human bra	217	32	64.0	394	3	AAG52870	Arabidops
145	32	64.0	43	4	ABG48190	Abg48190	Human liv	218	32	64.0	394	3	AAG19494	Arabidops
146	32	64.0	43	4	AAU02122	Aam02122	Peptide #	219	32	64.0	400	8	ADY08467	Plant ful
147	32	64.0	43	5	ABG36174	Abg36174	Human pep	220	32	64.0	419	7	ABO66272	Klebsiell
148	32	64.0	51	8	ABO54758	Abos4758	Human gen	221	32	64.0	427	3	AAG46725	Arabidops
149	32	64.0	56	4	ABE17838	Abb17838	Human ner	222	32	64.0	440	3	AAG46728	Arabidops
150	32	64.0	63	4	ABE23038	Abb23038	Protein #	223	32	64.0	440	3	AAG13314	Arabidops
151	32	64.0	63	5	ABG40618	Abg40618	Human pep	224	32	64.0	443	3	AAG14094	Arabidops
152	32	64.0	65	5	ADK35689	Adk35689	Novel hum	225	32	64.0	446	3	AAG46717	Arabidops
153	32	64.0	68	3	AAU00631	Aag00631	Human sec	226	32	64.0	450	8	ADX72022	Plant ful
154	32	64.0	69	2	AAU11991	Aay11991	Human 5'	227	32	64.0	464	4	AU38230	Salmonell
155	32	64.0	101	5	ABG98425	Abg98425	Thermus t	228	32	64.0	469	5	ABU47653	Listeria
156	32	64.0	120	7	ABO62070	Abos62070	Klebsiell	229	32	64.0	469	6	ABU41961	Protein e
157	32	64.0	127	3	AAG44713	Aag44713	Zea mays	230	32	64.0	480	7	ADC96533	E. faeciu
158	32	64.0	130	4	AU31276	Aau31276	Novel hum	231	32	64.0	481	2	ADP72095	Human mGI
159	32	64.0	135	8	ADX68453	Adx68453	Plant ful	232	32	64.0	493	2	AAR26898	Jojoba fa
160	32	64.0	148	6	ADB09809	Adb09809	Alloioococ	233	32	64.0	493	2	AAR37485	Jojoba wa
161	32	64.0	149	3	AAG05261	Aag05261	Arabidops	234	32	64.0	493	2	AAR76470	Jojoba fa
162	32	64.0	155	4	ADG07176	Adg07176	Novel hum	235	32	64.0	493	2	AAR79934	Jojoba fa
163	32	64.0	183	7	ABD36341	Abd36341	Human imm	236	32	64.0	493	2	AAR77163	Jojoba fa
164	32	64.0	194	3	AAG05260	Aag05260	Arabidops	237	32	64.0	493	2	AAR87509	Resynthes
165	32	64.0	202	9	ADY19135	Ady19135	PRO polyp	238	32	64.0	493	2	AAR87508	Jojoba fa
166	32	64.0	204	3	AAG05259	Aag05259	Arabidops	239	32	64.0	493	5	ABG97573	Jojoba fa
167	32	64.0	206	6	ABU35095	Abu35095	Protein e	240	32	64.0	493	7	ADU77055	Jojoba fa
168	32	64.0	208	8	ADX73900	Adx73900	Plant ful	241	32	64.0	502	3	ADU77055	Jojoba fa
169	32	64.0	226	6	ABU48522	Abu48522	Protein e	242	32	64.0	502	3	AAG46724	Arabidops
170	32	64.0	229	3	AAG19496	Aag19496	Arabidops	243	32	64.0	502	9	ABE42120	L. pneumo



244	32	64.0	502	9	ABE38966	Aeb38966	L. pneumo	317	31	62.0	73	8	ADN41061	Adn41061	Novel hum
245	32	64.0	511	8	ADS15485	Ads15485	HSV-1 pol	318	31	62.0	73	8	ADU01131	Adu01131	Human pro
246	32	64.0	515	3	RAG13313	Rag13313	Arabidops	319	31	62.0	73	8	ADU15513	Adu15513	Novel hum
247	32	64.0	517	3	RAG46727	Rag46727	Arabidops	320	31	62.0	74	7	ADY02710	Ady02710	Human sec
248	32	64.0	515	3	RAG43745	Rag43745	Arabidops	321	31	62.0	74	7	ADY07389	Ady07389	Human sec
249	32	64.0	518	3	RAG14093	Rag14093	Arabidops	322	31	62.0	80	5	ABB97837	Abb97837	Human sec
250	32	64.0	521	3	RAG46716	Rag46716	Arabidops	323	31	62.0	87	3	AAG40274	Aag40274	Arabidops
251	32	64.0	522	3	RAG43744	Rag43744	Arabidops	324	31	62.0	87	3	AAG19973	Aag19973	Arabidops
252	32	64.0	552	3	RAG46723	Rag46723	Arabidops	325	31	62.0	87	3	AAG50777	Aag50777	Arabidops
253	32	64.0	562	5	ABB93783	Abb93783	Herbicida	326	31	62.0	99	6	ABU70455	Abu70455	Human adi
254	32	64.0	563	7	ADB65471	Adb65471	Human pro	327	31	62.0	113	4	AAB95774	Aab95774	Human pro
255	32	64.0	565	3	RAG13312	Rag13312	Arabidops	328	31	62.0	113	7	ADM04519	Adm04519	Human pro
256	32	64.0	565	3	RAG46726	Rag46726	Arabidops	329	31	62.0	117	5	ABP05341	Abp05341	Human ORF
257	32	64.0	568	3	RAG14092	Rag14092	Arabidops	330	31	62.0	125	3	AAG18530	Aag18530	Zea mayfs
258	32	64.0	571	3	RAG46715	Rag46715	Arabidops	331	31	62.0	125	6	ABM71087	Abm71087	Staphyloc
259	32	64.0	574	5	ABB91815	Abb91815	Herbicida	332	31	62.0	126	3	AAG14595	Aag14595	Arabidops
260	32	64.0	596	4	ABB67493	Abb67493	Drosophil	333	31	62.0	129	3	AAG50776	Aag50776	Arabidops
261	32	64.0	619	3	RAG43743	Rag43743	Arabidops	334	31	62.0	129	3	AAG19972	Aag19972	Arabidops
262	32	64.0	625	7	ADI60215	Adi60215	Secreted	335	31	62.0	129	3	AAG40273	Aag40273	Arabidops
263	32	64.0	715	8	ADN27191	Adn27191	Bacterial	336	31	62.0	135	6	ABU70663	Abu70663	Human adi
264	32	64.0	732	3	AABW97207	Aabw97207	A trehalo	337	31	62.0	139	5	ABP40482	Abp40482	Staphyloc
265	32	64.0	747	6	ABU38828	Abu38828	Protein e	338	31	62.0	139	9	ADY19137	Ady19137	PRO polyp
266	32	64.0	754	7	ABO84387	Ab084387	pseudomon	339	31	62.0	147	5	ABB47726	Abb47726	Listeria
267	32	64.0	799	5	ADI16874	Adi16874	Murine NO	340	31	62.0	153	3	AAG14594	Aag14594	Arabidops
268	32	64.0	799	5	ADI16880	Adi16880	Murine NO	341	31	62.0	161	3	AAG14593	Aag14593	Arabidops
269	32	64.0	828	3	AAB25559	Aab25559	Pinus rad	342	31	62.0	175	2	AAW82629	Aaw82629	Ehrlichia
270	32	64.0	867	2	AAR72093	Aar72093	Human mgl	343	31	62.0	175	3	AAW78549	Aaw78549	Ehrlichia
271	32	64.0	886	5	AAE16785	Aae16785	Human tra	344	31	62.0	175	5	ABG93401	Abg93401	Ehrlichia
272	32	64.0	898	9	ADZ67613	Adz67613	Chimeric	345	31	62.0	175	5	AAU73198	Aau73198	Human gra
273	32	64.0	907	9	ADZ67611	Adz67611	Chimeric	346	31	62.0	191	5	ABU05548	Abu05548	M. tuberc
274	32	64.0	910	9	ADZ67609	Adz67609	Chimeric	347	31	62.0	205	7	ADH86229	Adh86229	Enterococ
275	32	64.0	912	9	ADZ67607	Adz67607	Chimeric	348	31	62.0	205	7	ADH88302	Adh88302	Enterococ
276	32	64.0	915	2	AAR72097	Aar72097	Human mgl	349	31	62.0	220	4	ABBG69592	Abbg69592	Drosophil
277	32	64.0	915	2	AAR80479	Aar80479	Rat metab	350	31	62.0	222	5	ABP35380	Abp35380	Human ORF
278	32	64.0	915	5	ABG95165	Abg95165	Human GPC	351	31	62.0	223	5	ABP29267	Abp29267	Streptoco
279	32	64.0	915	5	ABG95155	Abg95155	Human GPC	352	31	62.0	229	5	ABBA49573	Abba49573	Listeria
280	32	64.0	915	5	ABG95164	Abg95164	Human GPC	353	31	62.0	229	6	ABU32499	Abu32499	Protein e
281	32	64.0	915	5	ABG95166	Abg95166	Human GPC	354	31	62.0	247	7	ADF58774	Adf58774	Human pol
282	32	64.0	915	5	ABG95163	Abg95163	Human GPC	355	31	62.0	248	3	AAG56496	Aag56496	Arabidops
283	32	64.0	915	6	AAE30109	Aae30109	Rat metab	356	31	62.0	252	3	AAG56495	Aag56495	Arabidops
284	32	64.0	915	6	ABP81849	Abp81849	Human met	357	31	62.0	255	6	ABU19053	Abu19053	Protein e
285	32	64.0	915	7	ADD48384	Add48384	Rat Prote	358	31	62.0	259	6	ABU18774	Abu18774	Protein e
286	32	64.0	915	7	ADE55969	Ade55969	Human Pro	359	31	62.0	259	6	ADA36468	Ada36468	Acinetoba
287	32	64.0	915	7	ADE55967	Ade55967	Rat Prote	360	31	62.0	260	2	AA494114	Aay49114	Human mgl
288	32	64.0	915	7	ADJ93191	Adj93191	Human met	361	31	62.0	260	5	AAO15081	Aao15081	Human mgl
289	32	64.0	915	8	ADO29103	Ado29103	Human nov	362	31	62.0	261	6	ABR63985	Abre63985	B subtili
290	32	64.0	915	8	ADO29104	Ado29104	Mouse nov	363	31	62.0	262	5	AAO19490	Aao19490	Murine al
291	32	64.0	915	9	ADZ67603	Adz67603	Human met	364	31	62.0	269	8	ADQ66488	Adq66488	Novel hum
292	32	64.0	915	9	ABE87480	Aeb87480	Human met	365	31	62.0	272	7	ADQ67916	Ade07916	Novel pro
293	32	64.0	922	8	AAR72098	Aar72098	Human mgl	366	31	62.0	274	3	AAG56494	Aag56494	Arabidops
294	32	64.0	926	8	ADN24302	Adn24302	Bacterial	367	31	62.0	274	8	ADN72197	Adn72197	Thale cre
295	32	64.0	1072	7	ADC83636	Adc83636	LTPPC3-re	368	31	62.0	275	7	ADC21432	Adc21432	Staphyloc
296	32	64.0	1072	8	ADT93477	Adt93477	Murine tr	369	31	62.0	275	7	ADC25118	Adc25118	S. aureus
297	32	64.0	1180	4	ABG13178	Abg13178	Novel hum	370	31	62.0	275	7	ADD52620	Add52620	Staphyloc
298	32	64.0	1186	6	ABP71253	Abp71253	Zebrafish	371	31	62.0	280	5	AAO15351	Aao15351	Human cit
299	32	64.0	1264	7	ADC89806	Adc89806	Mouse 5'	372	31	62.0	284	5	ABP38525	Abp38525	Staphyloc
300	32	64.0	1586	7	ADM26435	Adm26435	Hyperther	373	31	62.0	284	8	ADSO5645	Adso5645	Staphyloc
301	31	62.0	21	2	AAR98468	Aar98468	Signal pe	374	31	62.0	285	5	ABJ11030	Abj11030	Yeast sel
302	31	62.0	24	8	ADT40922	Adt40922	hSARS vir	375	31	62.0	290	6	ABU19001	Abu19001	Pathogen
303	31	62.0	24	8	ADS80339	Ads80339	SARS viru	376	31	62.0	290	6	ABU16362	Abu16362	Protein e
304	31	62.0	24	8	ADT38452	Adt38452	hSARS vir	377	31	62.0	290	6	ABM71823	Abm71823	Staphyloc
305	31	62.0	32	4	AAM89043	Aam89043	Human imm	378	31	62.0	290	9	ADW94786	Adw94786	Prolifera
306	31	62.0	38	4	ABG00514	Abg00514	Novel hum	379	31	62.0	291	3	AAG09673	Aag09673	Arabidops
307	31	62.0	52	4	ABBA0456	Abba0456	Peptide #	380	31	62.0	299	5	ABP73250	Abp73250	Candida a
308	31	62.0	52	4	AAW34176	Aaw34176	Peptide #	381	31	62.0	300	3	AAE18216	Aae18216	Plasmodiu
309	31	62.0	52	4	AAW74001	Aaw74001	Human bon	382	31	62.0	309	2	AAW32799	Aaw32799	Polypeptl
310	31	62.0	52	4	AAW61278	Aaw61278	Human bra	383	31	62.0	332	4	AAG71799	Aag71799	Human oli
311	31	62.0	52	4	ABG55758	Abg55758	Human liv	384	31	62.0	335	6	ADA36769	Ada36769	Acinetoba
312	31	62.0	52	5	ABG43896	Abg43896	Human pep	385	31	62.0	366	2	AAR58687	Aar58687	Rat NR77
313	31	62.0	64	4	AAW24289	Aaw24289	Human EST	386	31	62.0	375	3	AAW43700	Aaw43700	Arabidops
314	31	62.0	65	3	AAG01207	Aag01207	Human sec	387	31	62.0	375	3	AAG06362	Aag06362	Arabidops
315	31	62.0	73	2	AAW37869	Aaw37869	Human pro	388	31	62.0	428	5	ADS43909	Ads43909	Bacterial
316	31	62.0	73	4	AAU21332	Aau21332	Human nov	389	31	62.0	428	5	ABB91603	Abb91603	Herbicida

390	31	62.0	435	4	AAB97165	Aab97165 Pseudomon	463	31	62.0	908	8	ADO29476	Ado29476 Human GPC
391	31	62.0	450	5	AB91192	Abg31192 Herbicida	464	31	62.0	908	8	ADQ89128	Adq89128 Human uro
392	31	62.0	453	3	AG43699	Aag43699 Arabidops	465	31	62.0	908	9	ADZ67605	Adz67605 Human met
393	31	62.0	453	3	AG06361	Aag06361 Arabidops	466	31	62.0	908	9	ABE68321	Abe68321 Human met
394	31	62.0	453	8	ADN74429	Adn74429 Thale cre	467	31	62.0	913	4	ABG29452	Abg29452 Novel hum
395	31	62.0	460	8	ADN22875	Adn22875 Bacterial	468	31	62.0	937	3	AAy92102	Aay92102 Human WFS
396	31	62.0	461	3	AG06360	Aag06360 Arabidops	469	31	62.0	1019	2	AAW43394	Aaw43394 Singapore
397	31	62.0	461	3	AG43698	Aag43698 Arabidops	470	31	62.0	1019	2	AAW05750	Aaw05750 Horseshoe
398	31	62.0	464	4	AAU34609	Aau34609 E. coli c	471	31	62.0	1019	2	AAW94302	Aaw94302 Horseshoe
399	31	62.0	475	8	ADS29861	Ads29861 Bacterial	472	31	62.0	1019	3	AAy42490	Aay42490 Recombina
400	31	62.0	479	4	AB862000	Ab862000 Drosophil	473	31	62.0	1019	4	AAW60935	Aaw60935 Horseshoe
401	31	62.0	486	8	AD943500	Ad943500 Bacterial	474	31	62.0	1019	6	ABP72334	Abp72334 Horseshoe
402	31	62.0	494	6	AB014787	Ab014787 Novel hum	475	31	62.0	1019	9	ADM39099	Adm39099 Southeast
403	31	62.0	494	6	AB014786	Ab014786 Novel hum	476	31	62.0	1059	2	AAy49130	Aay49130 Chimeric
404	31	62.0	497	7	ADS93890	Ads93890 Ixodes sc	477	31	62.0	1059	5	AAO15096	Aao15096 Chimeric
405	31	62.0	506	8	ADS98029	Ads98029 Protein f	478	31	62.0	1074	4	AAU40997	Aau40997 Propionib
406	31	62.0	533	6	ABU49311	Abu49311 Protein e	479	31	62.0	1074	6	ABM37516	Abm37516 Propionib
407	31	62.0	535	5	ABU74082	Abu74082 Candida a	480	31	62.0	1083	2	AAW43393	Aaw43393 Singapore
408	31	62.0	557	6	ADA54841	Ada54841 Human pro	481	31	62.0	1083	2	AAy05749	Aay05749 Horseshoe
409	31	62.0	569	4	AB859532	Ab859532 Drosophil	482	31	62.0	1083	2	AAW94301	Aaw94301 Horseshoe
410	31	62.0	580	7	ABM86384	Abm86384 Rice abio	483	31	62.0	1083	3	AAy42489	Aay42489 Horseshoe
411	31	62.0	591	6	AAE33778	Aae33778 Human nuc	484	31	62.0	1083	4	AAW60934	Aaw60934 Horseshoe
412	31	62.0	622	2	AAW41248	Aaw41248 Thermococ	485	31	62.0	1083	6	ABP72333	Abp72333 Horseshoe
413	31	62.0	622	6	ABG72741	Abg72741 Thermococ	486	31	62.0	1097	5	AAW52105	Aaw52105 Human fat
414	31	62.0	622	8	ADM47629	Adm47629 Thermococ	487	31	62.0	1142	4	ABG29451	Abg29451 Novel hum
415	31	62.0	622	8	ADM99181	Adm99181 Archaeal	488	31	62.0	1172	6	ADA34784	Ada34784 Acinetoba
416	31	62.0	623	2	AAW82651	Aaw82651 Ehrlichia	489	31	62.0	1215	8	ADP75036	Adp75036 Capsicum
417	31	62.0	623	3	AAW78550	Aaw78550 Ehrlichia	490	31	62.0	1262	5	ABP74021	Abp74021 Candida a
418	31	62.0	623	5	ABG93426	Abg93426 Ehrlichia	491	31	62.0	1418	2	AAy49131	Aay49131 mGluR8/Ca
419	31	62.0	623	5	AAU73223	Aau73223 Human gra	492	31	62.0	1418	5	AAO15097	Aao15097 Human mG1
420	31	62.0	647	3	AAy92106	Aay92106 Human WFS	493	31	62.0	1421	5	AAO15103	Aao15103 Human phm
421	31	62.0	649	8	ADS28790	Ads28790 Bacterial	494	31	62.0	2000	6	ABP53747	Abp53747 Protein s
422	31	62.0	663	8	ADN21318	Adn21318 Bacterial	495	31	62.0	2000	7	ADK64668	Adk64668 Disease t
423	31	62.0	680	4	AAQ91123	Aaq91123 C glutami	496	31	62.0	2000	8	ADP54026	Adp54026 Human PRO
424	31	62.0	682	7	ABO76173	Ab076173 Pseudomon	497	31	62.0	2335	5	AAE27902	Aae27902 Human LBD
425	31	62.0	686	3	AAy44246	Aay44246 Human cel	498	31	62.0	2335	6	ABO52998	Ab052998 Human spl
426	31	62.0	754	7	AD939382	Ad939382 Ixodes sc	499	31	62.0	2396	4	ABE64047	Ab664047 Drosophil
427	31	62.0	775	4	AAU48754	Aau48754 Propionib	500	31	62.0	2416	5	ABP73515	Abp73515 Candida a
428	31	62.0	775	6	ABM65954	Abm65954 Propionib	501	31	62.0	2747	6	ABP70795	Abp70795 Human ext
429	31	62.0	775	6	ABM45273	Abm45273 Propionib	502	31	62.0	2749	8	ADL92190	Adl92190 Thyroglob
430	31	62.0	811	2	AAy29146	Aay29146 Amino aci	503	31	62.0	3332	8	ADM34079	Adm34079 Toxoplasma
431	31	62.0	841	6	ABR62492	AbR62492 Human met	504	31	62.0	4472	4	ABE60101	Ab660101 Drosophil
432	31	62.0	862	6	ADA34240	Ada34240 Acinetoba	505	31	62.0	4544	5	ADH48738	Adh48738 NOV9 prot
433	31	62.0	878	8	ADM20748	Adm20748 Bacterial	506	31	62.0	4555	5	AAW52106	Aaw52106 Rat fat 3
434	31	62.0	885	3	AAy92103	Aay92103 Human WFS	507	31	62.0	4560	8	ADH18897	Adh18897 Human cel
435	31	62.0	890	3	AAy92101	Aay92101 Murine WF	508	31	62.0	4585	9	ADW80700	Adw80700 Novel hum
436	31	62.0	890	3	AAy92105	Aay92105 Human WFS	509	31	62.0	4585	9	ADY97348	Ady97348 Human pro
437	31	62.0	890	3	AAy92107	Aay92107 Human WFS	510	31	62.0	4588	9	ADW80702	Adw80702 Novel hum
438	31	62.0	890	3	AAy92110	Aay92110 Human WFS	511	31	62.0	4588	9	ADY97350	Ady97350 Human pro
439	31	62.0	890	3	AAy92109	Aay92109 Human WFS	512	31	62.0	4589	9	ADW80696	Adw80696 Novel hum
440	31	62.0	890	3	AAy92100	Aay92100 WFS1 poly	513	31	62.0	4589	9	ADY97344	Ady97344 Human pro
441	31	62.0	890	3	AAy92104	Aay92104 Human WFS	514	31	62.0	9913	9	ABE00351	Abe00351 SARS coro
442	31	62.0	890	3	AAy51606	Aay51606 Human wml	515	31	62.0	9914	8	ADT40602	Adt40602 HSARS vir
443	31	62.0	890	5	ABB78284	Abb78284 Amino aci	516	31	62.0	9914	8	ADT38132	Adt38132 HSARS vir
444	31	62.0	890	5	ABB78285	Abb78285 Amino aci	517	30.5	61.0	275	6	ABR63986	AbR63986 B subtili
445	31	62.0	890	5	ABB78282	Abb78282 Amino aci	518	30	60.0	275	4	AAU02231	Aau02231 HLA bindi
446	31	62.0	890	7	ADD46013	AdD46013 Human pro	519	30	60.0	9	AAU02250	Aau02250 HLA bindi	
447	31	62.0	890	7	ADF69127	Adf69127 Human MP5	520	30	60.0	9	ABP83368	Abp83368 G protein	
448	31	62.0	890	9	ADY70426	Ady70426 Human bet	521	30	60.0	12	AAy21123	Aay21123 Human bcl	
449	31	62.0	890	9	ADY70680	Ady70680 Human nic	522	30	60.0	30	ADQ27332	AdQ27332 Classical	
450	31	62.0	892	8	ADR08513	AdR08513 Human pro	523	30	60.0	42	AAO27332	Aao27332 Classical	
451	31	62.0	893	4	ABG26977	Abg26977 Novel hum	524	30	60.0	49	AAW91145	Aaw91145 Human imm	
452	31	62.0	904	5	ABP35661	Abp35661 Fungal ZB	525	30	60.0	55	AAW74367	Aaw74367 DNA clone	
453	31	62.0	908	2	AAW41568	Aaw41568 Human met	526	30	60.0	61	AAW87827	Aaw87827 Human imm	
454	31	62.0	908	2	AAW49928	Aaw49928 Human met	527	30	60.0	63	AAO11264	Aao11264 Human pol	
455	31	62.0	908	5	ABW09564	Abw09564 Human GRM	528	30	60.0	71	AAO11264	Aao11264 Human pol	
456	31	62.0	908	6	ABP81850	Abp81850 Human met	529	30	60.0	80	AAW92840	Aaw92840 Human dig	
457	31	62.0	908	6	ABR62488	AbR62488 Human met	530	30	60.0	87	ABG18437	Abg18437 Novel hum	
458	31	62.0	908	6	ABR62489	AbR62489 Human met	531	30	60.0	94	ABP04024	Abp04024 Human ORF	
459	31	62.0	908	6	ABR62491	AbR62491 Human met	532	30	60.0	96	AAW88401	Aaw88401 Human imm	
460	31	62.0	908	6	ABR62490	AbR62490 Human met	533	30	60.0	97	ADA34974	Ada34974 Acinetoba	
461	31	62.0	908	7	ADE31729	Ade31729 Human 255	534	30	60.0	98	AAW84281	Aaw84281 Human imm	
462	31	62.0	908	8	ADO29477	Ado29477 Mouse GPC	535	30	60.0	101	4	AAW91794	Aaw91794 Human imm

536	30	60.0	107	3	AAB40752
537	30	60.0	107	5	ABP31274
538	30	60.0	110	5	ADK34522
539	30	60.0	117	3	AAB18125
540	30	60.0	127	2	AAW62661
541	30	60.0	130	5	ABB04713
542	30	60.0	133	9	ADY66464
543	30	60.0	137	4	AAE93882
544	30	60.0	141	8	ADU02489
545	30	60.0	150	3	AAU05345
546	30	60.0	155	6	ABM69477
547	30	60.0	164	6	ABM69450
548	30	60.0	172	7	ADF06031
549	30	60.0	174	4	ABB11479
550	30	60.0	177	3	AAU05344
551	30	60.0	187	3	AAB18062
552	30	60.0	188	8	ADX95404
553	30	60.0	192	6	ABU01000
554	30	60.0	192	8	ADK48780
555	30	60.0	192	8	ADR96127
556	30	60.0	192	9	AEA59997
557	30	60.0	194	2	AAU27355
558	30	60.0	194	5	ABP26707
559	30	60.0	194	8	ADV88612
560	30	60.0	194	8	ADV82015
561	30	60.0	194	8	ADV79865
562	30	60.0	195	6	ABU44535
563	30	60.0	197	6	ADB07914
564	30	60.0	198	7	ADP06753
565	30	60.0	199	6	ABU33756
566	30	60.0	201	6	ABM15848
567	30	60.0	201	6	ABU36626
568	30	60.0	202	6	ABU34633
569	30	60.0	202	6	ABU25817
570	30	60.0	205	4	AAU19339
571	30	60.0	211	4	AAU79912
572	30	60.0	211	4	AAU25590
573	30	60.0	211	4	AAU91512
574	30	60.0	213	4	AAU19316
575	30	60.0	216	4	AAU48197
576	30	60.0	216	6	ABM44716
577	30	60.0	216	6	ADB07916
578	30	60.0	229	9	ABE49909
579	30	60.0	233	4	ABG32771
580	30	60.0	240	4	ADM19827
581	30	60.0	241	8	ADY12813
582	30	60.0	247	8	ADY06264
583	30	60.0	252	3	AAU49496
584	30	60.0	252	8	ADR09668
585	30	60.0	255	5	AAE14390
586	30	60.0	255	8	ADT58877
587	30	60.0	259	5	AAE17014
588	30	60.0	259	8	ADS41577
589	30	60.0	261	8	ADS42580
590	30	60.0	262	6	ADA05714
591	30	60.0	262	8	ADN62878
592	30	60.0	269	5	ABG76497
593	30	60.0	270	6	ABU29838
594	30	60.0	271	3	AAU49495
595	30	60.0	271	5	AAE17015
596	30	60.0	273	4	AAU01595
597	30	60.0	278	6	AAU01594
598	30	60.0	278	6	ABR52929
599	30	60.0	278	7	ADK62510
600	30	60.0	279	5	AAE17011
601	30	60.0	287	8	ADU91839
602	30	60.0	287	9	AEA10744
603	30	60.0	288	8	ADR42963
604	30	60.0	288	9	AEA10743
605	30	60.0	289	5	AAE1647
606	30	60.0	289	8	ADO29555
607	30	60.0	289	8	ADO29554
608	30	60.0	290	3	AAU82535

00	3	AAB43340	Aab43340	Human	ORF
00	5	ABP52843	Abp52843	Human	tum
00	8	ADP25195	Adp25195	PRO poly	
04	4	AAU02224	Aau02224	Human ext	
06	5	AAU82727	Aau82727	Human aci	
07	8	ADR42962	Adr42962	IPT-like	
05	5	AAG65908	Aag65908	Amino aci	
05	5	AAEL17013	Aael17013	Human eoa	
06	4	ABG67544	Abg67544	Amino aci	
08	7	ABO74347	Abot74347	Pseudomon	
08	8	ADT58783	Adt58783	Plant pol	
22	7	ADB80574	Adb80574	Ovarian c	
4	2	AAW77296	Aaw77296	Amino aci	
4	2	AAW77297	Aaw77297	Amino aci	
4	2	AAW97116	Aaw97116	A human e	
4	2	AAW06434	Aay06434	Human pro	
4	2	AAV13388	Aay13388	Amino aci	
4	3	ABC12132	Abc12132	Hydrophob	
4	4	ABG78569	Abg78569	Human PRO	
4	4	AAAB80256	Aab80256	Human PRO	
4	4	AAU02223	Aau02223	Human ext	
4	5	AAEL17010	Aael17010	Human eoa	
4	6	ABU71634	Abu71634	Human PRO	
4	6	ABU71489	Abu71489	Human PRO	
4	6	ABU71935	Abu71935	Human sec	
4	6	ABO01818	Abol01818	Novel hum	
4	6	ADA05716	Ada05716	Human NOV	
4	6	ADA054391	Adu54391	Human sec	
4	6	ABO47406	Abot47406	Human sec	
4	6	ABU64543	Abu64543	Human sec	
4	6	ABU67389	Abu67389	Human sec	
4	6	ABO14909	Abol14909	Human sec	
4	6	ABU69666	Abu69666	Novel hum	
4	6	ABO14848	Abol14848	Human sec	
4	6	ADB29462	Abd29462	Human sec	
4	6	ADA18318	Ada18318	Human sec	
4	6	ABO32800	Abol32800	Human sec	
4	6	ABO34860	Abol34860	Human PRO	
4	6	ADA16293	Ada16293	Human sec	
4	6	ADA42438	Ada42438	Human sec	
4	6	ABO17538	Abol17538	Human PRO	
4	7	ADA16717	Ada16717	Human sec	
4	7	ADA13146	Ada13146	Human sec	
4	7	ADA42014	Ada42014	Human sec	
4	7	ADA17361	Ada17361	Human sec	
4	7	ADA42864	Ada42864	Human sec	
4	7	ABO17599	Abol17599	Human PRO	
4	7	ADB80572	Adb80572	Ovarian c	
4	7	ADB77783	Adb77783	Human sec	
4	7	ADG74919	Adg74919	Human sec	
4	7	ADC28555	Adc28555	Human sec	
4	7	ADC39765	Adc39765	Human sec	
4	7	ADC40279	Adc40279	Human sec	
4	7	ADCL19103	Adcl19103	Human sec	
4	7	ADC34403	Adc34403	Human sec	
4	7	ADC29458	Adc29458	Human sec	
4	7	ADC28989	Adc28989	Human sec	
4	7	ADC40874	Adc40874	Human sec	
4	7	ADCL19531	Adcl19531	Human sec	
4	7	ADC33979	Adc33979	Human sec	
4	7	ADCL3049	Adcl3049	Human sec	
4	7	ADCL12501	Adcl12501	Human sec	
4	7	ADDO5056	Ado05056	Human sec	
4	7	ADDO4062	Ado04062	Human sec	
4	7	ADDO3638	Ado03638	Human sec	
4	7	ADBC34890	Adc34890	Human sec	
4	7	ADB89060	Adb89060	TAT246.1	
4	7	ADG38954	Adg38954	Human tes	
4	7	ADH59373	Adh59373	Human sec	
4	7	ADL38152	Adl38152	Human sec	
4	7	ADJ26420	Adj26420	Human sec	
4	7	ADN39222	Adn39222	Cancer/an	
4	8	ADN79335	Adn79335	Human sec	

682	30	60.0	314	8	ADP79759	Human sec
683	30	60.0	314	8	ADP73435	Human sec
684	30	60.0	314	8	ADP73970	Human sec
685	30	60.0	314	8	ADP95524	Human sec
686	30	60.0	314	8	ADP98643	Human sec
687	30	60.0	314	8	ADP99070	Human sec
688	30	60.0	314	8	ADG40540	Human sec
689	30	60.0	314	8	ADG40540	Human sec
690	30	60.0	314	8	ADP73934	Human sec
691	30	60.0	314	8	ADP73510	Human sec
692	30	60.0	314	8	ADG92353	Human sec
693	30	60.0	314	8	ADG92780	Human sec
694	30	60.0	314	8	ADH20569	Human sec
695	30	60.0	314	8	ADH07424	Human sec
696	30	60.0	314	8	ADH59969	Human sec
697	30	60.0	314	8	ADH06997	Human sec
698	30	60.0	314	8	ADH18739	Human sec
699	30	60.0	314	8	ADH65459	Human sec
700	30	60.0	314	8	ADH37718	Human sec
701	30	60.0	314	8	ADH97518	Human sec
702	30	60.0	314	8	ADH65886	Human sec
703	30	60.0	314	8	ADH60629	Human sec
704	30	60.0	314	8	ADJ99686	Human sec
705	30	60.0	314	8	ADL08879	Human sec
706	30	60.0	314	8	ADM25220	Human sec
707	30	60.0	314	8	ADM29970	Human sec
708	30	60.0	314	8	ADM06292	Human sec
709	30	60.0	314	8	ADM62880	Human sec
710	30	60.0	314	8	ADQ17735	Human sec
711	30	60.0	314	8	ADH11144	Human sec
712	30	60.0	314	8	ADH18053	Human sec
713	30	60.0	314	8	ADH81711	Tumour-as
714	30	60.0	314	8	ADH74632	Human sec
715	30	60.0	314	8	ADT03729	Human sec
716	30	60.0	314	9	ADH04414	Human Ova
717	30	60.0	314	9	ADH0746	Mutated h
718	30	60.0	314	9	ADH37967	Human sec
719	30	60.0	314	4	ADU01569	Human sec
720	30	60.0	317	3	ADG49494	Arabidops
721	30	60.0	318	5	ADH93084	Arabidops
722	30	60.0	318	5	ADG70980	Arabidops
723	30	60.0	318	8	ADH42955	IPT-like
724	30	60.0	318	8	ADH42964	IPT-like
725	30	60.0	318	9	ADH19041	Thale cre
726	30	60.0	319	5	ADH16638	Human NOV
727	30	60.0	320	8	ADH42292	Human nov
728	30	60.0	320	6	ADH69200	Photohab
729	30	60.0	320	9	ADH17730	PRO polyp
730	30	60.0	322	2	ADH30162	Human dor
731	30	60.0	322	4	ADG64294	Human GTP
732	30	60.0	322	4	ADH12794	Human G p
733	30	60.0	322	4	ADU04371	Human G-p
734	30	60.0	322	4	ADH20075	Protein e
735	30	60.0	322	5	ADH17074	Human G-p
736	30	60.0	322	5	ADH95617	Human GPC
737	30	60.0	322	5	ADH21288	Human Mrg
738	30	60.0	322	5	ADH16991	Human NOV
739	30	60.0	322	5	ADH16636	Human NOV
740	30	60.0	322	5	ADH16997	Human NOV
741	30	60.0	322	6	ADH96696	Human G p
742	30	60.0	322	6	ADH92666	Human Dor
743	30	60.0	322	7	ADH66445	Human GPC
744	30	60.0	322	7	ADH00803	Human GPC
745	30	60.0	322	7	ADH196466	Human G p
746	30	60.0	322	8	ADH08520	MrgX1 . 3/
747	30	60.0	322	8	ADH42290	Human nov
748	30	60.0	322	8	ADH29703	Human GPC
749	30	60.0	322	8	ADH36621	Human mas
750	30	60.0	322	9	ADH44787	Human RUP
751	30	60.0	322	9	ADH44639	Human RUP
752	30	60.0	322	9	ADH02566	Human sen
753	30	60.0	322	9	ADH02581	Human sen
754	30	60.0	322	9	ADH20823	Human RUP

755	30	60.0	323	4	ADU25612	Human G p
756	30	60.0	323	5	ADH06257	Human G p
757	30	60.0	327	3	ADY91871	Human can
758	30	60.0	330	4	ADG71688	Human Olf
759	30	60.0	332	9	ADH91136	M. xanthu
760	30	60.0	334	5	ADH17012	Human eos
761	30	60.0	336	8	ADY08955	Plant ful
762	30	60.0	339	5	ADH17009	Human eos
763	30	60.0	339	6	ADU50180	Protein e
764	30	60.0	340	4	ADU33548	Klebsiell
765	30	60.0	340	4	ADU91840	Testisin
766	30	60.0	340	9	ADH10745	Mutated h
767	30	60.0	341	4	ADU36133	Klebsiell
768	30	60.0	341	4	ADU34869	E. coli c
769	30	60.0	341	6	ADU28877	Protein e
770	30	60.0	341	6	ADU15491	Protein e
771	30	60.0	341	6	ADU28395	Protein e
772	30	60.0	341	6	ADU32035	Protein e
773	30	60.0	342	7	ADH062145	Klebsiell
774	30	60.0	344	5	ADH40722	Staphyloc
775	30	60.0	344	8	ADH08018	Staphyloc
776	30	60.0	348	6	ADH67677	Photohab
777	30	60.0	349	4	ADH19616	Novel hum
778	30	60.0	349	8	ADH25803	Bacterial
779	30	60.0	349	8	ADH25147	Bacterial
780	30	60.0	356	3	ADH43597	Arabidops
781	30	60.0	360	9	ADH40678	L. pneumo
782	30	60.0	360	9	ADH37358	L. pneumo
783	30	60.0	362	8	ADH22489	Bacterial
784	30	60.0	365	5	ADH91701	Herbicida
785	30	60.0	366	3	ADH53207	Arabidops
786	30	60.0	368	5	ADH89466	Human pol
787	30	60.0	368	5	ADH74073	Candida a
788	30	60.0	369	5	ADH48238	Listeria
789	30	60.0	373	8	ADH57280	Plant pol
790	30	60.0	384	8	ADH68375	Swine fav
791	30	60.0	385	8	ADH47662	Thermococ
792	30	60.0	386	8	ADH07890	Plant ful
793	30	60.0	386	8	ADH86225	Aspergill
794	30	60.0	390	8	ADH19384	Bacterial
795	30	60.0	391	6	ADH69144	Photohab
796	30	60.0	399	3	ADH44614	Zea maye
797	30	60.0	400	8	ADH11960	Plant ful
798	30	60.0	403	8	ADH30152	Bacterial
799	30	60.0	406	8	ADH42055	Bacterial
800	30	60.0	410	3	ADH21144	Arabidops
801	30	60.0	412	3	ADH43596	Arabidops
802	30	60.0	421	8	ADH21994	Bacterial
803	30	60.0	425	3	ADH21143	Arabidops
804	30	60.0	426	5	ADH47737	NOV7 prot
805	30	60.0	426	7	ADH68273	Human NOV
806	30	60.0	426	7	ADH25620	Human dia
807	30	60.0	429	5	ADH14389	Caenorhab
808	30	60.0	430	9	ADH95249	M. xanthu
809	30	60.0	431	8	ADH26162	Bacterial
810	30	60.0	431	8	ADH25681	Bacterial
811	30	60.0	431	8	ADH22512	Bacterial
812	30	60.0	436	8	ADH27960	Bacterial
813	30	60.0	439	8	ADH43274	IPT-like
814	30	60.0	441	4	ADH66859	Drosophil
815	30	60.0	441	4	ADH60529	Drosophil
816	30	60.0	442	8	ADH71086	Plant ful
817	30	60.0	444	8	ADH97055	Plant ful
818	30	60.0	446	9	ADH74344	Drosophil
819	30	60.0	446	9	ADH55415	Drosophil
820	30	60.0	447	4	ADH63609	Drosophil
821	30	60.0	447	4	ADH38827	Human pol
822	30	60.0	447	5	ADH21720	Human PKI
823	30	60.0	447	7	ADH05515	Human pro
824	30	60.0	450	3	ADH53206	Arabidops
825	30	60.0	450	3	ADH34636	Arabidops
826	30	60.0	450	8	ADH32596	Ovine GFP
827	30	60.0	451	7	ADH86128	Rice abio

828	30	60.0	453	8	ADI32543	Adi32543	Ovine GDF	901	30	60.0	1006	7	ADK61814	Adk61814	Disease t
829	30	60.0	453	8	ADI32545	Adi32545	Ovine GDF	902	30	60.0	1006	8	ADN20224	Adn20224	Bacterial
830	30	60.0	456	6	AAO16378	Aao16378	Murine pa	903	30	60.0	1019	2	AAR14118	Aar14118	Human GAP
831	30	60.0	457	3	AAG21142	Aag21142	Arabidops	904	30	60.0	1019	6	ABU04976	Abu04976	Human exp
832	30	60.0	460	4	AAM40613	Aam40613	Human pol	905	30	60.0	1019	6	ABU04977	Abu04977	Human exp
833	30	60.0	460	6	AAO16374	Aao16374	Human pan	906	30	60.0	1037	8	ADL70579	Adl70579	Cervical c
834	30	60.0	464	3	AAB58437	Aab58437	Lung canc	907	30	60.0	1051	2	AAR14117	Aar14117	Hamster G
835	30	60.0	465	8	ADN27288	Adn27288	Bacterial	908	30	60.0	1051	2	AAW54032	Aaw54032	Human alp
836	30	60.0	473	6	ABU50396	Abu50396	Protein e	909	30	60.0	1051	6	ABR58637	AbR58637	Human cer
837	30	60.0	476	6	ABU18192	Abu18192	Protein e	910	30	60.0	1051	6	ABR58637	AbR58637	Human cer
838	30	60.0	479	8	ADS30073	Ads30073	Bacterial	911	30	60.0	1051	6	ABU04978	Abu04978	Human exp
839	30	60.0	488	3	AGS34635	AgS34635	Arabidops	912	30	60.0	1051	6	ABU04979	Abu04979	Human exp
840	30	60.0	488	3	AGS3205	AgS3205	Arabidops	913	30	60.0	1051	6	ABU04975	Abu04975	Human exp
841	30	60.0	491	5	ABB48506	Abb48506	Listeria	914	30	60.0	1051	7	ADB80582	AdB80582	Ovarian c
842	30	60.0	491	6	ABU32789	Abu32789	Protein e	915	30	60.0	1051	9	ADY25776	AdY25776	MRAC ITGA
843	30	60.0	508	8	ADN22626	Adn22626	Bacterial	916	30	60.0	1051	9	ABE78066	Aeb78066	Human int
844	30	60.0	510	8	ADJ48617	Adj48617	Oil-aseoc	917	30	60.0	1053	9	AEA55084	Aea55084	Mouse int
845	30	60.0	512	3	AGS34634	AgS34634	Arabidops	918	30	60.0	1053	9	AEA55031	Aea55031	Mouse int
846	30	60.0	516	5	ABB91981	Abb91981	Herbicida	919	30	60.0	1066	5	ABG96350	AbG96350	Human ova
847	30	60.0	517	8	ADS23050	Ads23050	Bacterial	920	30	60.0	1066	6	ABR58638	AbR58638	Human can
848	30	60.0	527	4	ABB62569	Abb62569	Drosophil	921	30	60.0	1066	6	ABR92095	AbR92095	Human cer
849	30	60.0	529	8	ADX92928	Adx92928	Plant ful	922	30	60.0	1066	6	ABU04981	Abu04981	Human exp
850	30	60.0	532	5	ABB91619	Abb91619	Herbicida	923	30	60.0	1066	6	ABU04980	Abu04980	Human exp
851	30	60.0	544	8	ADN23316	Adn23316	Bacterial	924	30	60.0	1066	7	ABB80584	Abb80584	Ovarian c
852	30	60.0	546	6	ABU50592	Abu50592	Protein e	925	30	60.0	1066	9	ABE78074	Aeb78074	Human int
853	30	60.0	560	6	ABU39828	Abu39828	Protein e	926	30	60.0	1070	2	AAR21521	Aar21521	Alpha gal
854	30	60.0	570	7	ABM86595	Abm86595	Rice abio	927	30	60.0	1079	4	ABE69644	Abb69644	Drosophil
855	30	60.0	560	9	ABE49961	Aeb49961	P. putida	928	30	60.0	1119	4	ABE63999	Abb63999	Drosophil
856	30	60.0	561	7	ADF70484	Adf70484	Orphan re	929	30	60.0	1119	6	ABU21548	Abu21548	Protein e
857	30	60.0	562	6	ABU41726	Abu41726	Protein e	930	30	60.0	1137	8	ABM84163	Abm84163	Human dia
858	30	60.0	565	7	ADO71376	Ado71376	Pseudomon	931	30	60.0	1180	8	ADU02401	AdU02401	Novel hum
859	30	60.0	576	7	ADH88595	Adh88595	Enterococ	932	30	60.0	1186	5	ABR55149	AbR55149	Lactococc
860	30	60.0	625	6	ABU38933	Abu38933	Protein e	933	30	60.0	1196	8	ADS29458	AdS29458	Bacterial
861	30	60.0	581	5	ABP29275	Abp29275	Streptoco	934	30	60.0	1233	8	ADJ48692	Adj48692	Oil-aseoc
862	30	60.0	592	6	ABU20377	Abu20377	Protein e	935	30	60.0	1224	7	ABO84134	AbO84134	Pseudomon
863	30	60.0	594	8	ADN22333	Adn22333	Bacterial	936	30	60.0	1236	4	ABE67049	Abb67049	Drosophil
864	30	60.0	604	3	AAE16602	Aae16602	Bacteriop	937	30	60.0	1236	5	ABP52136	AbP52136	Schizosac
865	30	60.0	625	6	ABU20337	Abu20337	Protein e	938	30	60.0	1571	8	ADN19123	Adn19123	Bacterial
866	30	60.0	634	5	ABR97150	AbR97150	Human tum	939	30	60.0	1589	5	ADN16996	Adn16996	Human NOV
867	30	60.0	644	3	AAV57584	Aav57584	Human pap	940	30	60.0	1589	5	ADN16992	Adn16992	Human NOV
868	30	60.0	644	4	ABR98444	Abr98444	Human pap	941	30	60.0	1612	8	ADN18975	Adn18975	Bacterial
869	30	60.0	665	5	ABP65389	AbP65389	Bifidobac	942	30	60.0	2217	4	ABE71700	Abb71700	Drosophil
870	30	60.0	676	8	ADK16185	Adk16185	Nanoarcha	943	30	60.0	3998	2	AAR10473	Aar10473	Hog chole
871	30	60.0	679	9	AEA20243	Aea20243	Novel hum	944	29.5	59.0	15	5	AAO15251	Aao15251	Human pap
872	30	60.0	696	2	AAR75366	Aar75366	Adhesin.	945	29.5	59.0	153	4	AAU29305	Aau29305	Human PRO
873	30	60.0	696	7	ADC00149	Adc00149	Enterohae	946	29.5	59.0	153	6	ABU58681	Abu58681	Human PRO
874	30	60.0	702	8	ADR13763	Adr13763	Amidase,	947	29.5	59.0	153	6	ABU88229	Abu88229	Novel hum
875	30	60.0	735	6	ABG72972	Abg72972	Lactococc	948	29.5	59.0	153	6	ABU84544	Abu84544	Human sec
876	30	60.0	737	9	ADU91825	Adu91825	Chondroit	949	29.5	59.0	153	6	ABR68357	AbR68357	Human sec
877	30	60.0	746	4	ABE68562	Abe68562	Human GTP	950	29.5	59.0	153	6	ABU96410	Abu96410	Novel hum
878	30	60.0	746	8	ADM87226	Adm87226	Human pro	951	29.5	59.0	153	6	ABU92841	Abu92841	Human sec
879	30	60.0	746	8	ADP55016	Adp55016	Human PRO	952	29.5	59.0	153	6	ABO08918	AbO08918	Human sec
880	30	60.0	746	9	ADY16812	Ady16812	PRO poly	953	29.5	59.0	153	6	ABU02970	Abu02970	Human sec
881	30	60.0	748	8	ADS28266	Ads28266	Bacterial	954	29.5	59.0	153	6	ABR68357	AbR68357	Human sec
882	30	60.0	752	8	ADP98846	Adp98846	C. albica	955	29.5	59.0	153	6	ABU96410	Abu96410	Novel hum
883	30	60.0	767	2	AAV31227	Aav31227	Sea urchi	956	29.5	59.0	153	6	ABU92841	Abu92841	Human sec
884	30	60.0	768	5	ABP66175	Abp66175	Bifidobac	957	29.5	59.0	153	6	ABO08918	AbO08918	Human sec
885	30	60.0	779	4	ABG70899	Abg70899	C. albican	958	29.5	59.0	153	6	ABU02970	Abu02970	Human sec
886	30	60.0	817	4	ABE64090	Abe64090	Drosophil	959	29.5	59.0	153	6	ABR75124	AbR75124	Human sec
887	30	60.0	823	4	ABE65453	Abe65453	Drosophil	960	29.5	59.0	153	6	ABR94886	AbR94886	Human sec
888	30	60.0	855	4	ABBS59695	Abbs59695	Drosophil	961	29.5	59.0	153	6	ABU85859	Abu85859	Human PRO
889	30	60.0	873	3	AAV97877	Aav97877	Eucalyptu	962	29.5	59.0	153	6	ABU99019	Abu99019	Novel hum
890	30	60.0	873	3	AAV97876	Aav97876	Eucalyptu	963	29.5	59.0	153	6	ABU98234	Abu98234	Novel hum
891	30	60.0	875	4	ABB71072	Abb71072	Drosophil	964	29.5	59.0	153	6	ABU91940	Abu91940	Novel hum
892	30	60.0	900	6	ABU48917	Abu48917	Protein e	965	29.5	59.0	153	6	ABU89633	Abu89633	Human PRO
893	30	60.0	901	6	ABM72914	Abm72914	Staphyloc	966	29.5	59.0	153	6	ABU86474	Abu86474	Human sec
894	30	60.0	930	7	ADJ70833	Adj70833	Human hea	967	29.5	59.0	153	6	ABU67687	Abu67687	Human sec
895	30	60.0	949	4	ABBS59631	Abbs59631	Drosophil	968	29.5	59.0	153	6	ABU80715	Abu80715	Human PRO
896	30	60.0	949	4	ABBS59856	Abbs59856	Drosophil	969	29.5	59.0	153	6	ABR99633	AbR99633	Human sec
897	30	60.0	985	8	ABM84164	Abm84164	Human dia	970	29.5	59.0	153	6	ABR99023	AbR99023	Human sec
898	30	60.0	998	7	ABO72722	AbO72722	Pseudomon	971	29.5	59.0	153	6	ABO16546	AbO16546	Human sec
899	30	60.0	998	6	ABU38844	Abu38844	Protein e	972	29.5	59.0	153	6	ABR92446	AbR92446	Human sec
900	30	60.0	1006	6	ABR52681	AbR52681	Protein s	973	29.5	59.0	153	6	ABO19087	AbO19087	Human sec

974 29.5 59.0 153 6 ABR78508 Human sec  
 975 29.5 59.0 153 6 ABR85244 Novel hum  
 976 29.5 59.0 153 6 ABO00383 Novel hum  
 977 29.5 59.0 153 6 ABO11715 Human sec  
 978 29.5 59.0 153 6 ABO02360 Human sec  
 979 29.5 59.0 153 6 ABU88934 Novel hum  
 980 29.5 59.0 153 6 ABU83629 Human sec  
 981 29.5 59.0 153 6 ABO06430 Novel hum  
 982 29.5 59.0 153 6 ABR59466 Human sec  
 983 29.5 59.0 153 6 ABO09528 Human sec  
 984 29.5 59.0 153 6 ABO19392 Novel hum  
 985 29.5 59.0 153 6 ABO11410 Human sec  
 986 29.5 59.0 153 6 ABR67028 Human sec  
 987 29.5 59.0 153 6 ABO16241 Human sec  
 988 29.5 59.0 153 6 ABO13947 Human sec  
 989 29.5 59.0 153 6 ABO65850 Human sec  
 990 29.5 59.0 153 6 ABO07698 Human PRO  
 991 29.5 59.0 153 6 ABO03885 Human sec  
 992 29.5 59.0 153 6 ABR67333 Human sec  
 993 29.5 59.0 153 6 ABO15936 Human sec  
 994 29.5 59.0 153 6 ABO56217 Human sec  
 995 29.5 59.0 153 6 ABR65545 Human PRO  
 996 29.5 59.0 153 6 ABU95490 Novel hum  
 997 29.5 59.0 153 6 ABO71393 Human PRO  
 998 29.5 59.0 153 6 ABO08003 Human PRO  
 999 29.5 59.0 153 6 ABR70244 Human sec  
 1000 29.5 59.0 153 6 ABR69577 Human sec

## ALIGNMENTS

RESULT 1  
 ABB08363  
 ID ABB08363 standard; protein; 9 AA.  
 AC ABB08363;  
 XX  
 XX 07-MAY-2002 (first entry)  
 XX  
 DE Synthetic epitope 3 of human cancer antigen eIF3.  
 XX  
 KW Human; melanoma antigen eukaryotic initiation factor 3; eIF3;  
 KW ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;  
 KW anti-cancer; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain  
 FT /note= "HLA-2 binding residue"  
 FT Domain  
 FT /note= "HLA-2 binding residue"  
 FT Domain  
 FT 3..8  
 FT /note= "T-cell receptor (TCR) binding domain"  
 FT Domain  
 FT /note= "HLA-2 binding residue"  
 FT  
 XX WO200192307-A2.  
 PN  
 XX  
 XX 06-DEC-2001.  
 PD  
 XX  
 XX 30-MAY-2001; 2001WO-US017456.  
 XX  
 XX 31-MAY-2000; 2000US-0209391P.  
 PR 17-AUG-2000; 2000US-0226258P.  
 PR 20-DEC-2000; 2000US-0257008P.  
 XX  
 XX (GENZ ) GENZYME CORP.  
 PA  
 XX Nicolette CA;  
 PI  
 XX WPI; 2002-139606/18.  
 XX

DR N-PSDB; ABA97214.  
 XX  
 PT New therapeutic compounds useful against human ovarian cancer, for  
 PT modulating immune response in a subject, and for generating antibodies  
 PT that specifically recognize and bind to these molecules.  
 XX  
 XX  
 PS Claim 29; Page 59; 68pp; English.  
 CC  
 CC The invention relates to novel therapeutic compounds, that are designed  
 CC to enhance binding to MHC molecules and to enhance immunoregulatory  
 CC properties relative to their natural counterparts. The activity of the  
 CC compounds of the invention may be described as cytostatic and  
 CC immunomodulatory. The compounds are useful against human ovarian cancer,  
 CC for modulating immune response in a subject, and for generating  
 CC antibodies that specifically recognize and bind to these molecules.  
 CC Compositions comprising the compounds are useful as components of anti-  
 CC cancer vaccines and to expand immune effector cells that are specific for  
 CC cells characterized by expression of antigen eIF3 (melanoma antigen  
 CC eukaryotic initiation factor). The peptides or polypeptides conjugated to  
 CC a detectable agent may be used in diagnostic procedures, such as in the  
 CC detection and purification of antibodies, and as immunogens for  
 CC production of antibodies. The polynucleotides can be used as primers for  
 CC detecting genes or gene transcripts expressed in APC to confirm  
 CC transduction of the polynucleotides into host cells. The current sequence  
 CC represents synthetic epitope 3 of human cancer antigen eIF3  
 XX  
 SQ Sequence 9 AA;  
 Query Match 100.0%; Score 50; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLWFEIDIV 9  
 Db 1 FLWFEIDIV 9  
 |||||  
 |||||  
 RESULT 2  
 ABR82215  
 ID ABR82215 standard; peptide; 9 AA.  
 XX  
 AC ABR82215;  
 XX  
 XX 13-OCT-2003 (first entry)  
 DT  
 XX  
 DE Human antigen eIF3 derived compound 3.  
 XX  
 KW Eukaryotic translation initiation factor 3; eIF3; neoplasia; cancer;  
 KW cytostatic; gene therapy; human; antigen.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 OS  
 XX WO2003050543-A1.  
 PN  
 XX 19-JUN-2003.  
 PD  
 XX  
 XX 05-DEC-2001; 2001WO-US047997.  
 PF  
 XX  
 XX 05-DEC-2001; 2001WO-US047997.  
 PR  
 XX (GENZ ) GENZYME CORP.  
 PA  
 XX Nicolette CA;  
 PI  
 XX WPI; 2003-532936/50.  
 DR N-PSDB; ACC85032.  
 DR  
 XX  
 XX Aiding in the diagnosis of a neoplastic condition, useful for treating  
 PT cancer and related malignancies comprises determining the amount of  
 PT expression of an eIF3 protein in a test sample isolated from the cell or  
 PT tissue.  
 XX

PS Claim 12; Page 30; 77pp; English.

XX The invention relates to aiding in the diagnosis of a neoplastic

CC condition or susceptibility to a neoplastic condition of an animal cell

CC or tissue. The method involves determining the amount of expression of an

CC eukaryotic translation initiation factor 3 (eIF3) protein in a test

CC sample isolated from the cell or tissue, and diagnosing a neoplastic

CC condition or susceptibility to a neoplastic condition based on the amount

CC of expression of the eIF3 protein. The methods, compounds and kits are

CC useful in therapeutics, diagnostic and screening methods for human cancer

CC and related malignancies, e.g. ovarian, breast, lung, colon, prostate,

CC pancreatic or gastrointestinal cancer, or melanoma. Sequences ABB82213-16

CC represent compounds derived from the human antigen eIF3

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;

QY 1 FLWFEIDIV 9

Db |||||

1 FLWFEIDIV 9

RESULT 3

ABB08368

ID ABB08368 standard; protein; 352 AA.

XX

AC ABB08368;

XX

DT 07-MAY-2002 (first entry)

XX

DE Human cancer antigen eIF3 variant 3 amino acid sequence.

XX

XX Human; melanoma antigen eukaryotic initiation factor 3; eIF3;

KW ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;

XX anti-cancer; vaccine.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Misc-difference 242 /note= "wild-type Asn is replaced by Phe"

FT Domain 242 /note= "HLA-2 binding residue"

FT Domain 243

FT Domain /note= "HLA-2 binding residue"

FT Domain 244..249

FT Misc-difference 244 /note= "T-cell receptor (TCR) binding domain"

FT Misc-difference 245 /note= "wild-type Gln is replaced by Trp"

FT Misc-difference 246 /note= "wild-type Leu is replaced by Phe"

FT Misc-difference 247 /note= "wild-type Leu is replaced by Glu"

FT Misc-difference 249 /note= "wild-type Met is replaced by Ile"

FT Misc-difference 249 /note= "wild-type Arg is replaced by Ile"

FT Domain 250

FT /note= "HLA-2 binding residue"

XX

PN WQ200192307-A2.

XX

PD 06-DEC-2001.

XX

XX 30-MAY-2001; 2001WO-US017456.

XX

XX 31-MAY-2000; 2000US-0209391P.

PR 17-AUG-2000; 2000US-0226258P.

XX

XX 20-DEC-2000; 2000US-0257008P.

XX

PA (GENZ ) GENZYME CORP.

XX

PI Nicolette CA;

XX

DR WPI; 2002-139606/18.

XX

XX New therapeutic compounds useful against human ovarian cancer, for

PT modulating immune response in a subject, and for generating antibodies

FT that specifically recognize and bind to these molecules.

XX

PS Claim 8; Page; 68pp; English.

XX

CC The invention relates to novel therapeutic compounds, that are designed

CC to enhance binding to MHC molecules and to enhance immunoregulatory

CC properties relative to their natural counterparts. The activity of the

CC compounds of the invention may be described as cytostatic and

CC immunomodulatory. The compounds are useful against human ovarian cancer,

CC for modulating immune response in a subject, and for generating

CC antibodies that specifically recognize and bind to these molecules.

CC Compositions comprising the compounds are useful as components of anti-

CC cancer vaccines and to expand immune effector cells that are specific for

CC cells characterised by expression of antigen eIF3 (melanoma antigen

CC eukaryotic initiation factor). The peptides or polypeptides conjugated to

CC a detectable agent may be used in diagnostic procedures, such as in the

CC detection and purification of antibodies, and as immunogens for

CC production of antibodies. The polynucleotides can be used as primers for

CC detecting genes or gene transcripts expressed in APC to confirm

CC transduction of the polynucleotides into host cells. The current sequence

CC represents the human cancer antigen eIF3 variant 3 amino acid sequence.

CC Note: This sequence is not present in the specification, but may be

CC created from the sequence of the wild-type human cancer antigen eIF3

CC sequence given in ABB08360

XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9

Db |||||

242 FLWFEIDIV 250

RESULT 4

ABO67351

ID ABO67351 standard; protein; 585 AA.

XX

AC ABO67351;

XX

DT 29-JUL-2004 (first entry)

XX

DE Klebsiella pneumoniae polypeptide seqid 13868.

XX

XX Recombinant expression vector; transcription regulatory element;

KW Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX

OS Klebsiella pneumoniae.

XX

PN US6610836-B1.

XX

PD 26-AUG-2003.

XX

PF 27-JAN-2000; 2000US-00489039.

XX

PR 29-JAN-1999; 99US-0117747P.

XX

XX (GENO-) GENOME THERAPEUTICS CORP.

XX

XX Breton GL, Osborne M;

PI WPI; 2003-895346/82.

XX

DR N-PSDB; ABD00922.

XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.  
XX Disclosure; SEQ ID NO 13868; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
CC Klebsiella pneumoniae polypeptide of the invention  
XX  
SQ Sequence 585 AA;

Query Match 78.0%; Score 39; DB 7; Length 585;  
Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
DB 273 WFEIDVW 279

RESULT 5  
AAO30104  
ID AAO30104 standard; protein; 587 AA.

AC AAO30104;

XX 03-SEP-2003 (first entry)

XX Yersinia pestis 2G5 mutant protein.

DE Infection; tuberculosis; veterinary treatment; antimicrobial drug;

KW vaccine; mutant; mutein.

XX Yersinia pestis.

OS Synthetic.

XX WO2003044047-A2.

XX 30-MAY-2003.

XX 18-NOV-2002; 2002WO-GB005212.

XX 19-NOV-2001; 2001GB-00027657.

XX (UNLO ) LONDON SCHOOL HYGIENE & TROPICAL MEDICIN.

XX Karlyshev AV, Wren BW;

XX WPI; 2003-457588/43.

DR N-PSDB; AAL60720.

XX New virulence peptides encoded by a gene of Yersinia pseudotuberculosis,  
PT useful for treating or preventing a condition associated with infection  
PT by Yersinia, e.g. tuberculosis, particularly in veterinary treatment.

XX Claim 4; Page 96-99; 130pp; English.

XX The present invention relates to virulence genes of Yersinia species and  
CC proteins encoded by such genes. Sequences of the invention are useful in  
CC the manufacture of a medicament for treating or preventing a condition  
CC associated with infection by Yersinia e.g. tuberculosis particularly in  
CC veterinary treatment. They are useful in screening assays for identifying  
CC antimicrobial drugs. They are also used to prepare vaccines. The present  
CC sequence is Yersinia pestis 2G5 mutant protein  
XX  
SQ Sequence 587 AA;

Query Match 78.0%; Score 39; DB 6; Length 587;

Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
DB 272 WFEIDVW 278

RESULT 6

AAO20498

ID AAO20498 standard; protein; 1717 AA.

XX AAO20498;

XX 06-AUG-2003 (revised)

DT 09-JUL-2001 (first entry)

XX Ostrinia nubilalis Bt toxin receptor.

XX European corn borer; ECB; Bacillus thuringiensis; Bt toxin; receptor;  
KW crystal protein; CryIA; biological control; insecticide; crop protection.

XX Ostrinia nubilalis.

XX Key Location/Qualifiers

FT Binding-site 1293..1462

FT /label= CryIA\_binding\_site

FT Domain 1571..1589

FT /label= Transmembrane\_domain

XX WO200136639-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-US031674.

XX 18-NOV-1999; 99US-0166285P.

XX 21-SEP-2000; 2000US-0234099P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Flannagan RD, Mathis JP, Meyer TE;

XX WPI; 2001-329223/34.

XX N-PSDB; AAF30933.

XX New nucleic acid encoding Bt toxin receptor, useful for screening and  
PT identifying new Bt toxin receptor ligands useful as new insecticidal  
toxins.

XX Claim 4(a); Page 57-61; 85pp; English.

XX The present sequence of is that of the Bacillus thuringiensis (Bt) toxin  
CC receptor of the European corn borer (ECB), Ostrinia nubilalis. The  
CC sequence was deduced from cDNA isolated from an ECB larva midgut cDNA.  
CC The receptor protein binds CryIA toxins, particularly CryIA(b) toxins.  
CC The invention provides compositions and methods for modulating the  
CC susceptibility of a cell to Bt toxins. The compositions include Bt toxin  
CC receptor proteins from the lepidopteran insects ECB, corn earworm  
CC (Heliothis zea) and fall armyworm (Spodoptera frugiperda). Nucleic acids  
CC encoding the polypeptides, antibodies specific to the polypeptides, and  
CC nucleic acid constructs for expressing the polypeptides in cells are also  
CC provided. The methods of the invention are useful for investigating the  
CC structure-function relationships of Bt toxin receptors, investigating  
CC toxin-receptor interactions, elucidating the mode of action of Bt toxins,  
CC screening and identifying novel Bt toxin receptor ligands including novel  
CC insecticidal toxins, and designing and developing novel Bt toxin receptor  
CC ligands. The methods are useful for managing Bt toxin resistance in plant  
CC pests, and protecting plants against damage by plant pests. (Updated on  
CC 06-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 1717 AA;



Query Match 78.0%; Score 39; DB 4; Length 1717;  
Best Local Similarity 85.7%; Pred. No. 5.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
:|||||  
Db 650 YLWFEID 656

RESULT 7  
ADS76164  
ID ADS76164 standard; protein; 1717 AA.  
XX  
AC ADS76164;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE European corn borer Bt toxin receptor, SEQ ID 8.  
XX  
KW Bacillus thuringiensis; Bt; toxin; receptor; black cutworm moth;  
KW insecticide; european corn borer.  
XX  
OS Ostrinia nubilalis.

Key Location/Qualifiers  
FH Peptide 1..25  
FT /label= Signal\_peptide  
FT Protein 26..1717  
FT /label= Mature\_protein  
FT Domain 1293..1462  
FT /label = Cys1A\_binding\_domain  
FT Domain 1570..1589  
FT /label = Transmembrane\_domain

XX WO2004083436-A2.  
XX  
XX 30-SEP-2004.  
XX  
XX 11-MAR-2004; 2004WO-US007460.  
XX  
XX 14-MAR-2003; 2003US-0455085P.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX Mathis JP;  
XX WPI; 2004-728483/71.  
XX  
XX Novel isolated Bacillus thuringiensis receptor polypeptide, useful for  
XX screening test compounds to identify compounds binding to polypeptide,  
XX and for developing new insecticides.  
XX  
XX Disclosure; SEQ ID NO 8; 83pp; English.  
XX  
XX The present invention relates to a novel Bacillus thuringiensis (Bt)  
XX toxin receptor (I; ADS76158) and its coding sequence (II; ADS76157) from  
XX the black cutworm moth (BCW, *Agrotis ipsilon*). (I) and (II) are useful in  
XX developing new insecticides, for carrying out intact cell or in vitro  
XX receptor binding assays and/or intact cell toxicity assays. (II) is  
XX useful for isolating homologous sequences in insects species other than  
XX *Agrotis*, particularly other lepidopteran species such as *Noctuoidea* sp.  
XX The present sequence is a Bt toxin receptor used in a sequence homology  
XX alignment with the BCW Bt toxin receptor of the invention.  
XX

Seq Sequence 1717 AA;  
Query Match 78.0%; Score 39; DB 8; Length 1717;  
Best Local Similarity 85.7%; Pred. No. 5.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
:|||||  
Db 650 YLWFEID 656

RESULT 8  
ABM69298  
ID ABM69298 standard; protein; 589 AA.  
XX  
AC ABM69298;

XX 20-NOV-2003 (first entry)  
XX  
XX Photorhabdus luminescens protein sequence #2395.  
XX  
DE  
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
KW detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
KW whooping cough.  
XX  
XX Photorhabdus luminescens.  
XX  
XX WO200294867-A2.  
XX  
XX 28-NOV-2002.  
XX  
XX 07-FEB-2002; 2002WO-IB003040.  
XX  
XX 07-FEB-2001; 2001PR-00001659.  
XX (INSP ) INST PASTEUR.  
XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX

XX Duchaud B, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
XX Buchrieser C;  
XX WPI; 2003-148459/14.  
XX  
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX  
XX Claim 2; SEQ ID NO 2395; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded  
XX proteins from Photorhabdus luminescens. The isolated sequences are  
XX sources of probes and primers for detecting the genome of P. luminescens  
XX and related species; to study polymorphisms; for gene analysis and for  
XX detection/amplification of the genes. Antibodies (Ab) raised against the  
XX polypeptides encoded by the genes are used for detection/identification  
XX of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
XX carry a gene-containing vector are used to select compounds that  
XX modulate, regulate, induce or inhibit expression of the genes in plants,  
XX animals or microorganisms other than P. luminescens and are able to alter  
XX response or sensitivity to toxins and antibiotics produced by P.  
XX luminescens. Cells transformed to express the genes are useful for  
XX recombinant production of the proteins, particularly toxins and  
XX antibacterials useful as insecticides, bactericides and fungicides. The  
XX genes, proteins, vectors containing the genes and Ab are also useful  
XX therapeutically (to treat microbial infection by bacteria or fungi that  
XX are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
XX biopesticides. Other uses of the genes and the proteins are as virulence  
XX factors and for identifying targets of human diseases for which P.  
XX luminescens is a model (particularly plague and whooping cough). This  
XX sequence represents one of the isolated P. luminescens proteins  
XX  
XX Sequence 589 AA;

Query Match 76.0%; Score 38; DB 6; Length 589;  
Best Local Similarity 85.7%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
:|||||  
Db 273 WFEIDIV 279

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RESULT 9
ADY17237
ID ADY17237 standard; protein; 109 AA.
XX
XX AC ADY17237;
XX
XX DT 05-MAY-2005 (first entry)
XX
XX DE PRO polypeptide SEQ ID NO 3043.
XX
XX Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antidiabetic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW Antiallergic; ds; gene; diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN WO2005016962-A2.
XX
XX PD 24-FEB-2005.
XX
XX PF 11-AUG-2004; 2004WO-US026249.
XX
XX PR 11-AUG-2003; 2003US-0493546P.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX WPI; 2005-182330/19.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
XX Claim 8; SEQ ID NO 3043; 158pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX
XX SQ Sequence 109 AA;
Query Match 74.0%; Score 37; DB 9; Length 109;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
Db 10 FLWLQLDLV 18

RESULT 10
ABB49338
ID ABB49338 standard; protein; 150 AA.
XX
XX AC ABB49338;
XX
XX DT 05-FEB-2002 (first entry)
XX
XX DE Listeria monocytogenes protein #2042.
XX
XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
XX Listeria monocytogenes.
OS
XX WO200177335-A2.
PN

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PD 18-OCT-2001.
XX
XX PF 11-APR-2001; 2001WO-FR001118.
XX
XX PR 11-APR-2000; 2000FR-00004629.
XX
XX PA (INSP ) INST PASTEUR.
XX
XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Faihi H, Dehoux P;
PI Duesurget O, Chetoui F, Nedjari H, Glaeser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kref J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend L;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
XX WPI; 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.
XX
XX Claim 6; SEQ ID NO 2043; 192pp; French.
XX
XX The present invention relates to the genome sequence of Listeria
CC monocytogenes EGB-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccine compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 150 AA;
Query Match 74.0%; Score 37; DB 5; Length 150;
Best Local Similarity 77.8%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
Db 116 FKWFEIDKV 124

RESULT 11
ABP64842
ID ABP64842 standard; protein; 273 AA.
XX
XX AC ABP64842;
XX
XX DT 25-FEB-2003 (first entry)
XX
XX DE Human protein SEQ ID 502.
XX
XX Human; expressed sequence tag; EST; haematopoietic disorder;
KW central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective.

```

XX OS Homo sapiens.  
 XX PN WO200259260-A2.  
 XX PD 01-AUG-2002.  
 XX PF 16-NOV-2001; 2001WO-US042950.  
 XX PR 17-NOV-2000; 2000US-00714936.  
 XX PA (HYSB-) HYSEQ INC.  
 XX PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;  
 XX PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
 XX DR WPI; 2002-590824/63.  
 XX DR N-PSDB; ABQ99428.  
 XX PT New isolated polynucleotide, useful in research, diagnostic or  
 PT therapeutic methods, e.g. preventing or treating disorders involving  
 PT aberrant protein expression or biological activity.  
 XX PS Claim 20; SEQ ID NO 502; 394pp; English.  
 XX CC The present invention relates to novel human coding sequences (ABQ99268-  
 CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in  
 CC therapeutic, diagnostic and research methods. The polynucleotides may be  
 CC used in the field of molecular biology as hybridisation probes, primers  
 CC for PCR, for chromosome and gene mapping, for the recombinant production  
 CC of protein, or in generation of anti-sense DNA or RNA. The  
 CC polynucleotides are useful in diagnostics as expressed sequence tags  
 CC (ESTs) for identifying expressed genes or for physical mapping of the  
 CC human genome. The proteins may be used as molecular weight markers, or as  
 CC nutritional sources or supplements. The proteins may be used to maintain  
 CC and expand cell population in a totipotential or pluripotential state  
 CC useful for re-engineering damaged or diseased tissues, transplantation,  
 CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The  
 CC polynucleotides and proteins are useful for preventing, treating or  
 CC ameliorating disorders involving aberrant protein expression or  
 CC biological activity, e.g. haematopoietic disorders, central/peripheral  
 CC nervous system diseases, mechanical and traumatic disorders, non-healing  
 CC wounds, immune deficiencies and disorders, infectious diseases caused by  
 CC viral, bacterial or fungal infection, autoimmune disorders, allergic  
 CC reactions and conditions, coagulation disorders, or cancer. The  
 CC polynucleotide sequences of the invention were assembled from ESTs  
 CC isolated mainly by sequencing by hybridisation, and in some cases,  
 CC sequences obtained from one or more public databases. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 273 AA;  
 Query Match 74.0%; Score 37; DB 5; Length 273;  
 Best Local Similarity 55.6%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLWFEIDIV 9  
 DB 10 FLWLQDLV 18  
 RESULT 12  
 ABB54865  
 ID ABB54865 standard; protein; 528 AA.  
 XX AC ABB54865;  
 XX 29-AUG-2003 (revised)  
 DT 16-MAY-2002 (first entry)  
 XX DE Lactococcus lactis protein ypgD.

XX KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
 XX OS Lactococcus lactis; IL1403.  
 XX PN FR2807446-A1.  
 XX PD 12-OCT-2001.  
 XX PF 11-APR-2000; 2000FR-00004630.  
 XX PR 11-APR-2000; 2000FR-00004630.  
 XX PI (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
 XX DR WPI; 2002-043418/06.  
 XX PT New nucleotide sequence useful in the identification or Lactococcus  
 PT lactis and related species.  
 XX PS Claim 6; SEQ ID NO 1567; 2504pp; French.  
 XX CC The present invention is related to a Lactococcus lactis nucleotide  
 CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
 CC acid sequence is useful in the detection and/or amplification of nucleic  
 CC acid sequence, particularly to identify Lactococcus lactis or related  
 CC species. The proteins of the invention are useful for the biosynthesis or  
 CC biodegradation of a composition of interest. The invention helps research  
 CC in lactic bacteria, particularly useful in the production of yogurt and  
 CC cheese. Note: The sequence data for this patent is based on equivalent  
 CC patent WO200177334 (published 18-OCT-2001) which is available in  
 CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
 CC standardise OS field)  
 XX SQ Sequence 528 AA;  
 Query Match 74.0%; Score 37; DB 5; Length 528;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FLWFEIDIV 9  
 DB 49 FLWLADII 57  
 RESULT 13  
 ADS29413  
 ID ADS29413 standard; protein; 529 AA.  
 XX AC ADS29413;  
 XX 02-DEC-2004 (first entry)  
 DT Bacterial polypeptide #18446.  
 DE Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX OS Bacteria.  
 XX PN US2003233675-A1.  
 XX PD 18-DEC-2003.  
 XX PF 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.  
PR (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
PI WPI; 2004-061375/06.  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX Claim 1; SEQ ID NO 18446; 122pp; English.  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX Sequence 529 AA;  
SQ Query Match 74.0%; Score 37; DB 8; Length 529;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FLWFEIDIV 9  
DB 49 FLWLAIDII 57  
RESULT 14  
ABM70700  
ID ABM70700 standard; protein; 587 AA.  
XX ABM70700;  
XX ABM70700;  
XX 20-NOV-2003 (first entry)  
XX Photorhabdus luminescens protein sequence #3797.  
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
KW detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
KW whooping cough.  
XX Photorhabdus luminescens.  
XX WO200294867-A2.  
XX

XX 28-NOV-2002.  
XX 07-FEB-2002; 2002WO-IB003040.  
XX 07-FEB-2001; 2001FR-00001659.  
XX (INSP ) INST PASTEUR.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
PI Buchrieser C;  
XX WPI; 2003-148459/14.  
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX Claim 2; SEQ ID NO 3797; 1205pp; French.  
XX The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
SQ Sequence 587 AA;  
Query Match 74.0%; Score 37; DB 6; Length 587;  
Best Local Similarity 71.4%; Pred. No. 4.2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 WFEIDIV 9  
DB 272 WFEIDV 278  
RESULT 15  
ABBS3431  
ID ABBS3431 standard; protein; 269 AA.  
XX ABBS3431;  
XX 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
XX Lactococcus lactis protein ybdC.  
XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
XX Lactococcus lactis; IL1403.  
XX PR2807446-A1.  
XX 12-OCT-2001.  
XX 11-APR-2000; 2000FR-00004630.  
XX



CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences ABQ67826-  
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 373 AA;

Query Match 72.0%; Score 36; DB 7; Length 373;  
 Best Local Similarity 55.6%; Pred. No. 3.9e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 :|||:|:  
 Db 307 YLWVELDIV 315

RESULT 18  
 ADS41622  
 ID ADS41622 standard; protein; 402 AA.

XX ADS41622;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #20052.

XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 20052; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 402 AA;

Query Match 72.0%; Score 36; DB 8; Length 402;  
 Best Local Similarity 71.4%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
 :|||:|:  
 Db 245 WFEVDIL 251

RESULT 19

ABG01159

ID ABG01159 standard; protein; 410 AA.

XX ABG01159;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #1150.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS65346.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX Claim 20; SEQ ID NO 31518; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activities. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX SQ Sequence 410 AA;

Query Match 72.0%; Score 36; DB 4; Length 410;  
 Best Local Similarity 62.5%; Pred. No. 4.3e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWPEIDI 8  
 | : | | | |  
 Db 200 FFWFEDDV 207

RESULT 20  
 ABM68497  
 ID ABM68497 standard; protein; 591 AA.  
 AC ABM68497;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 DE Photorhabdus luminescens protein sequence #1594.  
 XX  
 XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
 KW detection; food; gene expression; plant; animal; microorganism; toxin;  
 KW antibiotic; biopesticide; virulence factor; disease model; plague;  
 KW whooping cough.  
 XX  
 XX Photorhabdus luminescens.  
 OS  
 XX WO200294867-A2.  
 PN  
 XX 28-NOV-2002.  
 PD  
 XX 07-FEB-2002; 2002WO-IB003040.  
 PF  
 XX 07-FEB-2001; 2001FR-00001659.  
 PR  
 XX (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA  
 XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
 PI Buchrieser C;  
 PI  
 XX WPI; 2003-148459/14.  
 DR  
 XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
 PT  
 XX Claim 2; SEQ ID NO 1594; 1205pp; French.  
 PS  
 XX The invention relates to the isolation of genes and their encoded  
 CC proteins from Photorhabdus luminescens. The isolated sequences are  
 CC sources of probes and primers for detecting the genome of P. luminescens

CC and related species; to study polymorphisms; for gene analysis and for  
 CC detection/amplification of the genes. Antibodies (Ab) raised against the  
 CC polypeptides encoded by the genes are used for detection/identification  
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
 CC carry a gene-containing vector are used to select compounds that  
 CC modulate, regulate, induce or inhibit expression of the genes in plants,  
 CC animals or microorganisms other than P. luminescens and are able to alter  
 CC response or sensitivity to toxins and antibiotics produced by P.  
 CC luminescens. Cells transformed to express the genes are useful for  
 CC recombinant production of the proteins, particularly toxins and  
 CC antibacterials useful as insecticides, bactericides and fungicides. The  
 CC genes, proteins, vectors containing the genes and Ab are also useful  
 CC therapeutically (to treat microbial infection by bacteria or fungi that  
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
 CC biopesticides. Other uses of the genes and the proteins are as virulence  
 CC factors and for identifying targets of human diseases for which P.  
 CC luminescens is a model (particularly plague and whooping cough). This  
 CC sequence represents one of the isolated P. luminescens proteins  
 XX  
 XX SQ Sequence 591 AA;

Query Match 72.0%; Score 36; DB 6; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEID 7  
 | : | | | | |  
 Db 255 LWFEID 260

RESULT 21  
 ABO14689  
 ID ABO14689 standard; protein; 652 AA.  
 AC ABO14689;  
 XX  
 XX 25-AUG-2003 (first entry)  
 DT  
 DE Novel human protein #62.  
 XX  
 XX Human; NOV; gene therapy; endocrine related disease; diabetes;  
 KW metabolism-related disease; obesity; central nervous system disorder;  
 KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
 KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
 KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
 KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
 KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;  
 KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
 KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
 KW stroke; infection.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2003023002-A2.  
 PN  
 XX 20-MAR-2003.  
 PD  
 XX 09-SEP-2002; 2002WO-US028539.  
 PF  
 XX 07-SEP-2001; 2001US-0318120P.  
 PR 07-SEP-2001; 2001US-0318130P.  
 PR 10-SEP-2001; 2001US-0318430P.  
 PR 17-SEP-2001; 2001US-0322636P.  
 PR 17-SEP-2001; 2001US-0322781P.  
 PR 17-SEP-2001; 2001US-0322816P.  
 PR 17-SEP-2001; 2001US-0322817P.  
 PR 19-SEP-2001; 2001US-0323519P.  
 PR 20-SEP-2001; 2001US-0323631P.  
 PR 20-SEP-2001; 2001US-0323636P.  
 PR 25-SEP-2001; 2001US-0324969P.  
 PR 25-SEP-2001; 2001US-0325091P.  
 PR 26-SEP-2001; 2001US-0324990P.  
 PR 17-APR-2002; 2002US-0373212P.

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PR 06-SEP-2002; 2002US-00236177.
XX (CURA-) CURAGEN CORP.
PA
XX
XX
XX Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;
PI Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;
PI Shinkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
PI Lepley DM, Edinger SR, Burgess CE;
XX
XX WPI; 2003-313242/30.
DR N-PSDB; ACD19382.
XX
XX New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)
PT and polynucleotides, useful in gene therapy, e.g. for treating or
PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
PT stroke or infections.
XX
XX Claim 1; Page 195-196; 586pp; English.
PS
XX The invention describes a new isolated polypeptide (NOVX). The NOVX
CC polypeptide, nucleic acid and antibody are useful as therapeutics,
CC particularly in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, which includes a pathology associated
CC with NOVX polypeptide. The DNA encoding the protein is useful in gene
CC therapy for treating the disease or condition. In particular, the NOVX
CC polypeptide or polynucleotide is useful for treating endocrine/
CC metabolism-related diseases (e.g. obesity or diabetes), central nervous
CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,
CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune
CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,
CC asthma, inflammatory bowel disease, rheumatoid arthritis or
CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver
CC cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
CC haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
CC These are also useful in developing powerful assay system for functional
CC analysis of various human disorders, as well as in diagnostic
CC applications, and for monitoring the effects of drugs during clinical
CC trials. This is the amino acid sequence of a novel human NOV protein
XX
XX Sequence 652 AA;
SQ
Query Match 72.0%; Score 36; DB 6; Length 652;
Best Local Similarity 75.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 FLWFEIDI 8
DB 564 FLWFENDM 571
RESULT 22
ABO14690
ID ABO14690 standard; protein; 700 AA.
XX
XX ABO14690;
AC
XX
XX 25-AUG-2003 (first entry)
DT
XX
XX Novel human protein #63.
DE
XX
XX Human; NOV; gene therapy; endocrine related disease; diabetes;
KW metabolism-related disease; obesity; central nervous system disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;
KW stroke; infection.
XX

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OS Homo sapiens.
XX
XX WO20030233002-A2.
XX
XX 20-MAR-2003.
XX
XX 09-SEP-2002; 2002WO-US028539.
XX
XX 07-SEP-2001; 2001US-0318120P.
XX 07-SEP-2001; 2001US-0318130P.
XX 10-SEP-2001; 2001US-0318430P.
XX 17-SEP-2001; 2001US-0322636P.
XX 17-SEP-2001; 2001US-0322781P.
XX 17-SEP-2001; 2001US-0322816P.
XX 17-SEP-2001; 2001US-0322817P.
XX 19-SEP-2001; 2001US-0323519P.
XX 20-SEP-2001; 2001US-0323631P.
XX 20-SEP-2001; 2001US-0323636P.
XX 25-SEP-2001; 2001US-0324969P.
XX 25-SEP-2001; 2001US-0325091P.
XX 26-SEP-2001; 2001US-0324990P.
XX 17-APR-2002; 2002US-0373212P.
XX 06-SEP-2002; 2002US-00236177.
XX (CURA-) CURAGEN CORP.
XX
XX Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;
PI Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;
PI Shinkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
PI Lepley DM, Edinger SR, Burgess CE;
XX
XX WPI; 2003-313242/30.
DR N-PSDB; ACD19383.
XX
XX New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)
PT and polynucleotides, useful in gene therapy, e.g. for treating or
PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
PT stroke or infections.
XX
XX Claim 1; Page 196; 586pp; English.
XX
XX The invention describes a new isolated polypeptide (NOVX). The NOVX
CC polypeptide, nucleic acid and antibody are useful as therapeutics,
CC particularly in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, which includes a pathology associated
CC with NOVX polypeptide. The DNA encoding the protein is useful in gene
CC therapy for treating the disease or condition. In particular, the NOVX
CC polypeptide or polynucleotide is useful for treating endocrine/
CC metabolism-related diseases (e.g. obesity or diabetes), central nervous
CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,
CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune
CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,
CC asthma, inflammatory bowel disease, rheumatoid arthritis or
CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver
CC cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
CC haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
CC These are also useful in developing powerful assay system for functional
CC analysis of various human disorders, as well as in diagnostic
CC applications, and for monitoring the effects of drugs during clinical
CC trials. This is the amino acid sequence of a novel human NOV protein
XX
XX Sequence 700 AA;
SQ
Query Match 72.0%; Score 36; DB 6; Length 700;
Best Local Similarity 75.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 FLWFEIDI 8
DB 612 FLWFENDM 619

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RESULT 23
ADD14125
ID ADD14125 standard; protein; 700 AA.
XX
AC ADD14125;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human src biomarker polypeptide SEQ ID NO:314.
XX
KW predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytoskeletal;
KW gene therapy; drug sensitivity; genetic profile; cancer; human.
XX
OS Homo sapiens.
XX
PN W02003062395-A2.
XX
PD 31-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-US001981.
XX
PR 18-JAN-2002; 2002US-0350061P.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Huang F, Fairchild CR, Lee FY, Shaw P;
XX
DR WPI; 2003-636735/60.
XX
N-PSDB; ADD14725.
XX
PT New polynucleotides and polypeptides for predicting the activity of
PT compounds that interact with protein tyrosine kinases and/or protein
PT tyrosine kinase pathways.
XX
PS Claim 10; SEQ ID NO 314; 139pp; English.
XX
XX The present invention describes a predictor set comprising a plurality of
XX polynucleotides or polypeptides whose expression pattern is predictive of
XX the response of cells to treatment with a compound that modulates protein
XX tyrosine kinase activity or members of the protein tyrosine kinase
XX pathway. Also described: (1) predicting whether a compound is capable of
XX modulating the activity of cells, comprising obtaining a sample of cells,
XX determining whether the cells express a plurality of markers, and
XX correlating the expression of the markers to the compound's ability to
XX modulate the activity of the cells; (2) a plurality of cell lines for
XX identifying polynucleotides and polypeptides whose expression levels
XX correlate with compound sensitivity or resistance of cells associated
XX with a disease state; and (3) identifying polynucleotides and
XX polypeptides that predict compound sensitivity or resistance of cells
XX associated with a disease state, comprising subjecting the plurality of
XX cell lines to one or more compounds, analysing the expression pattern of
XX a microarray of polynucleotides or polypeptides, and selecting
XX polynucleotides or polypeptides that predict the sensitivity or
XX resistance of cells associated with a disease state by using the
XX expression pattern of the microarray. The polynucleotides and
XX polypeptides have cytostatic activities, and can be used in gene therapy.
XX The polynucleotides and polypeptides are useful in predicting the
XX activity of compounds that interact with protein tyrosine kinases and/or
XX protein tyrosine kinase pathways. These may be used in determining drug
XX sensitivity in patients to allow the development of individualized
XX genetic profiles which aid in treating diseases and disorders (e.g.
XX cancer) based on patient response at a molecular level. The present
XX sequence is used in the exemplification of the present invention.
XX
SQ Sequence 700 AA;
Query Match 72.0%; Score 36; DB 7; Length 700;
Best Local Similarity 75.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FLWFEIDI 8
||||| |
612 FLWFENDM 619
RESULT 24
ADJ70236
ID ADJ70236 standard; protein; 700 AA.
XX
AC ADJ70236;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID2042.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN W02003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
XX Warnock DE;
XX WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
XX comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX
XX Claim 1; SEQ ID NO 2042; 180pp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
XX for therapeutic intervention in treating a disease associated with
XX altered mitochondrial function. Specifically, it refers to a method for
XX identifying proteins of the human heart mitochondrial proteome that are
XX useful for drug screening assays, as well as therapeutic targets. The
XX present invention describes a method for identifying such proteins that
XX can be used in the treatment of various diseases associated with altered
XX mitochondrial function including diabetes mellitus, Huntington's disease,
XX osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX compositions have neuroprotective, nontropic, antidiabetic,
XX anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX cytostatic activities. This polypeptide sequence is a human heart
XX mitochondrial protein of the invention.
XX
SQ Sequence 700 AA;
Query Match 72.0%; Score 36; DB 7; Length 700;
Best Local Similarity 75.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FLWFEIDI 8
||||| |
612 FLWFENDM 619

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Db          612 FLWFENDM 619

RESULT 25
ABG01151
ID ABG01151 standard; protein; 1097 AA.
XX
AC ABG01151;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #1142.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
PD WO200175067-A2.
XX
WPI; 2001-639362/73.
DR N-PSDB; AAS65338.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 31510; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1097 AA;

Query Match          72.0%; Score 36; DB 4; Length 1097;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 FLWFEDI 8
          |:|:|:|:|:|
Db          270 FIWFEDDV 277

RESULT 26
ADS76158
ID ADS76158 standard; protein; 1759 AA.
XX
AC ADS76158;
XX
DT 16-DEC-2004 (first entry)
XX
DE Black cutworm moth Bt toxin receptor, SEQ ID 2.
XX
KW Bacillus thuringiensis; Bt; toxin; receptor; black cutworm moth;
KW insecticide.
XX
OS Agrotis ipsilon.
XX
FH Key Location/Qualifiers
FH Peptide 1..25
FT /label= Signal_peptide
FT Protein 26..1759
FT /label= Mature_protein
FT Domain 1333..1500
FT /label = Cry1A_binding_domain
FT Domain 1608..1627
FT /label = Transmembrane_domain
XX
PN WO2004083436-A2.
XX
PD 30-SEP-2004.
XX
PF 11-MAR-2004; 2004WO-US007460.
XX
PR 14-MAR-2003; 2003US-0455085P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
PI Mathis JP;
XX
WPI; 2004-728483/71.
DR N-PSDB; ADS76157.
XX
PT Novel isolated Bacillus thuringiensis receptor polypeptide, useful for
PT screening test compounds to identify compounds binding to polypeptide,
PT and for developing new insecticides.
XX
PS Claim 4; SEQ ID NO 2; 83pp; English.
XX
CC The present invention relates to a novel Bacillus thuringiensis (Bt)
CC toxin receptor (I; ADS76158) and its coding sequence (II; ADS76157) from
CC the black cutworm moth (BCW, Agrotis ipsilon). (I) and (II) are useful in
CC developing new insecticides, for carrying out intact cell or in vitro
CC receptor binding assays and/or intact cell toxicity assays. (II) is
CC useful for isolating homologous sequences in insects species other than
CC Agrotis, particularly other lepidopteran species such as Noctuoidea sp.
XX
SQ Sequence 1759 AA;

Query Match          72.0%; Score 36; DB 8; Length 1759;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 LWFEID 7
          |||||
Db          668 LWFEID 673

RESULT 27
ADI17021
ID ADI17021 standard; protein; 217 AA.
XX
AC ADI17021;
XX
DT 15-APR-2004 (first entry)

```

XX Human NOVX protein homologue SeqID 557.  
DE human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;  
XX inflammation; autoimmune disorder; allergy; blood disorder;  
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;  
KW immunoglobulin (IgA nephropathy; cirrhosis; arthritis;  
KW Alzheimer's disease; infection; str.  
XX  
OS Homo sapiens.  
XX  
XX WO200268649-A2.  
XX  
PD 06-SEP-2002.  
XX  
XX 31-JAN-2002; 2002WO-US002785.  
XX  
XX 31-JAN-2001; 2001US-0265395P.  
XX 31-JAN-2001; 2001US-0265412P.  
XX 31-JAN-2001; 2001US-0265514P.  
XX 31-JAN-2001; 2001US-0265517P.  
XX 02-FEB-2001; 2001US-0266406P.  
XX 05-FEB-2001; 2001US-0266767P.  
XX 07-FEB-2001; 2001US-0266975P.  
XX 07-FEB-2001; 2001US-0267057P.  
XX 08-FEB-2001; 2001US-0267459P.  
XX 09-FEB-2001; 2001US-0267823P.  
XX 15-FEB-2001; 2001US-0268974P.  
XX 26-FEB-2001; 2001US-0271664P.  
XX 27-FEB-2001; 2001US-0271839P.  
XX 27-FEB-2001; 2001US-0271855P.  
XX 02-MAR-2001; 2001US-0272788P.  
XX 02-MAR-2001; 2001US-0273046P.  
XX 14-MAR-2001; 2001US-0275925P.  
XX 14-MAR-2001; 2001US-0275947P.  
XX 14-MAR-2001; 2001US-0275950P.  
XX 14-MAR-2001; 2001US-0275989P.  
XX 15-MAR-2001; 2001US-0276448P.  
XX 15-MAR-2001; 2001US-0276450P.  
XX 16-MAR-2001; 2001US-0276397P.  
XX 16-MAR-2001; 2001US-0276768P.  
XX 26-MAR-2001; 2001US-0278652P.  
XX 26-MAR-2001; 2001US-0278775P.  
XX 26-MAR-2001; 2001US-0278778P.  
XX 29-MAR-2001; 2001US-0279882P.  
XX 29-MAR-2001; 2001US-0279884P.  
XX 30-MAR-2001; 2001US-0280147P.  
XX 11-APR-2001; 2001US-0282992P.  
XX 11-APR-2001; 2001US-0283083P.  
XX 20-APR-2001; 2001US-0285133P.  
XX 23-APR-2001; 2001US-0285749P.  
XX 03-MAY-2001; 2001US-0288327P.  
XX 03-MAY-2001; 2001US-0288504P.  
XX 29-MAY-2001; 2001US-0294047P.  
XX 30-MAY-2001; 2001US-0294473P.  
XX 08-JUN-2001; 2001US-0296964P.  
XX 18-JUN-2001; 2001US-0298959P.  
XX 19-JUN-2001; 2001US-0299324P.  
XX 13-AUG-2001; 2001US-0312020P.  
XX 16-AUG-2001; 2001US-0312889P.  
XX 16-AUG-2001; 2001US-0312908P.  
XX 21-AUG-2001; 2001US-0313390P.  
XX 28-AUG-2001; 2001US-0315470P.  
XX 31-AUG-2001; 2001US-0316447P.  
XX 07-SEP-2001; 2001US-0318115P.  
XX 07-SEP-2001; 2001US-0318118P.  
XX 12-SEP-2001; 2001US-0318740P.  
XX 19-SEP-2001; 2001US-0323379P.  
XX 18-OCT-2001; 2001US-0330245P.  
XX 18-OCT-2001; 2001US-0330308P.  
XX 14-NOV-2001; 2001US-0332701P.  
XX  
XX (CURA-) CURAGEN CORP.

XX Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkete RA;  
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;  
PI Gerlach VL, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CEA;  
XX Purak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;  
XX WPI; 2002-706998/76.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
XX Disclosure; SEQ ID NO 557; 1498pp; English.  
XX  
XX This invention relates to a novel nucleic acids, and encoded polypeptides  
CC thereof, which have properties related to the stimulation of biochemical  
CC or physiological responses in a cell, tissue, organ or organism.  
CC Specifically, it refers to the use of biologically active fragments for  
CC diagnostic and prognostic assays and furthermore in the treatment of  
CC diverse pathological conditions. The present invention describes novel  
CC human and murine NOVX proteins, as well as methods to modulate their  
CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
CC The NOVX polypeptides, polynucleotides and antibodies are useful in  
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,  
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in  
CC treating or preventing diseases such as inflammation, autoimmune  
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome  
CC (AIDS), obesity, asthma, immunoglobulin (IgA) nephropathy, cirrhosis,  
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy  
CC and epilepsy. Accordingly, these molecules have many activities including  
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,  
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,  
CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,  
CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,  
CC relaxant and anticonvulsant. In addition, they are useful in screening  
CC assays to identify small molecules that modulate or inhibit, for example,  
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
CC used as in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein  
XX of the invention.  
XX  
XX Sequence 217 AA;  
SQ

Query Match 70.0%; Score 35; DB 5; Length 217;  
Best Local Similarity 77.8%; Pred. No. 3.3e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
||| |  
Db 86 FLWFLIPIV 94

RESULT 28  
ADC86399  
ID ADC86399 standard; protein; 232 AA.  
XX  
XX ADC86399;  
XX  
XX 01-JAN-2004 (first entry)  
XX  
XX Human GPCR protein SEQ ID NO:852.  
XX  
XX human; GPCR; guanosine triphosphate-binding protein coupled receptor;  
KW gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX EP1270724-A2.  
XX  
XX 02-JAN-2003.  
XX  
XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.  
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 XX Suwa M, Asai K, Akiyama Y, Aburatani H;  
 XX WPI; 2003-315783/31.  
 DR N-PSDB; ADC86398.  
 XX New polynucleotide, useful for preparing a composition for treating a  
 PT patient in need of increased or suppressed activity or expression of the  
 PT guanosine triphosphate-binding protein coupled receptor.  
 XX Claim 2; SEQ ID NO 852; 28pp; English.  
 XX The invention relates to a novel polynucleotide encoding a guanosine  
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
 CC the invention may have a use in gene therapy. The polynucleotide and  
 CC polypeptide are useful for preparing a composition for treating a patient  
 CC in need of increased or suppressed activity or expression of the  
 CC guanosine triphosphate-binding protein coupled receptor. The protein  
 CC sequences shown in ADC8549-ADC87617 represent GPCR's of the invention.  
 XX Sequence 232 AA;  
 SQ

Query Match 70.0%; Score 35; DB 7; Length 232;  
 Best Local Similarity 77.8%; Pred. No. 3.5e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 |||||  
 Db 168 FLWFLPIV 176

RESULT 29  
 AAG71459  
 ID AAG71459 standard; protein; 307 AA.  
 XX AAG71459;  
 AC  
 XX 31-JUL-2001 (first entry)  
 DT  
 XX Human olfactory receptor polypeptide, SEQ ID NO: 1140.  
 DE  
 XX Human; olfactory receptor; OR; primary scent determination;  
 KW secondary scent determination; polypeptide library; odour receptor;  
 KW scent profile; scent fingerprint; scent representation.  
 XX Homo sapiens.  
 OS  
 XX WO200127158-A2.  
 PN  
 XX 19-APR-2001.  
 PD  
 XX 06-OCT-2000; 2000WO-US027582.  
 PF  
 XX 08-OCT-1999; 99US-0158615P.  
 PR 24-FEB-2000; 2000US-0184809P.  
 XX (DIGI-) DIGISCENTS.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;  
 PI WPI; 2001-290713/30.  
 XX  
 XX New polynucleotides which encode polypeptides involved in olfactory  
 PT sensation for identifying olfactory agonists and antagonists.  
 XX Claim 11; Page 661-662; 1857pp; English.

CC The present sequence is an olfactory receptor which is encoded by one of  
 CC a number of novel polynucleotides. The polynucleotides can be used in  
 CC screening for olfactory agonists and antagonists. The methods allow for  
 CC the determination of primary scents and the identification of the odour  
 CC receptors used to detect these primary scents. The methods also enable  
 CC determination of secondary scents and the identification of combinations  
 CC of odour receptors that are involved in detecting such secondary scents.  
 CC This enables the construction of a scent representation (also called a  
 CC scent fingerprint or scent profile), which may be used to re-create and  
 CC edit scents. Libraries of olfactory receptors are useful for determining  
 CC the interaction pattern of a composition with the receptors, and can be  
 CC used for determining differences in the olfactory faculties of different  
 CC individuals  
 XX Sequence 307 AA;  
 SQ

Query Match 70.0%; Score 35; DB 4; Length 307;  
 Best Local Similarity 77.8%; Pred. No. 4.8e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 |||||  
 Db 146 FLWFLPIV 154

RESULT 30  
 AAG72215  
 ID AAG72215 standard; protein; 315 AA.  
 XX AAG72215;  
 AC  
 XX 30-JUL-2001 (first entry)  
 DT  
 XX Human olfactory receptor polypeptide, SEQ ID NO: 1896.  
 DE  
 XX Human; olfactory receptor; OR; primary scent determination;  
 KW secondary scent determination; polypeptide library; odour receptor;  
 KW scent profile; scent fingerprint; scent representation.  
 XX Homo sapiens.  
 OS  
 XX WO200127158-A2.  
 PN  
 XX 19-APR-2001.  
 PD  
 XX 06-OCT-2000; 2000WO-US027582.  
 PF  
 XX 08-OCT-1999; 99US-0158615P.  
 PR 24-FEB-2000; 2000US-0184809P.  
 XX (DIGI-) DIGISCENTS.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;  
 PI WPI; 2001-290713/30.  
 XX  
 XX New polynucleotides which encode polypeptides involved in olfactory  
 PT sensation for identifying olfactory agonists and antagonists.  
 XX Claim 11; Page 1258-1259; 1857pp; English.

CC The present sequence is an olfactory receptor which is encoded by one of  
 CC a number of novel polynucleotides. The polynucleotides can be used in  
 CC screening for olfactory agonists and antagonists. The methods allow for  
 CC the determination of primary scents and the identification of the odour  
 CC receptors used to detect these primary scents. The methods also enable  
 CC determination of secondary scents and the identification of combinations  
 CC of odour receptors that are involved in detecting such secondary scents.  
 CC This enables the construction of a scent representation (also called a  
 CC scent fingerprint or scent profile), which may be used to re-create and  
 CC edit scents. Libraries of olfactory receptors are useful for determining  
 CC the interaction pattern of a composition with the receptors, and can be

CC used for determining differences in the olfactory faculties of different  
 CC individuals

SQ Sequence 315 AA;

Query Match 70.0%; Score 35; DB 4; Length 315;  
 Best Local Similarity 77.8%; Pred. NO. 4.9e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLWFEIDIV 9  
 |||||  
 Db 157 FLWFLPIV 165

RESULT 31

ABG79345

ID ABG79345 standard; protein; 315 AA.

XX

AC ABG79345;

XX

DT 15-NOV-2002 (first entry)

XX Human GPCR7 protein.

XX G protein coupled receptor related protein; human; GPCR; cardiomyopathy;  
 KW atherosclerosis; diabetes; cancer; stroke; Von Hippel-Lindau syndrome;  
 KW Alzheimer's disease; tuberculous sclerosis; hypercalcaemia;  
 KW Parkinson's disease; Huntington's disease; cerebral palsy; epilepsy;  
 KW Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia;  
 KW leukodystrophy; addiction; anxiety; depression; pain; obesity;  
 KW Crohn's disease; osteoporosis; haemophilia; asthma;  
 KW inflammatory bowel disease; infertility; hypertension; scleroderma;  
 KW arthritis; human immunodeficiency virus; autoimmune disease; HIV;  
 KW infection; graft-versus-host disease.

XX Homo sapiens.

OS WO200264793-A2.

XX 22-AUG-2002.

XX 03-JAN-2002; 2002WO-US0000056.

XX 03-JAN-2001; 2001US-0259552P.

XX 09-JAN-2001; 2001US-0260544P.

XX 20-MAR-2001; 2001US-0277405P.

XX (CURA-) CURAGEN CORP.

XX Casman SV, Edinger SR, Ellerman K, Smithson G, Kekuda R;

PI Muralidhara P;

XX WPI; 2002-643487/69.

DR N-PSDB; ABS64714.

XX New isolated G protein coupled receptor polypeptides and polynucleotides,  
 PT useful in gene therapy, particularly for treating or preventing  
 PT cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, Crohn's  
 PT disease or cancer.

XX Claim 1; Page 50; 252pp; English.

XX This invention relates to a new isolated G-protein coupled receptor  
 CC (GPCR) polypeptide sequence and the cDNA encoding it. The GPCR  
 CC polypeptide, GPCR nucleic acid and an antibody specific to the protein  
 CC are useful for treating, preventing or alleviating a GPCR-associated  
 CC disorder or a pathological state in a subject, particularly a human. In  
 CC particular, the disorder is cardiomyopathy, atherosclerosis, diabetes, or  
 CC a disorder related to cell signal processing and metabolic pathway  
 CC modulation. The GPCR polypeptide and nucleic acid are also useful for  
 CC diagnosing the presence of or predisposition to a disease associated with  
 CC altered levels of GPCR, particularly cancer. The GPCR nucleic acid and  
 CC polypeptide are especially useful in the manufacture of a medicament for

CC therapeutic or prophylactic applications for disorders associated with  
 CC aberrant GPCR expression or activity, e.g. Von Hippel-Lindau syndrome,  
 CC Alzheimer's disease, stroke, tuberculous sclerosis, hypercalcaemia,  
 CC Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy,  
 CC Lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia,  
 CC leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's  
 CC disease, osteoporosis, inflammatory bowel disease, infertility,  
 CC hypertension, scleroderma, haemophilia, asthma, arthritis, human  
 CC immunodeficiency virus; autoimmune disease; HIV, viral, fungal, bacterial  
 CC or protozoal infections, or graft-versus-host disease. The DNA encoding  
 CC the protein is useful in gene therapy for treating the above conditions.  
 CC The polypeptides can be used as immunogens to produce antibodies and as  
 CC vaccines. The nucleic acids are further used as hybridisation probes, in  
 CC chromosome mapping, tissue typing, preventive medicine, and  
 CC pharmacogenomics. These are also useful in developing powerful assay  
 CC system for functional analysis of various human disorders, as well as in  
 CC diagnostic applications. The present sequence represents a human G  
 CC protein coupled receptor related protein (GPCR) of the invention  
 XX  
 XX Sequence 315 AA;

Query Match 70.0%; Score 35; DB 5; Length 315;

Best Local Similarity 77.8%; Pred. NO. 4.9e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLWFEIDIV 9

|||||

Db 157 FLWFLPIV 165

RESULT 32

AD116656

ID AD116656 standard; protein; 315 AA.

XX

AC AD116656;

XX

DT 15-APR-2004 (first entry)

XX Human NOVX protein to treat human pathological conditions SeqID192.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;  
 KW inflammation; autoimmune disorder; allergy; blood disorder;  
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;  
 KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;  
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;  
 KW cytostatic; cardiac; antiinflammatory; immunosuppressive; antiallergic;  
 KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;  
 KW antiasthmatic; nephrotropic; antiarthritis; hepatotropic;  
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;  
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;  
 KW chromosome mapping; tissue typing; pharmacogenomic.

XX Homo sapiens.

XX WO200268649-A2.

XX 06-SEP-2002.

XX 31-JAN-2002; 2002WO-US002785.

XX 31-JAN-2001; 2001US-0265395P.

XX 31-JAN-2001; 2001US-0265412P.

XX 31-JAN-2001; 2001US-0265514P.

XX 31-JAN-2001; 2001US-0265517P.

XX 02-FEB-2001; 2001US-0266406P.

XX 05-FEB-2001; 2001US-0266767P.

XX 07-FEB-2001; 2001US-0266975P.

XX 07-FEB-2001; 2001US-0267057P.

XX 08-FEB-2001; 2001US-0267459P.

XX 09-FEB-2001; 2001US-0267823P.

XX 15-FEB-2001; 2001US-0268974P.

XX 26-FEB-2001; 2001US-0271664P.

XX 27-FEB-2001; 2001US-0271839P.

PR 27-FEB-2001; 2001US-0271855P.  
PR 02-MAR-2001; 2001US-0272788P.  
PR 02-MAR-2001; 2001US-0273046P.  
PR 14-MAR-2001; 2001US-0275925P.  
PR 14-MAR-2001; 2001US-0275947P.  
PR 14-MAR-2001; 2001US-0275950P.  
PR 14-MAR-2001; 2001US-0275989P.  
PR 15-MAR-2001; 2001US-0276448P.  
PR 15-MAR-2001; 2001US-0276450P.  
PR 16-MAR-2001; 2001US-0276397P.  
PR 16-MAR-2001; 2001US-0276768P.  
PR 20-MAR-2001; 2001US-0278652P.  
PR 26-MAR-2001; 2001US-0278775P.  
PR 26-MAR-2001; 2001US-0278778P.  
PR 29-MAR-2001; 2001US-0279882P.  
PR 29-MAR-2001; 2001US-0279884P.  
PR 30-MAR-2001; 2001US-0280147P.  
PR 11-APR-2001; 2001US-0282992P.  
PR 11-APR-2001; 2001US-0283083P.  
PR 20-APR-2001; 2001US-0285133P.  
PR 23-APR-2001; 2001US-0285749P.  
PR 03-MAY-2001; 2001US-0288327P.  
PR 03-MAY-2001; 2001US-0288504P.  
PR 29-MAY-2001; 2001US-0294047P.  
PR 30-MAY-2001; 2001US-0294473P.  
PR 08-JUN-2001; 2001US-0296964P.  
PR 18-JUN-2001; 2001US-0298959P.  
PR 19-JUN-2001; 2001US-0299324P.  
PR 13-AUG-2001; 2001US-0312020P.  
PR 16-AUG-2001; 2001US-0312889P.  
PR 16-AUG-2001; 2001US-0312908P.  
PR 21-AUG-2001; 2001US-0313390P.  
PR 28-AUG-2001; 2001US-0315470P.  
PR 31-AUG-2001; 2001US-0316447P.  
PR 07-SEP-2001; 2001US-0318115P.  
PR 07-SEP-2001; 2001US-0318118P.  
PR 12-SEP-2001; 2001US-0318740P.  
PR 19-SEP-2001; 2001US-0323379P.  
PR 18-OCT-2001; 2001US-0330245P.  
PR 18-OCT-2001; 2001US-0330308P.  
PR 14-NOV-2001; 2001US-0332701P.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;  
PI Li L, Gangolli EA, Padigar M, Anderson DW, Rastelli L, Miller CE;  
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;  
PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;  
XX  
XX WPI: 2002-706998/76.  
XX N-PSDB; AD116655.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
XX Claim 1; SEQ ID NO 192; 1498pp; English.  
XX  
XX This invention relates to a novel nucleic acids, and encoded polypeptides  
CC thereof, which have properties related to the stimulation of biochemical  
CC or physiological responses in a cell, tissue, organ or organism.  
CC Specifically, it refers to the use of biologically active fragments for  
CC diagnostic and prognostic assays and furthermore in the treatment of  
CC diverse pathological conditions. The present invention describes novel  
CC human and murine NOVX proteins, as well as methods to modulate their  
CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
CC The NOVX polypeptides, polynucleotides and antibodies are useful in  
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,  
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in  
CC treating or preventing diseases such as inflammation, autoimmune  
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome  
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,  
CC

CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy  
CC and epilepsy. Accordingly, these molecules have many activities including  
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,  
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,  
CC antiasthmatic, nephrotropic, antiarthritic, virucide, antiparasitic,  
CC neuroprotective, nootropic, antibacterial, hepatotropic,  
CC relaxant and anticonvulsant. In addition, they are useful in screening  
CC assays to identify small molecules that modulate or inhibit, for example,  
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
CC used as in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. This polypeptide is a human NOVX protein of the  
XX invention.

SQ Sequence 315 AA;

Query Match 70.0%; Score 35; DB 5; Length 315;  
Best Local Similarity 77.8%; Pred. No. 4.9e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
||| |||  
Db 157 FLWFLPIIV 165

RESULT 33

ABR01643

ID ABR01643 standard; protein; 315 AA.

XX ABR01643;

XX 17-APR-2003 (first entry)

XX Human G protein coupled receptor SEQ ID 146.

XX Human; anorectic; antiasthmatic; antidiabetic; hypotensive; receptor;  
KW antiparkinsonian; nootropic; neuroprotective; tranquiliser;  
KW antirheumatic; antiinflammatory; osteopathic; cardiant; neuroleptic;  
KW antiarthritic; gene therapy; olfactory G protein-coupled receptor; GPCR;  
KW infection; obesity; diabetes; hypertension; malnutrition;  
KW Parkinson's disease; Alzheimer's disease; Korsakoff's psychosis; anxiety;  
KW rheumatoid arthritis; chronic obstructive pulmonary disease;  
KW osteoporosis; asthma; myocardial infarction; schizophrenia;  
KW osteoarthritis.

XX Homo sapiens.

XX WO2003000735-A2.

XX 03-JAN-2003.

XX 24-JUN-2002; 2002WO-IB002481.

XX 26-JUN-2001; 2001US-0301095P.

PR 06-NOV-2001; 2001US-0332758P.

XX (DECO-) DECODE GENETICS EHF.

XX Martinez RAM, Sigurdsson GT;

XX WPI; 2003-175284/17.

DR N-PSDB; ABZ77944.

XX New olfactory G protein-coupled receptor gene nucleic acid and  
PT polypeptide, useful for diagnosing or treating a disease or condition  
PT associated with GPCR, e.g. obesity, diabetes, hypertension, malnutrition  
PT or Alzheimer's disease.

XX Claim 9; Page 90; 383pp; English.

XX The present invention relates to novel human olfactory G protein-coupled  
CC receptors (GPCR) and their coding sequences (ABZ77872-ABZ77986 and  
CC ABR01571-ABR01685). The GPCRs and coding sequences are useful for  
CC diagnosing or treating a disease or condition associated with GPCR, e.g.

CC infections, obesity, diabetes, hypertension, malnutrition, Parkinson's  
 CC disease, Alzheimer's disease, Korsakoff's psychosis, anxiety, rheumatoid  
 CC arthritis, chronic obstructive pulmonary disease, osteoporosis, asthma,  
 CC myocardial infarction, schizophrenia, or osteoarthritis  
 XX  
 SQ Sequence 315 AA;

Query Match 70.0%; Score 35; DB 6; Length 315;  
 Best Local Similarity 77.8%; Pred. No. 4.9e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLWPEIDIV 9  
 |||||  
 Db 154 FLWFLPIV 162

## RESULT 34

ADN42310  
 ID ADN42310 standard; protein; 315 AA.

XX AC ADN42310;

XX DT 17-JUN-2004 (first entry)

XX DE Human novel protein NOV 51.

XX KW Human; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis.

XX OS Homo sapiens.

XX FN US2004033493-A1.

XX PD 19-FEB-2004.

XX PF 31-JAN-2002; 2002US-00072012.

XX PR 31-JAN-2001; 2001US-0265395P.

XX PR 31-JAN-2001; 2001US-0265412P.

XX PR 31-JAN-2001; 2001US-0265514P.

XX PR 02-FEB-2001; 2001US-0265517P.

XX PR 02-FEB-2001; 2001US-0266406P.

XX PR 05-FEB-2001; 2001US-0266767P.

XX PR 07-FEB-2001; 2001US-0266975P.

XX PR 07-FEB-2001; 2001US-0267057P.

XX PR 08-FEB-2001; 2001US-0267459P.

XX PR 09-FEB-2001; 2001US-0267823P.

XX PR 15-FEB-2001; 2001US-0268974P.

XX PR 26-FEB-2001; 2001US-0271664P.

XX PR 27-FEB-2001; 2001US-0271839P.

XX PR 02-MAR-2001; 2001US-0271855P.

XX PR 02-MAR-2001; 2001US-0272788P.

XX PR 02-MAR-2001; 2001US-0273046P.

XX PR 14-MAR-2001; 2001US-0275925P.

XX PR 14-MAR-2001; 2001US-0275947P.

XX PR 14-MAR-2001; 2001US-0275950P.

XX PR 14-MAR-2001; 2001US-0275989P.

XX PR 15-MAR-2001; 2001US-0276448P.

XX PR 16-MAR-2001; 2001US-0276450P.

PR 30-MAY-2001; 2001US-0294473P.  
 PR 08-JUN-2001; 2001US-0296964P.  
 PR 18-JUN-2001; 2001US-0298959P.  
 PR 19-JUN-2001; 2001US-0299324P.  
 PR 13-AUG-2001; 2001US-0312020P.  
 PR 16-AUG-2001; 2001US-0312889P.  
 PR 16-AUG-2001; 2001US-0312908P.  
 PR 21-AUG-2001; 2001US-0313930P.  
 PR 28-AUG-2001; 2001US-0315470P.  
 PR 31-AUG-2001; 2001US-0316447P.  
 PR 07-SEP-2001; 2001US-0318115P.  
 PR 07-SEP-2001; 2001US-0318118P.  
 PR 12-SEP-2001; 2001US-0318740P.  
 PR 19-SEP-2001; 2001US-0323379P.  
 PR 18-OCT-2001; 2001US-0330245P.  
 PR 18-OCT-2001; 2001US-0330308P.  
 PR 14-NOV-2001; 2001US-0332701P.

XX (TCHE/) TCHERNEV V T.

PA (SPYT/) SPYTEK K A.

PA (ZERH/) ZERHUSEN B D.

PA (PATT/) PATTURAJAN M.

PA (SHIM/) SHIMKETS R A.

PA (LILL/) LI L.

PA (GANG/) GANGOLLI E A.

PA (PADI/) PADIGARU M.

PA (ANDE/) ANDERSON D W.

PA (RAST/) RASTELLI L.

PA (MILL/) MILLER C E.

PA (GERL/) GERLACH V.

PA (TAUP/) TAUPIER R J.

PA (GUSE/) GUSEV V Y.

PA (COLM/) COLMAN S D.

PA (WOLE/) WOLENC A R.

PA (PENA/) PENNA C E A.

PA (FURT/) FURTAK K.

PA (GROS/) GROSSE W M.

PA (ALSO/) ALSOBROOK J P.

PA (LEPL/) LEPLEY D M.

PA (RIEG/) RIEGER D K.

PA (BURG/) BURGESS C B.

XX

PI Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;

PI Li L, Gangolli EA, Padigar M, Anderson DW, Rastelli L, Miller CE;

PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;

PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;

XX WPI; 2004-180039/17.

DR N-PSDB; ADN42309.

XX

PT Isolated NOVX polypeptides and polynucleotides, useful for preventing

PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and

PT atherosclerosis.

XX Claim 1; SEQ ID NO 192; 1309pp; English.

XX

CC The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,

CC including splice variants) and the nucleic acids (NA) that encode them.

CC Also included are the mature NOVX proteins (and their encoding

CC polynucleotides), a vector comprising NOVX NA, a cell comprising the

CC vector, an antibody that binds immunospecifically to NOVX, determining

CC the presence or amount of NOVX in a sample, determining the presence or

CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,

CC modulating the activity of NOVX, treating or preventing a NOVX-associated

CC disorder, determining the presence of or predisposition to a disease

CC associated with altered levels of NOVX and treating a pathological state

CC in a mammal comprising administering a polypeptide which is at least 95%

CC identical to NOVX (or fragment). NOVX and NA may be used in the

CC prevention, treatment and diagnosis of diseases associated with

CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,

CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and

CC antagonists may also be used to down regulate expression and activity of

CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for

CC detecting the presence of NOVX in samples (e.g. by enzyme linked  
 CC immunosorbant assay (ELISA). The agents and methods may be used in this  
 CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy  
 CC and/or atherosclerosis. The present sequence represents a NOVX protein.  
 XX  
 SQ Sequence 315 AA;

Query Match 70.0%; Score 35; DB 8; Length 315;  
 Best Local Similarity 77.8%; Pred. No. 4.9e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 |||||  
 DB 157 FLWFLIPV 165

RESULT 35

ID ABP95915 standard; protein; 326 AA.

XX AC ABP95915;  
 XX

DT 06-MAR-2003 (first entry)

DE Human GPCR polypeptide SEQ ID NO 640.

XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;  
 KW drug development; gustatory; taste; fragrance; receptor.  
 XX

OS Homo sapiens.

PN WO200216548-A2.

PD 28-FEB-2002.

XX 30-JUL-2001; 2001WO-IB001446.

XX 04-AUG-2000; 2000JP-00237818.

PR 13-FEB-2001; 2001JP-00034434.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Haga T, Takeda S, Mitaku S;

XX WPI; 2002-304118/34.

DR N-PSDB; AB243189.

XX Database global search for G protein-coupled receptors, proteins and  
 PT encoded genes for studying in vivo signal transduction mechanism and  
 PT identifying targets for drug development.

XX Claim 10; SEQ ID NO 640; 97pp + Sequence Listing; Japanese.

XX The invention relates to a method for screening G protein-coupled  
 CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-  
 CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane  
 CC domains with 250-1000 amino acid residues to give a gene homologous with  
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for  
 CC studying in vivo signal transduction mechanism and identifying targets  
 CC for drug development e.g. based on olfactory and gustatory receptors in  
 CC form of agonists and antagonists by screening intrinsic and extrinsic  
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance  
 CC improvers. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 XX

SQ Sequence 326 AA;

Query Match 70.0%; Score 35; DB 5; Length 326;  
 Best Local Similarity 77.8%; Pred. No. 5.1e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9

DB 168 FLWFLIPV 176  
 |||||  
 |||||

RESULT 36

AAU95516

ID AAU95516 standard; protein; 326 AA.

XX AC AAU95516;

DT 02-JUL-2002 (first entry)

XX Human olfactory and pheromone G protein-coupled receptor #3.

XX Human; olfactory and pheromone G protein coupled; receptor; GPCR;  
 KW tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;  
 KW anorectic; taste; fragrance; food additive; cosmetic; cell migration;  
 KW sterility; psychotic disorder; neurological disorder; anxiety;  
 KW schizophrenia; manic depression; depression; axonal growth;  
 KW menstrual cycle; appetite sexual motivation; sexual attraction;  
 KW aggression.

XX Homo sapiens.

PN WO200224726-A2.

XX 28-MAR-2002.

XX 21-SEP-2001; 2001WO-BE000162.

XX 22-SEP-2000; 2000EP-00870211.

XX (CHEM-) CHEMCOM SA.

XX Veithen A;

XX WPI; 2002-330013/36.

DR N-PSDB; ABK68403.

XX Novel pheromone G-protein coupled receptor and receptor-derived agonists,  
 PT antagonists or inhibitors useful in food or cosmetic products or in the  
 PT treatment or prevention of neurological disorders such as anxiety and  
 PT schizophrenia.

XX Disclosure; Page 23-25; 833pp; English.

XX The invention relates to olfactory and Pheromone G-protein coupled  
 CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active  
 CC portion and its encoding polynucleotide. Also included are an agonist,  
 CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector  
 CC comprising the polynucleotide, a cell transformed by the vector, a non-  
 CC human mammal comprising a partial or total deletion of the polynucleotide  
 CC encoding the receptor and screening (detection and possibly, recovering)  
 CC of compounds which are known or not known to be agonist, antagonists or  
 CC inhibitors of natural compounds to the GPCR. The receptor-derived  
 CC agonists, antagonists, inhibitors or compounds are used as an  
 CC improvement, elimination or substitution of an existing taste and/or a  
 CC fragrance of (or in) the food and/or cosmetic products. They can also be  
 CC used in the preparation of medicament in the treatment and/or prevention  
 CC of a mammalian disorder, such as cell migration, sterility, psychotic and  
 CC neurological disorders, including anxiety, schizophrenia, manic  
 CC depression, depression, for promoting axonal growth, nerve cell  
 CC connection and nerve regeneration for modulating male and female  
 CC endocrine functions, hormone production and the menstrual cycle, for the  
 CC prevention or the treatment by stimulation of several mammalian  
 CC behaviours, such as stimulation or suppression of appetite, sexual  
 CC motivation, sexual attraction, aggression and for promoting or  
 CC suppressing chemical communication between organisms. The present  
 CC sequence is a human olfactory and pheromone GPCR protein sequence

XX Sequence 326 AA;

SQ Query Match 70.0%; Score 35; DB 5; Length 326;



```

Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
Db 168 FLWFLIPV 176

RESULT 37
ADC85959
ID ADC85959 standard; protein; 326 AA.
XX
AC ADC85959;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR protein SEQ ID NO:412.
XX
KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
WPI; 2003-315783/31.
DR N-PSDB; ADC85958.
XX
PT New polynucleotide, useful for preparing a composition for treating a
patient in need of increased or suppressed activity or expression of the
guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 2; SEQ ID NO 412; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
SQ Sequence 326 AA;

Query Match 70.0%; Score 35; DB 7; Length 326;
Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
Db 168 FLWFLIPV 176

RESULT 39
ADG83292
ID ADG83292 standard; protein; 326 AA.
XX
AC ADG83292;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human Olfactory and pheromone GPCR #3.
XX
KW Olfactory; pheromone; GPCR; G protein-coupled receptor; receptor; human;
flavour; detergent; soap; shampoo; fragrance; appetite control;
KW odour trap; receptor-mediated disorder; cell migration; cell death;
cell growth; psychotic disorder; neurological disorder; anxiety;
schizophrenia; maniac depression; depression; mound modification.
XX
OS Homo sapiens.
XX
PN US2003221205-A1.
XX
PD 27-NOV-2003.
XX
PF 13-MAR-2003; 2003US-00387629.
XX
PR 21-SEP-2001; 2001WO-BE000162.
XX

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PA (VEIT/) VEITHEN A.  
XX Veithen A;  
FI WPI; 2004-010900/01.  
XX New isolated pheromone G-protein coupled receptor, or its active portion,  
PT useful for treating disorders affecting cell migration, death and growth,  
PT or psychotic and neurological disorders.  
XX  
PS Disclosure; SEQ ID NO 6; 7pp; English.  
XX  
XX The invention relates to an isolated olfactory and pheromone G protein-  
CC coupled receptor (GPCR), or its active portion. Also included are an  
CC isolated polynucleotide encoding the GPCR, a vector comprising the  
CC polynucleotide, a cell comprising the vector, a non-human mammal  
CC comprising a deletion of the polynucleotide, a transgenic non-human  
CC mammal that overexpresses the polynucleotide, screening for compounds  
CC that bind to the receptor polypeptide molecules, identifying a compound  
CC as a ligand, agonist or antagonist of GPCR and a pharmaceutical  
CC composition comprising the receptor, vector or cell, and a carrier. The  
CC protein, polynucleotide, vector, cell and composition are useful for  
CC preventing or treating receptor-mediated disorders, e.g. disorders  
CC affecting cell migration, cell death, cell growth, or psychotic and  
CC neurological disorders, including anxiety, schizophrenia, maniac  
CC depression, depression or mood modification. They may also be useful in  
CC developing detergents, soaps, shampoo, fragrances, in appetite control  
CC and as an odour trap. The present sequence is an olfactory and pheromone  
CC G protein-coupled receptor. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030221205.  
XX  
SQ Sequence 326 AA;

Query Match 70.0%; Score 35; DB 8; Length 326;  
Best Local Similarity 77.8%; Pred. No. 5.1e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
Db 168 FLWFLPIV 176

RESULT 40  
ADM42835  
ID ADM42835 standard; protein; 379 AA.

AC ADM42835;

XX 03-JUN-2004 (first entry)

DE Rat odourant receptor MOR106-2 SeqID 79.

XX rat; odourant receptor; chemical sensor system; taste; smell;  
KW artificial sensory organ; olfactory stimulation; food industry;  
KW hygiene inspection; environmental examination; disease diagnosis;  
KW carvone.

XX Rattus norvegicus.

XX WO2003100057-A1.

PD 04-DEC-2003.

XX 28-MAY-2003; 2003WO-JP006719.

XX 28-MAY-2002; 2003JP-00154239.

PR 13-JUN-2002; 2002JP-00172412.

PR 14-JAN-2003; 2003JP-00005175.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PI Sato T, Hirono J, Hamana H, Miyake M, Yoshikawa T, Miyake J;  
XX WPI; 2004-023356/02.  
DR N-PSDB; ADM42834.  
XX  
PT Chemical sensor systems based on chemical receptors introduced into cells  
PT for immobilization onto support to form chip as component of sensor,  
PT useful in detecting stimuli e.g. taste and smell applicable in food  
PT industry.

XX PS Disclosure; SEQ ID NO 79; 521pp; Japanese.

XX This invention relates to a novel chemical sensor system method.  
CC Specifically, it refers to an isolated nucleic acid molecule that encodes  
CC a receptor protein, which binds to chemicals that can stimulate the sense  
CC of taste or smell for example. The present invention describes the  
CC manufacture of a chip that acts as a support to immobilise transfected  
CC cells expressing the receptor gene, such that this chip can be employed  
CC as a component of the chemical sensor model. Furthermore, this chip is  
CC useable as an artificial sensory organ where the chemical receptor  
CC contains an olfactory receptor the sensor can react to olfactory  
CC stimulation. Accordingly, these sensors are useful in the food industry  
CC for analysing freshness of meat, fruit and vegetables, hygiene  
CC inspection, environmental examination and disease diagnosis. Furthermore,  
CC such systems are automatable for high throughput applications under  
CC various conditions, even for differentiating optical isomers of R(-)-  
CC carvone from S(+)-carvone easily. This polypeptide sequence is a rat  
CC odourant receptor protein of the invention.

XX Sequence 379 AA;

Query Match 70.0%; Score 35; DB 8; Length 379;  
Best Local Similarity 55.6%; Pred. No. 6e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
Db 154 FLWFPVPII 162

RESULT 41  
ADL04719  
ID ADL04719 standard; protein; 543 AA.

AC ADL04719;

XX 06-MAY-2004 (first entry)

DE M. catarrhalis protein #485.

XX Moraxella catarrhalis; infection.

XX Moraxella catarrhalis.

XX US6673910-B1.

PD 06-JAN-2004.

PF 04-APR-2000; 2000US-00540236.

PR 08-APR-1999; 99US-0128416P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL;

DR WPI; 2004-178127/17.

XX N-PSDB; ADL02799.

PT New nucleic acid encoding a Moraxella catarrhalis polypeptide, useful for  
PT preparing a composition for diagnosing, preventing or treating infection  
PT caused by Moraxella catarrhalis.

XX



CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.

XX  
 SQ Sequence 720 AA;  
 Query Match 70.0%; Score 35; DB 8; Length 720;  
 Best Local Similarity 57.1%; Pred. NO. 1.2e+03;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
 Db 528 YWFEVD 534

RESULT 44  
 AAB25508  
 ID AAB25508 standard; protein; 816 AA.  
 XX  
 AC AAB25508;  
 XX  
 DT 27-NOV-2000 (first entry)  
 XX  
 DE Eucalyptus grandis cell signalling involved protein SEQ ID NO:827.  
 XX  
 KW Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;  
 KW plant cell signalling; modulation; transgenic plant; pathogen; growth;  
 KW environmental change; development; cell proliferation; differentiation;  
 KW elongation; survival; disease resistance; nutrient metabolism.  
 XX  
 OS Eucalyptus grandis.  
 XX  
 PN WO200042171-A1.  
 XX  
 PD 20-JUL-2000.  
 XX  
 PF 11-JAN-2000; 2000WO-US000724.  
 XX  
 PR 12-JAN-1999; 99US-00228986.  
 BR 01-NOV-1999; 99US-0162866P.  
 XX  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA  
 XX Strabala TJ, Nieuwenhuizen NJ;  
 PI  
 XX WPI; 2000-476052/41.  
 DR  
 XX Isolated polynucleotide encoding a polypeptide involved in cell signaling  
 PT used for generating transgenic plants with modified responses to external  
 PT signals.  
 XX  
 PS Claim 3; Page 394-395; 527pp; English.  
 XX  
 CC AAA9263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide  
 CC and protein sequences isolated from eucalyptus (Eucalyptus grandis) or  
 CC pine (Pinus radiata also known as Monterey pine). The protein sequences  
 CC are involved in cell signalling. The polynucleotide and protein sequences  
 CC can be used to modify the response of plant cells to external signals  
 CC e.g. environmental changes or pathogens during the growth and development  
 CC of a plant. They can be used to modify cell proliferation,  
 CC differentiation, elongation and survival, resistance to disease and  
 CC nutrient metabolism. Examples of modifications which can be produced are  
 CC altered fruit ripening and senescence of leaves and flowers e.g. to delay  
 CC senescence and prolong the life of cut flowers or enhance senescence of  
 CC reproductive organs to engineer sterile plants. Other modifications can  
 CC be used to delay senescence in selected cell types or organs providing  
 CC fruit and vegetables which have a longer shelf life between harvest and  
 CC consumption, or to decrease branching frequency in forest tree species  
 CC giving long stretches of valuable knot-free clear wood which can be used  
 CC in solid timber furniture and veneers

XX  
 SQ Sequence 816 AA;  
 Query Match 70.0%; Score 35; DB 3; Length 816;  
 Best Local Similarity 83.3%; Pred. NO. 1.4e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEID 7  
 Db 250 LWFEVD 255

RESULT 45  
 ADA33169  
 ID ADA33169 standard; protein; 951 AA.  
 XX  
 AC ADA33169;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Acinetobacter baumannii protein #330.  
 XX  
 KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;  
 KW plant biocontrol agent.  
 XX  
 OS Acinetobacter baumannii.  
 XX  
 PN US6562958-B1.  
 XX  
 PD 13-MAY-2003.  
 XX  
 PF 04-JUN-1999; 99US-00328352.  
 XX  
 PR 09-JUN-1998; 98US-0088701P.  
 XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 PI Breton G, Bush D;  
 XX  
 DR WPI; 2003-576092/54.  
 DR N-PSDB; ADA29043.  
 XX  
 XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents  
 PT for diagnosing a bacterial disease, as components of antibacterial  
 PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for  
 PT plants.  
 XX  
 PS Example; SEQ ID NO 4456; 328pp; English.  
 XX  
 CC The invention relates to isolated Acinetobacter baumannii nucleic acids.  
 CC The A. baumannii nucleic acids and polypeptides are useful as reagents  
 CC for diagnosing a bacterial disease, as components of antibacterial  
 CC vaccines, as targets for antibacterial drugs, to detect the presence of  
 CC A. baumannii and other Acinetobacter species in a sample, in screening  
 CC compounds for the ability to interfere with the A. baumannii life cycle  
 CC or to inhibit A. baumannii infection, and as biocontrol agents for  
 CC plants. The present sequence represents the amino acid sequence of an A.  
 CC baumannii protein.  
 XX  
 SQ Sequence 951 AA;  
 Query Match 70.0%; Score 35; DB 6; Length 951;  
 Best Local Similarity 50.0%; Pred. NO. 1.6e+03;  
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9  
 Db 801 VMFKYDVV 808

RESULT 46  
 AAM88375  
 ID AAM88375 standard; protein; 37 AA.

XX AC AM88375;  
XX DT 07-NOV-2001 (first entry)  
XX DE Human immune/haematopoietic antigen SEQ ID NO:15968.  
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis.  
XX OS Homo sapiens.  
XX PN WO200157182-A2.  
XX PD 09-AUG-2001.  
XX PF 17-JAN-2001; 2001WO-US001354.  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 14-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 03-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239335P.  
PR 13-OCT-2000; 2000US-0239337P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 01-DEC-2000; 2000US-0250300P.  
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PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.

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PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX N-PSDB; AAK61156.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Claim 11; SEQ ID NO 15968; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 37 AA;
XX
Query Match 68.0%; Score 34; DB 4; Length 37;
Best Local Similarity 33.3%; Pred. No. 75;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLWFEIDIV 9
Db |||:::
17 FLWWQLEVI 25
RESULT 47
AAM89032
ID AAM89032 standard; protein; 73 AA.
AC AAM89032;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen SEQ ID NO:16625.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis.
XX Homo sapiens.
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX
XX 04-FEB-2000; 2000US-0180628P.
PR
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
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PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214866P.
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PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229144P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0234548P.
PR 27-SEP-2000; 2000US-0235634P.
PR 27-SEP-2000; 2000US-0235636P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
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PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
```



transcription, translation, protein transport, adaptation to atypical conditions, sensitivity to medicines and/or analogues, functions related to transposons, biosynthesis of cofactors, prosthetic groups and transporters, cell membrane proteins and cellular machinery. (I) are useful for the detection and/or amplification of nucleic acids. CC Pharmaceutical composition comprising (I) or (II) are useful for treatment of a bacterial S. agalactiae infection. Note: WO200292818A2 is CC equivalent for the present basic patent FR2824074A1. WO200292818A2 CC contains 6617 sequence whereas the present patent only contains 2344 CC sequences.

XX Sequence 81 AA;

Query Match 68.0%; Score 34; DB 8; Length 81;  
Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
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Db 64 WYEIDLI 70

RESULT 49

ADV79936

ID ADV79936 standard; protein; 81 AA.

XX ADV79936;

XX 24-FEB-2005 (first entry)

XX Streptococcus agalactiae protein, SEQ ID 1077.

XX Antibacterial; vaccine; bacterial infection.

XX Streptococcus agalactiae.

XX WO200292818-A2.

XX 21-NOV-2002.

XX 26-APR-2002; 2002WO-IB003059.

XX 26-APR-2001; 2001FR-00005642.

XX (INSP ) INST PASTEUR.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Glaeser P, Ruaniok C, Chevalier F, Frangeul L, Lalioui L;

PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu-Cuot P, Kunst F;

XX WPI; 2004-101891/11.

XX Genomic nucleotide sequences encoding polypeptides of Streptococcus  
PT agalactiae for the development of vaccines, diagnostic tools, DNA chips  
PT and identification of therapeutic targets.

PS Claim 6; SEQ ID NO 1077; 439pp; French.

XX The present invention relates to novel Streptococcus agalactiae  
CC nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and  
CC novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The  
CC nucleotide sequences encode polypeptides of S. agalactiae involved in the  
CC synthesis of amino acids, cell membranes, intermediate (central)  
CC metabolism, energetic metabolism, fatty acid and phospholipid metabolism,  
CC nucleotide metabolism including purines, pyrimidines and/or nucleosides,  
CC regulatory functions, replication, transcription, translation, protein  
CC transport, adaptation to atypical conditions, sensitivity to medicines  
CC and/or analogues, functions related to transposons, biosynthesis of  
CC cofactors, prosthetic groups and transporters, cell membrane proteins and  
CC cellular machinery. (I) are useful for the detection and/or amplification  
CC of nucleic acids. Pharmaceutical composition comprising (I) or (II) are  
CC useful for treatment of a bacterial S. agalactiae infection. The complete  
CC genome of Streptococcus agalactiae is given in ADV81204. Note: The

CC present patent is an equivalent for the basic patent FR2824074A1, which  
CC contains only 2344 sequences.

XX Sequence 81 AA;

Query Match 68.0%; Score 34; DB 8; Length 81;  
Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
|:||||:|  
Db 64 WYEIDLI 70

RESULT 50

AAG21340

ID AAG21340 standard; protein; 195 AA.

XX AAG21340;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 23863.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

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XX 08-APR-1999; 99US-0128714P.

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XX 28-APR-1999; 99US-0130891P.

XX 30-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 04-MAY-1999; 99US-0132407P.

XX 05-MAY-1999; 99US-0132484P.

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XX 14-MAY-1999; 99US-0134256P.

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XX 14-MAY-1999; 99US-0134221P.

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XX 19-MAY-1999; 99US-0134941P.

XX 20-MAY-1999; 99US-0135124P.

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XX 24-MAY-1999; 99US-0135629P.

XX 25-MAY-1999; 99US-0136021P.

XX 27-MAY-1999; 99US-0136392P.

XX 28-MAY-1999; 99US-0136782P.

XX 01-JUN-1999; 99US-0137222P.

XX 03-JUN-1999; 99US-0137528P.



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PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 68.0%; Score 34; DB 3; Length 195;  
Best Local Similarity 62.5%; Pred. No. 4.4e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLWPEIDI 8  
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Db 113 FLWTELDL 120

Search completed: May 9, 2006, 02:17:01  
Job time : 128.4 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 02:17:29 ; Search time 16.4 Seconds  
(without alignments)  
52.802 Million cell updates/sec

Title: US-09-870-216C-7  
Perfect score: 50  
Sequence: 1 FLWFEIDIV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

PIR 90:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	78.0	474	T38905	probable valine-py
2	39	78.0	587	A10180	conserved hypotet
3	37	74.0	110	S40136	T-cell receptor V-
4	37	74.0	134	C29774	T-cell receptor al
5	37	74.0	150	AG1585	hypothetical prote
6	37	74.0	150	AH1231	hypothetical prote
7	37	74.0	529	B86815	hypothetical prote
8	36	72.0	269	A86641	hypothetical prote
9	36	72.0	413	E64815	ybH protein - Esc
10	36	72.0	413	D85587	probable synthetas
11	36	72.0	413	C90737	cardiolipin synthe
12	35	70.0	250	D69457	hypothetical prote
13	35	70.0	280	B82372	SpoOM-related prot
14	35	70.0	648	T08856	hypothetical prote
15	35	70.0	848	T25325	hypothetical prote
16	35	70.0	1190	T00842	probable histidine
17	35	70.0	1207	T52459	sensory transducti
18	34	68.0	121	A12244	dihydroneopterin a
19	34	68.0	175	AB0185	probable membrane
20	34	68.0	209	F71612	glycosyl transfera
21	34	68.0	229	AB1468	ribosomal protein
22	34	68.0	254	C90024	hypothetical prote
23	34	68.0	422	T05592	tyrosine transamin
24	34	68.0	469	S44620	C50C3.1 protein -
25	34	68.0	643	S55593	membrane protein S
26	34	68.0	912	T43399	hypothetical prote
27	34	68.0	2363	T38841	probable pre-mRNA
28	33	66.0	55	C82565	hypothetical prote
29	33	66.0	126	A82519	hypothetical prote

30	33	66.0	143	2	A11511	hypothetical prote
31	33	66.0	150	1	S76177	dihydroneopterin a
32	33	66.0	190	2	A82343	conserved hypotet
33	33	66.0	218	2	G86612	hypothetical prote
34	33	66.0	226	2	A86316	protein T10022.3 l
35	33	66.0	269	2	H82616	hypothetical prote
36	33	66.0	269	2	D95396	probable polyketid
37	33	66.0	283	2	B71876	probable prolipopr
38	33	66.0	284	1	C64639	prolipoprotein dia
39	33	66.0	285	2	AG2429	delta-9 desaturase
40	33	66.0	343	2	F72011	hypothetical prote
41	33	66.0	461	2	G64206	hexosephosphate tr
42	33	66.0	470	2	T41409	probable valine-py
43	33	66.0	507	2	S75961	NADH2 dehydrogenas
44	33	66.0	516	2	S42093	cellulose 1,4-beta
45	33	66.0	546	2	A69484	hypothetical prote
46	33	66.0	562	2	A85042	hypothetical prote
47	33	66.0	601	2	T48539	probable potassium
48	33	66.0	602	2	AG0155	probable substrate
49	33	66.0	611	2	F82442	probable peptide A
50	33	66.0	784	2	T13579	hypothetical prote
51	33	66.0	821	2	T16412	hypothetical prote
52	33	66.0	875	2	T45813	hypothetical prote
53	33	66.0	1374	2	S62524	probable RNA helic
54	32.5	65.0	335	2	A13111	hypothetical prote
55	32.5	65.0	335	2	D98175	hypothetical prote
56	32	64.0	79	2	D75327	hypothetical prote
57	32	64.0	101	2	S43389	ribosomal protein
58	32	64.0	143	2	H83935	hypothetical prote
59	32	64.0	144	2	S21349	hypothetical 16.3K
60	32	64.0	153	2	G70077	hypothetical prote
61	32	64.0	194	2	C82811	hypothetical prote
62	32	64.0	226	2	H71349	probable ribosomal
63	32	64.0	229	2	A97287	ribosomal protein
64	32	64.0	230	2	D89821	50S ribosomal prot
65	32	64.0	232	1	RS881	ribosomal protein
66	32	64.0	252	2	D95853	conserved hypotet
67	32	64.0	258	2	E75140	hypothetical prote
68	32	64.0	271	2	A81384	prolipoprotein dia
69	32	64.0	272	2	I64245	hypothetical prote
70	32	64.0	285	1	I38548	alcohol sulfofrans
71	32	64.0	287	1	I47697	probable methyltra
72	32	64.0	287	1	I39885	rRNA methylase erm
73	32	64.0	290	2	JS0202	esterase - Acineto
74	32	64.0	328	2	A95011	conserved hypotet
75	32	64.0	328	2	D97882	conserved hypotet
76	32	64.0	344	1	B65024	probable membrane-
77	32	64.0	357	2	A99272	inorganic phosphat
78	32	64.0	377	2	B89102	protein F25B5.3 [i
79	32	64.0	400	2	G83790	aminotransferase B
80	32	64.0	418	2	E96765	hypothetical prote
81	32	64.0	448	2	T05591	tyrosine transamin
82	32	64.0	464	2	AD0768	probable extracell
83	32	64.0	465	2	D82262	probable capsular
84	32	64.0	467	2	AG1203	hypothetical prote
85	32	64.0	493	2	T48934	acyl CoA reductase
86	32	64.0	511	1	VGBEF4	glycoprotein C - h
87	32	64.0	574	2	G84578	probable potassium
88	32	64.0	628	2	AG3357	peptidylprolyl iso
89	32	64.0	637	2	A72532	probable DNA-direc
90	32	64.0	639	2	T50793	hypothetical prote
91	32	64.0	732	2	T00130	trehalose synthase
92	32	64.0	747	2	B83029	conserved hypotet
93	32	64.0	782	2	T35696	methionyl tRNA syn
94	32	64.0	825	2	T00818	hypothetical prote
95	32	64.0	878	2	F64425	valine-tRNA ligase
96	32	64.0	912	2	H85470	hypothetical prote
97	32	64.0	915	2	A49874	metabotropic gluta
98	32	64.0	925	2	T05012	hypothetical prote
99	32	64.0	926	2	T24923	hypothetical prote
100	32	64.0	950	2	S64405	MiCl protein - yea
101	32	64.0	1342	1	S32680	DNA-directed RNA p
102	32	64.0	1370	2	G84384	DNA polymerase typ

103	32	64.0	3498	2	T22330	hypothetical prote	176	31	62.0	569	2	A43317	germ cell-less pro
104	31.5	63.0	259	2	D72425	conserved hypothet	177	31	62.0	610	2	F95898	probable nodulatio
105	31	62.0	64	2	E37815	hypothetical prote	178	31	62.0	624	2	C83389	hypothetical prote
106	31	62.0	69	2	D95850	hypothetical prote	179	31	62.0	627	2	D90452	hypothetical prote
107	31	62.0	83	2	S74468	hemagglutinin prec	180	31	62.0	638	2	B34285	NADH2 dehydrogenas
108	31	62.0	108	2	A04069	hypothetical prote	181	31	62.0	663	2	T49685	RNA polymerase II
109	31	62.0	111	2	A12312	hypothetical prote	182	31	62.0	693	2	A10996	4-alpha-glucanotra
110	31	62.0	122	2	T48951	hypothetical prote	183	31	62.0	719	2	B95325	conserved hypothet
111	31	62.0	133	2	B82586	hypothetical prote	184	31	62.0	728	2	T05151	hypothetical prote
112	31	62.0	140	2	C49829	T-cell receptor va	185	31	62.0	731	2	SL6595	gene CARSR12 prote
113	31	62.0	147	2	AH1152	hypothetical prote	186	31	62.0	811	2	AB1980	two-component hybr
114	31	62.0	158	2	AH1902	hypothetical prote	187	31	62.0	821	2	C64461	hypothetical prote
115	31	62.0	166	2	AF3051	cytochrome c2 Act4	188	31	62.0	904	1	RGBYP1	regulatory protein
116	31	62.0	166	2	F98234	cytochrome c2 limp	189	31	62.0	908	2	T49142	metabotropic gluta
117	31	62.0	173	2	T40346	hypothetical prote	190	31	62.0	924	1	JC1269	DNA-directed DNA p
118	31	62.0	191	2	GB7118	probable secreted	191	31	62.0	1131	2	T19442	hypothetical prote
119	31	62.0	197	2	AB2162	hypothetical prote	192	31	62.0	2329	2	S44625	C50C3.6 protein -
120	31	62.0	229	2	AB1106	ribosomal protein	193	31	62.0	2413	2	S34670	splicing factor PR
121	31	62.0	231	2	H83664	ribosomal protein	194	31	62.0	2767	1	UIHU	thyroglobulin prec
122	31	62.0	232	2	E69694	ribosomal protein	195	30	60.0	81	2	AD2104	hypothetical prote
123	31	62.0	236	2	B70488	cytochrome-c oxida	196	30	60.0	105	2	B30010	hypothetical ORF-5
124	31	62.0	237	2	T24759	hypothetical prote	197	30	60.0	140	2	AF2030	hypothetical prote
125	31	62.0	251	2	T08315	hypothetical prote	198	30	60.0	165	2	F97077	hypothetical prote
126	31	62.0	258	2	B45710	BRRF1 gene homolog	199	30	60.0	192	2	G95072	conserved hypothet
127	31	62.0	261	1	I40437	stage III sporulat	200	30	60.0	192	2	D97940	conserved hypothet
128	31	62.0	262	2	T47607	hypothetical prote	201	30	60.0	197	2	D75315	rrf2 protein - Dei
129	31	62.0	270	2	A24955	hypothetical prote	202	30	60.0	201	2	A70902	probable ribC prot
130	31	62.0	273	2	A11593	hypothetical prote	203	30	60.0	240	2	S61110	hypothetical prote
131	31	62.0	280	2	A83796	stage III sporulat	204	30	60.0	242	2	AC1646	hypothetical prote
132	31	62.0	287	2	T28367	hypothetical prote	205	30	60.0	244	2	C82063	probable thiamin A
133	31	62.0	288	2	S36953	cytochrome-c oxida	206	30	60.0	248	1	A46542	granulin - Trichop
134	31	62.0	289	2	G84026	proteinase (proces	207	30	60.0	259	2	S73911	protein phosphatase
135	31	62.0	290	2	H90001	lipoprotein precus	208	30	60.0	261	2	G90198	hypothetical prote
136	31	62.0	291	2	AC1029	hypothetical prote	209	30	60.0	266	2	E82713	hypothetical prote
137	31	62.0	300	1	S41759	ribosomal protein	210	30	60.0	276	2	D41044	octopine-binding p
138	31	62.0	300	2	T71616	RNA-binding protei	211	30	60.0	278	2	S48776	hypothetical prote
139	31	62.0	300	2	T47557	hypothetical prote	212	30	60.0	278	2	E83453	hypothetical prote
140	31	62.0	302	2	S75481	polysialic acid tr	213	30	60.0	280	2	B90536	lipoprotein (impor
141	31	62.0	311	2	D97058	SAW-dependent meth	214	30	60.0	284	2	G22848	cytochrome-c oxida
142	31	62.0	332	2	T21279	hypothetical prote	215	30	60.0	288	2	S36956	cytochrome-c oxida
143	31	62.0	344	2	S42648	photosystem II chl	216	30	60.0	297	1	OBPC2N	probable c-4 methy
144	31	62.0	344	2	A82306	photosystem II chl	217	30	60.0	300	2	T38986	MHC ChIA chain - c
145	31	62.0	347	2	AD3026	D-threo-aldose 1-d	218	30	60.0	308	2	I36956	hypothetical prote
146	31	62.0	357	2	E98258	probable oxidoredu	219	30	60.0	308	2	T20043	NADH dehydrogenase
147	31	62.0	363	2	B84832	hypothetical prote	220	30	60.0	314	2	H84221	hypothetical prote
148	31	62.0	366	2	A47385	serotonin receptor	221	30	60.0	317	2	D64233	hypothetical prote
149	31	62.0	367	2	F70036	capsular polysacch	222	30	60.0	318	2	T05569	phospholipase D (E
150	31	62.0	374	2	S66702	hypothetical prote	223	30	60.0	318	2	I39484	hypothetical prote
151	31	62.0	380	2	S66728	hypothetical prote	224	30	60.0	322	2	S76978	hypothetical prote
152	31	62.0	385	2	T32855	hypothetical prote	225	30	60.0	327	2	G88976	protein F54E2.6 li
153	31	62.0	406	2	A0240	imidazolonepropion	226	30	60.0	337	2	AT2360	hypothetical prote
154	31	62.0	406	2	T46988	hypothetical prote	227	30	60.0	339	2	AH0475	probable sugar tra
155	31	62.0	419	2	F97133	phage-related, hea	228	30	60.0	341	2	F95970	probable sugar upt
156	31	62.0	428	2	S66782	hypothetical prote	229	30	60.0	341	2	S56456	hypothetical 35.7K
157	31	62.0	447	2	A96639	protein tif9.18 li	230	30	60.0	341	2	G91279	probable transport
158	31	62.0	452	2	S58994	NADH2 dehydrogenas	231	30	60.0	341	2	G86120	probable transport
159	31	62.0	453	2	D86430	probable UDP-gulco	232	30	60.0	347	2	F22845	hypothetical prote
160	31	62.0	460	2	T27759	hypothetical prote	233	30	60.0	348	2	C98330	hypothetical prote
161	31	62.0	464	2	F64970	hypothetical prote	234	30	60.0	348	2	AB2953	hypothetical prote
162	31	62.0	464	2	D90985	hypothetical prote	235	30	60.0	349	2	D84347	hypothetical prote
163	31	62.0	464	2	G85830	hypothetical prote	236	30	60.0	354	2	T47965	hypothetical prote
164	31	62.0	478	2	T04519	hypothetical prote	237	30	60.0	358	2	S03538	class I histocompa
165	31	62.0	484	2	T6190	hypothetical prote	238	30	60.0	362	2	T36962	MHC class I protei
166	31	62.0	486	2	S64111	probable membrane	239	30	60.0	362	2	S77024	hypothetical prote
167	31	62.0	498	2	H82494	probable NADH dehy	240	30	60.0	363	2	JH0542	class I histocompa
168	31	62.0	512	2	G69670	glycine betaine tr	241	30	60.0	365	2	T00599	probable reverse t
169	31	62.0	525	2	A99557	hypothetical prote	242	30	60.0	366	2	D97002	sensory transducti
170	31	62.0	529	2	T22398	hypothetical prote	243	30	60.0	366	2	AB3184	oxidoreductase Atu
171	31	62.0	531	1	S54098	1-phosphatidylinos	244	30	60.0	368	2	AI1291	glycerol dehydroge
172	31	62.0	533	2	F82237	conserved hypothet	245	30	60.0	368	2	AG1663	glycerol dehydroge
173	31	62.0	561	2	B90414	hypothetical prote	246	30	60.0	390	2	S62553	conserved hypothet
174	31	62.0	562	2	T01855	probable chaperoni	247	30	60.0	392	2	F96707	hypothetical prote
175	31	62.0	566	2	F90406	succinate dehydrog	248	30	60.0	412	2	F86296	hypothetical prote

249	30	60.0	421	2	B84702	hypothetical prote	322	30	60.0	1051	2	A40021	integrin alpha-3 c
250	30	60.0	429	2	T22495	hypothetical prote	323	30	60.0	1053	2	I55534	VIA-3 alpha subuni
251	30	60.0	433	2	AG3391	adenylosuccinate l	324	30	60.0	1070	2	S19686	alpha-glucosidase
252	30	60.0	436	2	F87557	adenylosuccinate l	325	30	60.0	1117	2	A38227	RNA-eplicing regul
253	30	60.0	445	2	E97320	sugar, proton sympo	326	30	60.0	1154	2	S69206	regulator protein
254	30	60.0	447	2	S52437	CDP-diacylglycerol	327	30	60.0	1171	2	S57829	genome polyprotein
255	30	60.0	450	2	AG2802	adenylosuccinate l	328	30	60.0	1175	2	T34182	hypothetical prote
256	30	60.0	450	2	H97581	adenylosuccinate l	329	30	60.0	1196	2	H86849	hypothetical prote
257	30	60.0	454	1	T25203	probable membrane-	330	30	60.0	1230	2	T30517	complement C3-Q2 -
258	30	60.0	464	2	E90530	hypothetical prote	331	30	60.0	1253	2	P86436	hypothetical prote
259	30	60.0	472	2	S53866	cytosine methylase	332	30	60.0	1342	2	A84934	DNA-directed RNA p
260	30	60.0	473	1	A59200	acid phosphatase (	333	30	60.0	1330	2	S52239	brefeldin a resist
261	30	60.0	473	2	T46999	hypothetical prote	334	30	60.0	1530	2	T52010	hypothetical prote
262	30	60.0	473	2	AC0239	probable GntR-fam	335	30	60.0	1571	2	S50669	hypothetical prote
263	30	60.0	481	2	T39678	probable valine-py	336	30	60.0	1612	2	S51243	probable ATPase (E
264	30	60.0	491	2	AB1322	glucose-6-phosphat	337	30	60.0	2144	2	S71490	ash1 protein - fru
265	30	60.0	491	2	AC1693	hypothetical prote	338	30	60.0	3191	2	T22945	hypothetical prote
266	30	60.0	497	2	F90471	NADH2 dehydrogenas	339	30	60.0	3898	1	GNWVHB	genome polyprotein
267	30	60.0	498	2	T14236	hypothetical prote	340	30	60.0	3898	2	S57437	genome polyprotein
268	30	60.0	508	2	T26636	hypothetical prote	341	29.5	59.0	269	1	OTNC3	cytochrome-c oxida
269	30	60.0	508	2	AH2688	Na+/H+ antiporter	342	29	58.0	82	2	S52460	hypothetical prote
270	30	60.0	516	2	T00791	purple acid phosph	343	29	58.0	88	2	AF1846	hypothetical prote
271	30	60.0	525	2	C97470	probable NADH dehy	344	29	58.0	111	2	T11266	NADH2 dehydrogenas
272	30	60.0	532	2	A96792	probable phosphate	345	29	58.0	113	2	A81347	hypothetical prote
273	30	60.0	538	2	AB1856	l-2,4-diaminobuty	346	29	58.0	118	2	T43134	hypothetical prote
274	30	60.0	544	2	T32568	hypothetical prote	347	29	58.0	121	2	D72336	transcriptional regu
275	30	60.0	546	2	AB0498	probable membrane	348	29	58.0	121	2	T12467	hypothetical prote
276	30	60.0	560	1	JQ1221	probable 60K inner	349	29	58.0	125	2	S73412	MG055 homolog D09
277	30	60.0	568	2	S42225	major envelope gly	350	29	58.0	130	2	D29774	T-cell receptor al
278	30	60.0	574	2	T51799	CLB1-like protein	351	29	58.0	130	2	T27126	hypothetical prote
279	30	60.0	578	2	G82950	conserved hypothet	352	29	58.0	131	2	AH1046	fumarate reductase
280	30	60.0	579	2	B82085	sensory box/GGDEF	353	29	58.0	131	2	E86111	succinate dehydrog
281	30	60.0	583	2	T00091	rgpFc protein - St	354	29	58.0	131	2	S56380	succinate dehydrog
282	30	60.0	585	1	SXAD32	peripentonal hexon	355	29	58.0	131	2	E91270	succinate dehydrog
283	30	60.0	585	1	SXADH5	peripentonal hexon	356	29	58.0	131	2	F45893	T-cell receptor al
284	30	60.0	594	2	T15202	hypothetical prote	357	29	58.0	132	2	AF2023	hypothetical prote
285	30	60.0	614	2	D64630	hypothetical prote	358	29	58.0	133	2	S78886	T cell receptor al
286	30	60.0	614	2	B71884	hypothetical prote	359	29	58.0	135	2	T13489	T-cell receptor al
287	30	60.0	616	2	E97649	probable permealase	360	29	58.0	137	2	E81355	hypothetical prote
288	30	60.0	621	2	T48187	hypothetical prote	361	29	58.0	143	2	C40590	hypothetical prote
289	30	60.0	632	2	T22052	hypothetical prote	362	29	58.0	144	2	F32536	hypothetical prote
290	30	60.0	638	2	T17554	hypothetical prote	363	29	58.0	156	2	S65219	probable membrane
291	30	60.0	644	1	W1WLJ33	E1 protein - human	364	29	58.0	160	2	F70082	hypothetical prote
292	30	60.0	644	1	W1WLJ58	E1 protein - human	365	29	58.0	174	2	E82315	probable type IV p
293	30	60.0	663	2	T33244	hypothetical prote	366	29	58.0	177	2	S34207	hypothetical prote
294	30	60.0	684	2	C84434	hypothetical prote	367	29	58.0	189	2	AH3634	diamine N-acetyltr
295	30	60.0	686	2	H90798	hypothetical prote	368	29	58.0	180	2	G86826	hypothetical prote
296	30	60.0	696	2	G85607	Iha adhesin [impor	369	29	58.0	180	2	S28716	conserved hypothet
297	30	60.0	696	2	T01951	probable receptor	370	29	58.0	181	2	H69428	transcription regu
298	30	60.0	710	2	T50469	hypothetical prote	371	29	58.0	188	2	A86806	norE protein [impo
299	30	60.0	710	2	A25657	hypothetical prote	372	29	58.0	189	2	WMXP30	p30 phosphoprotein
300	30	60.0	720	2	A44819	alpha-galactosidas	373	29	58.0	194	1	WMXP30	ribosomal protein
301	30	60.0	720	2	T50475	hypothetical prote	374	29	58.0	194	2	G69539	hypothetical prote
302	30	60.0	742	2	T48930	hypothetical prote	375	29	58.0	200	2	T34104	hypothetical prote
303	30	60.0	746	2	S74219	alpha-galactosidas	376	29	58.0	204	2	A45683	phosphoprotein p32
304	30	60.0	748	2	G83927	alpha-galactosidas	377	29	58.0	206	2	AH0466	threonine efflux p
305	30	60.0	770	2	H84463	hypothetical prote	378	29	58.0	210	2	JCS448	serine proteinase
306	30	60.0	775	2	A84526	hypothetical prote	379	29	58.0	213	2	AC3389	uracil-DNA glycosy
307	30	60.0	780	2	T29580	hypothetical prote	380	29	58.0	214	2	T20683	hypothetical prote
308	30	60.0	789	2	E84514	hypothetical prote	381	29	58.0	215	2	T35666	hypothetical prote
309	30	60.0	792	2	E84525	hypothetical prote	382	29	58.0	218	1	S23664	helb protein - Rho
310	30	60.0	795	2	D84477	hypothetical prote	383	29	58.0	219	2	S68364	nitrate lyase (EC
311	30	60.0	820	2	T12972	hypothetical prote	384	29	58.0	223	2	S60088	pyruvate reductase
312	30	60.0	836	2	T01473	hypothetical prote	385	29	58.0	227	2	AB0018	conserved hypothet
313	30	60.0	893	2	S64926	probable membrane	386	29	58.0	227	2	G70414	two-component resp
314	30	60.0	900	2	G82894	isoletucyl-CRNA syn	387	29	58.0	232	2	C83744	probable membrane
315	30	60.0	901	2	F89910	aconitate hydratase	388	29	58.0	233	2	AB0156	hypothetical prote
316	30	60.0	967	2	T15680	hypothetical prote	389	29	58.0	240	2	B72336	hypothetical prote
317	30	60.0	993	2	T25624	hypothetical prote	390	29	58.0	260	2	E98219	probable permealase
318	30	60.0	998	2	G83022	probable two-compo	391	29	58.0	260	2	AE3067	hypothetical prote
319	30	60.0	1006	2	S76892	hypothetical prote	392	29	58.0	262	2	H82114	probable permealase
320	30	60.0	1006	2	S20126	exoribonuclease RA	393	29	58.0	263	2	S85619	probable transport
321	30	60.0	1051	2	A35761	cell surface glyco	394	29	58.0	263	2	A90756	probable transport

395	29	58.0	263	2	AF2534	hypothetical prote	468	29	58.0	420	2	T08005	flavonol 3-O-gluc
396	29	58.0	264	2	G81252	NADH2 dehydrogen	469	29	58.0	420	2	E95982	probable transport
397	29	58.0	265	2	AC0441	probable aliphatic	470	29	58.0	420	2	A47649	probable inner mem
398	29	58.0	266	2	D82581	probable signal pe	471	29	58.0	422	2	F70018	multiple sugar-bin
399	29	58.0	271	2	T33613	hypothetical prote	472	29	58.0	422	1	MMXRWV	structural protein
400	29	58.0	274	2	E83215	probable permease	473	29	58.0	433	2	A83728	adenylosuccinate l
401	29	58.0	275	1	G69963	lipoprotein SpoII	474	29	58.0	435	2	T43749	cytochrome oxidase
402	29	58.0	275	2	T47063	hypothetical prote	475	29	58.0	441	2	S45284	growth/differentia
403	29	58.0	275	2	AB0231	probable binding-p	476	29	58.0	461	1	T43248	dihydrofolate redu
404	29	58.0	275	2	AC1247	B. subtilis SpoII	477	29	58.0	467	2	H84699	probable flavonol
405	29	58.0	275	2	AG1609	B. subtilis SpoII	478	29	58.0	467	2	F84699	probable flavonol
406	29	58.0	276	2	T08773	hypothetical prote	479	29	58.0	468	2	H87044	probable solute-bi
407	29	58.0	278	1	E64833	nitrate transport	480	29	58.0	469	2	T45201	hypothetical prote
408	29	58.0	280	2	E87652	conserved hypothet	481	29	58.0	479	1	VGBEF2	glycoprotein F - h
409	29	58.0	281	2	AB1921	ABC transporter pe	482	29	58.0	483	2	AI1130	amino acid antipor
410	29	58.0	282	2	T44707	DNA-formamidopyrim	483	29	58.0	484	2	T24238	hypothetical prote
411	29	58.0	283	2	G83754	transcription regu	484	29	58.0	503	2	C86786	glutamate-gamma-am
412	29	58.0	287	2	A25877	cytochrome-c oxida	485	29	58.0	507	2	AB1370	amino acid antipor
413	29	58.0	287	2	AD2075	tetracenomycin C s	486	29	58.0	507	2	AI1739	amino acid antipor
414	29	58.0	289	2	B83153	acyl-CoA thioester	487	29	58.0	512	2	AC3399	probable colanic b
415	29	58.0	293	2	H82184	glycerol-3-phospha	488	29	58.0	514	2	G97118	levanase imported
416	29	58.0	299	2	A90457	hypothetical prote	489	29	58.0	514	2	T19579	hypothetical prote
417	29	58.0	302	2	T24187	hypothetical prote	490	29	58.0	521	2	B64181	probable cytochrom
418	29	58.0	314	2	C85955	hypothetical prote	491	29	58.0	524	2	T43050	cyclin E - Caenorh
419	29	58.0	314	2	A98110	hypothetical prote	492	29	58.0	528	2	D85048	hypothetical prote
420	29	58.0	317	2	C70863	hypothetical prote	493	29	58.0	529	2	S48388	probable membrane
421	29	58.0	321	2	F85090	hypothetical prote	494	29	58.0	531	2	T40575	major facilitator
422	29	58.0	321	2	T33680	hypothetical prote	495	29	58.0	531	2	T11596	hypothetical prote
423	29	58.0	322	2	A69963	hypothetical prote	496	29	58.0	532	2	G84931	60 kD inner-membra
424	29	58.0	322	2	G64388	hypothetical prote	497	29	58.0	541	1	H64163	probable 60K inner
425	29	58.0	323	2	T15808	hypothetical prote	498	29	58.0	541	2	E82375	inner membrane pro
426	29	58.0	326	2	T10166	restriction endonu	499	29	58.0	543	2	C84334	hypothetical prote
427	29	58.0	330	2	A70422	hypothetical prote	500	29	58.0	544	2	T27444	hypothetical prote
428	29	58.0	332	2	T41227	hypothetical prote	501	29	58.0	544	2	T43364	potassium channel
429	29	58.0	333	2	H98282	hypothetical prote	502	29	58.0	546	2	S52053	cytochrome-c oxida
430	29	58.0	334	2	B6372	Spermidine synthas	503	29	58.0	548	1	B65173	probable 60K inner
431	29	58.0	335	2	T34296	hypothetical prote	504	29	58.0	548	2	AF0957	probable membrane
432	29	58.0	337	2	F83839	hypothetical prote	505	29	58.0	548	2	H31208	60 kD inner-membra
433	29	58.0	337	2	T38814	probable role in N	506	29	58.0	548	2	B86055	60 kD inner-membra
434	29	58.0	340	2	T01492	spermidine synthas	507	29	58.0	566	2	T50536	succinate dehydrog
435	29	58.0	341	2	A72674	hypothetical prote	508	29	58.0	566	2	T15866	hypothetical prote
436	29	58.0	341	2	T36790	probable phosphotr	509	29	58.0	568	2	D90525	hypothetical prote
437	29	58.0	342	2	T15078	hypothetical prote	510	29	58.0	570	2	T30156	hypothetical prote
438	29	58.0	345	2	F90194	threonine synthase	511	29	58.0	572	2	T32636	hypothetical prote
439	29	58.0	349	2	H85985	hypothetical prote	512	29	58.0	576	2	T43363	potassium channel
440	29	58.0	349	2	E91140	hypothetical prote	513	29	58.0	577	2	A72283	maltose ABC transp
441	29	58.0	349	2	T27204	hypothetical prote	514	29	58.0	582	2	G81288	hypothetical prote
442	29	58.0	352	2	T45843	hypothetical prote	515	29	58.0	602	2	S72513	FOG2 protein - yea
443	29	58.0	355	2	G62565	endonuclease III (	516	29	58.0	613	2	T27469	hypothetical prote
444	29	58.0	359	2	T22950	hypothetical prote	517	29	58.0	615	2	S74277	probable membrane
445	29	58.0	360	2	F96902	aspartate-semialde	518	29	58.0	615	2	S40624	probable membrane
446	29	58.0	366	2	S26048	serotonin receptor	519	29	58.0	616	2	G82885	hypothetical prote
447	29	58.0	367	2	AD0907	conserved hypothet	520	29	58.0	622	1	S44859	serine/threonine-s
448	29	58.0	369	2	AC0555	probable ATP-bind	521	29	58.0	623	2	D88922	protein W03F9.4 [i
449	29	58.0	369	2	T46950	probable ATPase co	522	29	58.0	628	2	A82889	hypothetical prote
450	29	58.0	371	2	D83226	probable chaperone	523	29	58.0	630	2	A82783	peptidyl-prolyl ci
451	29	58.0	371	2	S44145	amib protein - Pse	524	29	58.0	630	2	H37562	hypothetical prote
452	29	58.0	372	2	B64717	LPS biosynthesis p	525	29	58.0	633	1	A36030	serine/threonine-s
453	29	58.0	375	2	F65113	hypothetical 43.3K	526	29	58.0	636	2	T18542	moic protein - lep
454	29	58.0	381	2	T43393	potassium channel	527	29	58.0	639	1	S45776	uracil transport p
455	29	58.0	391	2	H85063	hypothetical prote	528	29	58.0	646	2	T41545	hypothetical trans
456	29	58.0	395	2	S43746	MNN9 protein - yea	529	29	58.0	647	2	S36575	E1 protein - human
457	29	58.0	401	2	T21456	hypothetical prote	530	29	58.0	648	2	F69848	transcription anti
458	29	58.0	406	2	T24492	hypothetical prote	531	29	58.0	657	2	E75484	glycosyl hydrolase
459	29	58.0	408	2	T50894	hydroxyneurospore	532	29	58.0	664	2	H83962	serine/threonine p
460	29	58.0	408	2	C91062	hypothetical prote	533	29	58.0	674	2	T28274	ORF MSV113 probabl
461	29	58.0	408	2	G65038	hypothetical prote	534	29	58.0	693	2	A90110	26S proteasome reg
462	29	58.0	408	2	G85906	hypothetical prote	535	29	58.0	709	2	A70624	H+/K+-exchanging A
463	29	58.0	413	2	C71971	serine transport p	536	29	58.0	712	2	T16338	hypothetical prote
464	29	58.0	413	2	E64536	serine transport p	537	29	58.0	724	2	G70928	probable 4-ALPHA-G
465	29	58.0	414	2	B84275	hypothetical prote	538	29	58.0	733	2	E86345	hypothetical prote
466	29	58.0	415	2	AC3446	bacteroid developm	539	29	58.0	738	2	B69863	two-component sens
467	29	58.0	418	2	S41044	chromosomal protei	540	29	58.0	758	2	T38811	hypothetical prote

541	29	58.0	772	2	T52402	hypothetical prote	614	28	56.0	131	2	G70326	hypothetical prote
542	29	58.0	809	2	A12747	conserved hypotet	615	28	56.0	133	2	AB2856	conserved hypotet
543	29	58.0	827	2	T20492	hypothetical prote	616	28	56.0	133	2	G97632	hypothetical prote
544	29	58.0	849	2	H84668	Mutator-like trans	617	28	56.0	137	2	B64208	hypothetical prote
545	29	58.0	850	2	C83081	probable oxidoredu	618	28	56.0	139	2	C96550	hypothetical prote
546	29	58.0	861	2	S73648	isoleucine-CRNA li	619	28	56.0	142	2	T49256	hypothetical prote
547	29	58.0	873	2	H97528	hypothetical prote	620	28	56.0	147	2	D90416	hypothetical prote
548	29	58.0	889	2	JC6015	chitin synthase (E	621	28	56.0	150	2	S43955	probable NADH2 deh
549	29	58.0	921	2	AC1337	isoleucyl-tRNA syn	622	28	56.0	150	2	S76562	hypothetical prote
550	29	58.0	921	2	AE1698	isoleucyl-tRNA syn	623	28	56.0	152	2	AG3434	zinc-finger protei
551	29	58.0	921	2	D86293	FYH2.22 protein -	624	28	56.0	152	2	H71845	hypothetical prote
552	29	58.0	928	2	T47846	Arm repeat contain	625	28	56.0	159	2	D82848	conserved hypotet
553	29	58.0	941	2	B96553	hypothetical prote	626	28	56.0	162	2	AF0119	conserved hypotet
554	29	58.0	941	2	AP2415	two-component hybr	627	28	56.0	163	2	AD0179	conserved hypotet
555	29	58.0	945	2	S77052	cation-transportin	628	28	56.0	165	2	F72600	hypothetical prote
556	29	58.0	957	2	S66755	probable membrane	629	28	56.0	167	2	G82892	hypothetical prote
557	29	58.0	1006	2	JC5526	kinase-defective E	630	28	56.0	168	2	G83288	transcription elon
558	29	58.0	1015	2	I39697	beta-galactosidase	631	28	56.0	169	2	H72334	bioY protein - The
559	29	58.0	1038	2	D95252	fucosyltransferase	632	28	56.0	180	2	AI0919	probable membrane
560	29	58.0	1038	2	B98117	hypothetical prote	633	28	56.0	181	2	T45782	hypothetical prote
561	29	58.0	1039	2	C64418	isoleucine-CRNA li	634	28	56.0	187	2	T50621	hypothetical prote
562	29	58.0	1043	1	IJBOG1	desmoglein 1 precu	635	28	56.0	188	2	H95348	nitric-oxide reduc
563	29	58.0	1049	1	IJHUG1	desmoglein 1 precu	636	28	56.0	188	2	AC3096	nitric oxide reduc
564	29	58.0	1090	2	T30576	glucan synthase -	637	28	56.0	188	2	G98190	norE protein (AB03
565	29	58.0	1102	2	T17367	potassium channel	638	28	56.0	194	2	C75132	leu ribosomal prot
566	29	58.0	1151	2	S03722	DNA-directed DNA p	639	28	56.0	206	2	B82061	30S ribosomal prot
567	29	58.0	1159	2	I38465	probable potassium	640	28	56.0	206	2	AB0029	probable glutathio
568	29	58.0	1193	2	P83264	hypothetical prote	641	28	56.0	208	2	C83294	30S ribosomal prot
569	29	58.0	1208	2	T00362	hypothetical prote	642	28	56.0	208	2	H82714	hypothetical prote
570	29	58.0	1301	2	S18118	alpha-amylase - Al	643	28	56.0	212	2	T25905	hypothetical prote
571	29	58.0	1327	2	D70759	probable otasB prot	644	28	56.0	213	2	S29910	hypothetical prote
572	29	58.0	1417	2	H83132	probable sensor/re	645	28	56.0	215	2	T35768	hypothetical prote
573	29	58.0	1599	2	T15854	hypothetical prote	646	28	56.0	216	2	B86749	riboflavin synthas
574	29	58.0	1685	2	T02750	acetyl-CoA carboxy	647	28	56.0	217	2	A47483	cysteine-rich omeg
575	29	58.0	1785	2	T22595	hypothetical prote	648	28	56.0	222	2	S09770	hypothetical prote
576	29	58.0	1976	2	I56555	sodium channel pro	649	28	56.0	222	2	H82482	transcription regu
577	29	58.0	2224	1	KFH05	coagulation factor	650	28	56.0	223	2	A43331	orf3 5' of sor - D
578	29	58.0	2787	2	S45416	TBL1 protein - yea	651	28	56.0	224	1	B70106	conserved hypotet
579	29	58.0	4092	1	S38128	dynein heavy chain	652	28	56.0	225	2	T19811	hypothetical prote
580	29	58.0	4351	2	T00252	MSGF1 protein - ra	653	28	56.0	226	2	AI1115	hypothetical prote
581	28.5	57.0	279	2	C96721	hypothetical prote	654	28	56.0	226	2	AB1477	hypothetical prote
582	28.5	57.0	302	2	AB0857	ATP sulfurylase (A	655	28	56.0	229	2	T21393	hypothetical prote
583	28.5	57.0	302	2	D65056	sulfate adenylyltr	656	28	56.0	230	2	T37412	probable 27.1K pro
584	28.5	57.0	302	2	G85924	ATP sulfurylase su	657	28	56.0	233	2	T43896	conserved hypotet
585	28.5	57.0	302	2	F91079	ATP sulfurylase su	658	28	56.0	234	2	D84768	hypothetical prote
586	28.5	57.0	376	2	C97059	uncharacterized pr	659	28	56.0	235	2	AB3344	integral membrane
587	28.5	57.0	420	2	H90356	conserved hypotet	660	28	56.0	236	2	T52494	hypothetical prote
588	28	56.0	20	2	T46626	hypothetical prote	661	28	56.0	238	2	B71089	ribosomal protein
589	28	56.0	46	2	B69423	hypothetical prote	662	28	56.0	242	2	T41323	hypothetical prote
590	28	56.0	57	2	A33811	tracheobronchial m	663	28	56.0	243	2	AD1341	hypothetical prote
591	28	56.0	59	2	F70251	hypothetical prote	664	28	56.0	248	2	G97340	acyl-ACP thioester
592	28	56.0	68	2	T00309	hypothetical prote	665	28	56.0	249	2	AE1928	hypothetical prote
593	28	56.0	76	2	P83739	hypothetical prote	666	28	56.0	251	2	T33679	pyrroline-5-carbox
594	28	56.0	98	2	S54735	ribosomal protein	667	28	56.0	253	2	H69219	essential for sigm
595	28	56.0	101	2	G82061	conserved hypotet	668	28	56.0	257	2	H84157	hypothetical prote
596	28	56.0	104	2	S56386	hypothetical 12.6K	669	28	56.0	257	2	T00406	hypothetical prote
597	28	56.0	105	2	S53607	NADH2 dehydrogenas	670	28	56.0	259	2	B87314	conserved hypotet
598	28	56.0	106	2	C34879	NADH2 dehydrogenas	671	28	56.0	259	2	AG3607	probable hydroxlas
599	28	56.0	111	2	T07656	probable resistanc	672	28	56.0	264	2	D97344	amino acid (probab
600	28	56.0	114	2	H90467	NADH2 dehydrogenas	673	28	56.0	265	2	S25951	cytochrome-c oxid
601	28	56.0	114	2	T11159	conserved hypotet	674	28	56.0	265	2	D71838	nadh oxidoreductas
602	28	56.0	117	2	T11356	NADH2 dehydrogenas	675	28	56.0	266	2	F64677	NADH2 dehydrogenas
603	28	56.0	120	2	S50338	NADH2 dehydrogenas	676	28	56.0	267	2	C90411	ketopantoate hydro
604	28	56.0	121	2	AI0552	conserved hypotet	677	28	56.0	267	2	H86320	probable bis(5'-nu
605	28	56.0	122	2	T46207	hypothetical prote	678	28	56.0	269	2	H82322	probable bis(5'-nu
606	28	56.0	123	2	B84206	hypothetical prote	679	28	56.0	271	2	B96773	hypothetical prote
607	28	56.0	124	2	B82444	hypothetical prote	680	28	56.0	272	2	AI2005	delta-9 desaturase
608	28	56.0	127	2	S37901	hypothetical prote	681	28	56.0	272	2	C64351	imidazoleglycerol-
609	28	56.0	128	2	AF2239	hypothetical prote	682	28	56.0				
610	28	56.0	128	2	E90092	hypothetical prote	683	28	56.0				
611	28	56.0	129	2	S66831	probable membrane	684	28	56.0				
612	28	56.0	129	2	A95172	hypothetical prote	685	28	56.0				
613	28	56.0	129	2	A98038	hypothetical prote	686	28	56.0				

687	28	56.0	272	2	H90087	hypothetical prote	760	409	2	S37497	triose phosphate/3
688	28	56.0	274	2	T51714	probable formamido	761	410	2	T51692	phosphate/triose-p
689	28	56.0	275	2	T34626	hypothetical prote	762	411	2	G82159	integrase, phage f
690	28	56.0	276	2	T50896	hypothetical membr	763	413	2	G84921	hypothetical prote
691	28	56.0	277	2	AB1340	maltodextrase util	764	414	2	S34822	triose phosphate/3
692	28	56.0	277	2	AB1710	hypothetical prote	765	414	2	S23224	triose phosphate/3
693	28	56.0	279	2	D90258	hypothetical prote	766	417	2	C44038	tryptophan permeas
694	28	56.0	283	2	S34851	hypothetical 31-9K	767	421	2	C91109	integrase (limpoes
695	28	56.0	284	2	D83697	rRNA adenine N-6-m	768	421	2	F85954	probable pathogeni
696	28	56.0	285	2	T29804	hypothetical prote	769	423	2	G83573	conserved hypothet
697	28	56.0	288	2	S36954	cytochrome-c oxida	770	430	2	F96686	unknown protein F1
698	28	56.0	288	2	S36955	cytochrome-c oxida	771	431	2	G75017	histidyl-tRNA synt
699	28	56.0	289	2	C96656	unknown protein, 4	772	431	2	A84380	hypothetical prote
700	28	56.0	299	2	C86196	hypothetical prote	773	431	2	G82430	conserved hypothet
701	28	56.0	299	2	D86199	hypothetical prote	774	432	2	S22527	glutamate-ammonia
702	28	56.0	305	2	T52111	hypothetical prote	775	439	2	G97159	contains cell adhe
703	28	56.0	307	2	AD0807	stearoyl-CoA 9-des	776	441	2	T50689	proline transport
704	28	56.0	306	2	T52109	probable acyltrans	777	442	2	T50687	proline transport
705	28	56.0	310	2	C90277	hypothetical prote	778	442	2	H89770	hypothetical prote
706	28	56.0	311	2	G84719	delta 9 desaturase	779	443	2	AB1446	probable terminase
707	28	56.0	313	2	T24390	hypothetical prote	780	443	2	AU1362	probable terminase
708	28	56.0	315	2	T30162	hypothetical prote	781	446	2	S01187	NADH2 dehydrogenas
709	28	56.0	318	1	S75765	stearoyl-CoA 9-des	782	446	2	I25797	NADH2 dehydrogenas
710	28	56.0	318	2	A71830	magnesium and coba	783	447	2	S53982	hypothetical prote
711	28	56.0	318	2	H64687	magnesium and coba	784	448	2	A69747	ABC transporter (p
712	28	56.0	319	2	C86199	hypothetical prote	785	449	2	C95142	sensory box sensor
713	28	56.0	320	2	T22191	hypothetical prote	786	449	2	A39010	histidine kinase (
714	28	56.0	320	2	T41927	hypothetical prote	787	450	2	T23111	hypothetical prote
715	28	56.0	320	2	JC1311	cell protein precu	788	451	1	S56818	hypothetical prote
716	28	56.0	322	1	WMV21U	A-type inclusion p	789	451	2	T26587	hypothetical prote
717	28	56.0	324	2	T20681	hypothetical prote	790	454	2	H70167	xylokinaase (xylB
718	28	56.0	325	1	B40358	NADH2 dehydrogenas	791	457	1	G70116	histidine-tRNA lig
719	28	56.0	325	2	AG2082	iron(III) dicitrat	792	460	2	T51560	probable flavonol
720	28	56.0	327	2	B95266	probable ABC trans	793	465	2	T32738	hypothetical prote
721	28	56.0	328	2	A70145	prolipoprotein dia	794	468	1	B64896	hypothetical prote
722	28	56.0	331	1	DN0BU1	NADH2 dehydrogenas	795	468	2	D85734	hypothetical prote
723	28	56.0	332	2	T72509	probable 5-methylt	796	468	2	C90884	probable transcrip
724	28	56.0	334	2	T22366	hypothetical prote	797	468	2	H70521	probable papA2 pro
725	28	56.0	334	2	T24388	hypothetical prote	798	471	2	E83130	conserved hypothet
726	28	56.0	346	2	I79270	trab protein - Bsc	799	473	2	A11574	ethanolamine utili
727	28	56.0	347	2	T50963	related to cell pr	800	473	2	G70975	hypothetical prote
728	28	56.0	349	2	D84608	hypothetical prote	801	474	2	AF0669	probable regulator
729	28	56.0	349	2	A44507	licheninase (EC 3.	802	474	2	A40721	neuroblast prolife
730	28	56.0	355	2	AF3581	hypothetical prote	803	476	1	C70986	probable serine/th
731	28	56.0	359	2	T21840	hypothetical prote	804	477	2	H84160	hypothetical prote
732	28	56.0	363	2	T01354	herbicide safener	805	477	2	S53362	mucin SAC (clone J
733	28	56.0	363	2	T34631	probable integrat	806	479	2	A84588	probable tyrosine
734	28	56.0	364	2	H89973	conserved hypothet	807	479	2	S67202	probable membrane
735	28	56.0	372	2	AI0637	probable sarcosine	808	480	2	AH2333	cardiolipin syntha
736	28	56.0	375	2	D75591	probable cation tr	809	481	2	AB1927	hypothetical prote
737	28	56.0	379	2	T32778	hypothetical prote	810	481	2	E84860	hypothetical prote
738	28	56.0	380	2	S11187	REP1 protein - yea	811	484	2	C82567	GumD protein XF236
739	28	56.0	381	2	G84497	hypothetical prote	812	487	2	AD3643	adhesin aidA-I (lm
740	28	56.0	382	2	S40417	REP1 protein - yea	813	490	2	T23112	hypothetical prote
741	28	56.0	385	2	AG3059	cytochrome d oxida	814	498	2	C72167	A30L protein - var
742	28	56.0	385	2	A98227	cytochrome d oxida	815	498	2	C36851	A29L protein - var
743	28	56.0	388	2	T15075	hypothetical prote	816	498	2	T28571	hypothetical prote
744	28	56.0	388	2	T15948	hypothetical prote	817	500	2	AC1915	NADH dehydrogenase
745	28	56.0	389	2	G83317	conserved hypothet	818	500	2	AF2325	NADH dehydrogenase
746	28	56.0	390	2	E96565	hypothetical prote	819	503	2	AC1042	probable DNA helic
747	28	56.0	390	2	T51713	probable formamido	820	510	2	D96741	hypothetical prote
748	28	56.0	391	2	S75649	renin-binding prot	821	513	2	T45658	1-phosphatidylinos
749	28	56.0	393	2	B44767	L-mandelate dehydr	822	513	2	P95533	probable fucosyltr
750	28	56.0	395	2	T02185	probale translatio	823	514	2	B83360	hypothetical prote
751	28	56.0	398	2	JQ1245	hypothetical 43K p	824	521	2	S67491	phosphate transpor
752	28	56.0	399	2	AC0135	probable prophage	825	527	2	A84050	acetate-CoA ligase
753	28	56.0	401	2	T28223	SCG gene family pr	826	530	2	T20360	hypothetical prote
754	28	56.0	401	2	S42583	phosphate transloc	827	532	2	T08969	hypothetical prote
755	28	56.0	403	2	T02290	hypothetical prote	828	535	2	T47790	hypothetical prote
756	28	56.0	404	2	S03638	triose phosphate/3	829	535	2	H90716	hypothetical prote
757	28	56.0	405	2	T32361	hypothetical prote	830	554	2	H85566	asparagine synthet
758	28	56.0	407	2	S37550	triose phosphate/3	831	557	2	AC32694	interferon alpha/b
759	28	56.0	408	2	S37553	triose phosphate/3	832	558	2	C72391	conserved hypothet



833	28	56.0	559	2	C72732	probable medium-ch	906	28	56.0	884	2	E89010	protein R08P11.1 [
834	28	56.0	564	2	T21393	hypothetical prote	907	28	56.0	884	2	S61569	hypothetical prote
835	28	56.0	571	2	T20359	hypothetical prote	908	28	56.0	895	2	B64238	isoleucine-tRNA li
836	28	56.0	572	2	T22547	hypothetical prote	909	28	56.0	899	2	C84765	hypothetical prote
837	28	56.0	579	2	T72252	aspartate-tRNA lig	910	28	56.0	906	2	T45158	pre-mRNA splicing
838	28	56.0	583	2	T32266	hypothetical prote	911	28	56.0	953	2	S55156	probable membrane
839	28	56.0	585	2	T28884	hypothetical prote	912	28	56.0	954	2	S57108	hypothetical prote
840	28	56.0	587	2	T40849	succinate dehydrog	913	28	56.0	962	2	T53197	potassium channel
841	28	56.0	589	2	A29476	muscarinic acetylch	914	28	56.0	984	2	A55137	hyaluronate lyase
842	28	56.0	589	2	B29514	muscarinic acetylch	915	28	56.0	985	2	JC4217	alpha-glucosidase
843	28	56.0	590	2	B33448	succinate dehydrog	916	28	56.0	989	2	I48912	potassium channel
844	28	56.0	590	2	S01114	muscarinic acetylch	917	28	56.0	1010	2	T22712	hypothetical prote
845	28	56.0	590	2	S47572	muscarinic acetylch	918	28	56.0	1017	2	T31354	probable potassium
846	28	56.0	592	2	T52139	LRR-containing F-b	919	28	56.0	1040	1	A38306	alpha-mannosidase
847	28	56.0	603	2	B64444	hypothetical prote	920	28	56.0	1056	2	A53767	mucin MUC5B, trach
848	28	56.0	608	2	T28301	ORF MSV140 hypothe	921	28	56.0	1077	2	T38900	probable alpha-man
849	28	56.0	613	2	F69424	conserved hypoteth	922	28	56.0	1087	2	T31100	probable potassium
850	28	56.0	622	2	F71174	hypothetical prote	923	28	56.0	1108	2	A55915	guanylate cyclase
851	28	56.0	627	2	F84194	Hcr14 transducer l	924	28	56.0	1135	1	JQ1928	G2-G1 polyprotein
852	28	56.0	632	2	T50597	peptidase PAB1418	925	28	56.0	1168	2	T30935	reverse transcript
853	28	56.0	638	2	T20944	hypothetical prote	926	28	56.0	1249	2	H71404	hypothetical prote
854	28	56.0	638	2	S36723	FUN36 protein - ye	927	28	56.0	1277	2	E70224	hypothetical prote
855	28	56.0	639	2	A55019	muscarinic acetylch	928	28	56.0	1278	2	B70236	hypothetical prote
856	28	56.0	639	2	S62567	hypothetical prote	929	28	56.0	1289	2	B72354	conserved hypoteth
857	28	56.0	644	2	B70420	NADH2 dehydrogenas	930	28	56.0	1297	2	S25714	son-of-sevenless-2
858	28	56.0	650	2	T15972	hypothetical prote	931	28	56.0	1315	2	T41055	membrane atpase -
859	28	56.0	651	2	T27810	hypothetical prote	932	28	56.0	1324	2	S06187	rRNA2 polyprotein -
860	28	56.0	663	2	D83545	probable helicase	933	28	56.0	1333	2	A37488	Ras guanine nucleo
861	28	56.0	664	2	PC4002	phosphatidylinosit	934	28	56.0	1336	2	S25716	Ras guanine nucleo
862	28	56.0	667	2	S64915	EMP70 protein prec	935	28	56.0	1441	2	A88355	protein Y48B1A.1 [
863	28	56.0	676	2	AP1153	transcription anti	936	28	56.0	1490	2	T30550	ABC transport prot
864	28	56.0	682	2	T64113	methionine-tRNA li	937	28	56.0	1548	1	DVLNS	multidrug resistan
865	28	56.0	684	2	H82296	c-di-GMP phosphodi	938	28	56.0	1664	2	H82601	conserved hypoteth
866	28	56.0	694	2	G95314	probable site-spec	939	28	56.0	1715	2	G84429	hypothetical prote
867	28	56.0	703	2	H86588	thio, disulfide int	940	28	56.0	1737	2	T19606	hypothetical prote
868	28	56.0	703	2	H72034	thiol-disulfide in	941	28	56.0	2073	2	T39207	fatty acid synthas
869	28	56.0	703	2	S40710	hypothetical prote	942	28	56.0	2073	2	T43311	fatty acyl-CoA syn
870	28	56.0	707	2	S77094	glycogen operon pr	943	28	56.0	2167	2	S50658	genom polyprotein
871	28	56.0	710	2	B71374	probable soluble l	944	28	56.0	2238	1	RRVUBY	coagulation factor
872	28	56.0	714	2	G81503	thiol-disulfide in	945	28	56.0	2319	2	A47004	coagulation factor
873	28	56.0	717	2	S77190	hypothetical prote	946	28	56.0	2351	1	E2HU	splicing factor PR
874	28	56.0	717	2	T29816	hypothetical prote	947	28	56.0	2352	2	T06077	hypothetical prote
875	28	56.0	722	2	D90083	probable helicase-	948	28	56.0	2359	2	B96832	hypothetical prote
876	28	56.0	722	2	B75074	methionyl-tRNA syn	949	28	56.0	2823	2	F87908	protein T22A3.8 [i
877	28	56.0	723	2	D71091	methionine-tRNA li	950	28	56.0	2823	2	T23064	hypothetical prote
878	28	56.0	729	2	B70803	hypothetical prote	951	28	56.0	3102	2	T43291	laminin alpha chai
879	28	56.0	731	2	T17002	probable beta-gala	952	28	56.0	3570	2	T45025	mucin MUC5B, trach
880	28	56.0	734	2	F88098	protein F18A12.4 [	953	28	56.0	3623	2	T08618	intrinsic factor-B
881	28	56.0	742	2	T00371	hypothetical prote	954	28	56.0	3788	2	T13960	beige protein homo
882	28	56.0	748	2	T32654	hypothetical prote	955	28	56.0	3796	2	T18514	lysosomal traffick
883	28	56.0	765	2	B88924	protein R02C2.3 [i	956	28	56.0	3898	1	GNWVHC	genom polyprotein
884	28	56.0	775	2	B84828	probable WD-40 rep	957	27.5	55.0	363	2	G70145	glycerol-3-Phospha
885	28	56.0	782	2	T43277	host cell factor l	958	27.5	55.0	993	2	H86469	protein F21H2.13 [
886	28	56.0	785	2	A86299	hypothetical prote	959	27	54.0	24	2	D91209	tryptophanase lead
887	28	56.0	797	2	D86459	probable disease r	960	27	54.0	24	2	I54862	tryptophanase lead
888	28	56.0	798	2	C95202	primosomal protein	961	27	54.0	24	2	G86055	tryptophanase lead
889	28	56.0	798	2	C98069	primosomal replica	962	27	54.0	25	2	T12941	hypothetical prote
890	28	56.0	801	1	T52538	1-phosphatidylinos	963	27	54.0	34	2	A44038	leader peptide Tna
891	28	56.0	807	2	T12177	potassium channel	964	27	54.0	37	2	H82269	hypothetical prote
892	28	56.0	814	2	F59430	GTPase regulator a	965	27	54.0	44	2	S35146	photosystem II pro
893	28	56.0	835	2	T06590	probable beta-gala	966	27	54.0	46	2	F97214	hypothetical prote
894	28	56.0	838	2	S23606	potassium channel	967	27	54.0	50	2	B97826	hypothetical prote
895	28	56.0	841	2	T14520	probable S-recepto	968	27	54.0	53	2	T30721	hypothetical prote
896	28	56.0	850	2	S56015	gastric mucin MUC5	969	27	54.0	53	2	AB2328	hypothetical prote
897	28	56.0	855	2	A34810	3',5'-cyclic-GMP p	970	27	54.0	57	2	C84255	hypothetical prote
898	28	56.0	857	2	S62694	potassium channel	971	27	54.0	62	2	T06501	photosystem II pro
899	28	56.0	858	2	JC4520	3',5'-cyclic-GMP p	972	27	54.0	70	2	S28252	hypothetical prote
900	28	56.0	862	2	I50186	3',5'-cyclic-GMP p	973	27	54.0	79	2	AD1030	hypothetical prote
901	28	56.0	864	2	H85335	hypothetical prote	974	27	54.0	87	2	E69324	hypothetical prote
902	28	56.0	864	2	T04518	hypothetical prote	975	27	54.0	87	4	IMBP12	hypothetical immun
903	28	56.0	865	2	AG2023	hypothetical prote	976	27	54.0	94	2	G82024	hypothetical prote
904	28	56.0	867	2	H70411	alanine-tRNA ligas	977	27	54.0	94	2	B81244	conserved hypoteth
905	28	56.0	875	1	A36369	1-phosphatidylinos	978	27	54.0	96	2	C86649	hypothetical prote

```
979 27 54.0 97 2 T15891
980 27 54.0 98 2 AC2369
981 27 54.0 98 2 E84064
982 27 54.0 111 2 S22898
983 27 54.0 111 2 AF2121
984 27 54.0 112 2 S66865
985 27 54.0 115 2 A29156
986 27 54.0 115 2 A83056
987 27 54.0 117 2 S52966
988 27 54.0 117 2 S59150
989 27 54.0 117 2 S58996
990 27 54.0 118 2 JC2568
991 27 54.0 119 2 T34624
992 27 54.0 121 2 S76002
993 27 54.0 121 2 S78514
994 27 54.0 122 2 S73761
995 27 54.0 128 2 B70647
996 27 54.0 128 2 AH2322
997 27 54.0 128 2 AC3164
998 27 54.0 128 2 C82474
999 27 54.0 129 2 S73787
1000 27 54.0 132 2 C69850

ALIGNMENTS

RESULT 1
T38905
probable valine-pyruvate transaminase (BC 2.6.1.66) SPAC56E4.03 [similarity] - fission y
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38905
R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21813
A:Accession: T38905
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-474 <CON>
A:Cross-references: UNIPROT:O14192; UNIPARC:UPI000006A5B8; EMBL:Z99261; NID:g4038621; PI
A:Experimental source: strain 972h; cosmid c56E4
C:Genetics:
A:Gene: SPDB.SPAC56E4.03
A:Map position: 1
C:Superfamily: Escherichia coli valine-pyruvate transaminase
C:Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate
F:297/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 78.0%; Score 39; DB 2; Length 474;
Best Local Similarity 71.4%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2;

QY 1 FLWFEID 7
Db 390 FLWFEVD 396
|:|:|:|
|:|:|:|

RESULT 2
AI0180
conserved hypothetical protein YPO1485 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AI0180
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AI0180
A:Status: preliminary
A:Molecule type: DNA
```

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A:Residues: 1-587 <KUR>
A:Cross-references: UNIPROT:Q8ZG34; UNIPARC:UPI00000DC814; GB:AL590842; PIDN:CAC90308.1
C:Genetics:
A:Gene: YPO1485
C:Superfamily: uncharacterized conserved protein

Query Match 78.0%; Score 39; DB 2; Length 587;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9
Db 272 WFEIDVV 278
|:|:|:|
|:|:|:|

RESULT 3
S40136
T-cell receptor V-alpha 8.1b - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S40136
R:Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40133
A:Accession: S40136
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-110 <PLA>
A:Cross-references: UNIPARC:UPI0000116115; EMBL:X70308; NID:g437034; PIDN:CAA49787.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 74.0%; Score 37; DB 2; Length 110;
Best Local Similarity 55.6%; Pred. No. 6.2;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
Db 10 FLWLQDLV 18
|:|:|:|
|:|:|:|

RESULT 4
C29774
T-cell receptor alpha chain precursor V region (HAP41) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-May-1997
C:Accession: C29774
R:Yoshikai, Y.; Kimura, N.; Toyonaga, B.; Mak, T.W.
J. Exp. Med. 164, 90-103, 1986
A:title: Sequences and repertoire of human T cell receptor alpha chain variable region
A:Reference number: A92778; MUID:86253078; PMID:3088203
A:Accession: C29774
A:Molecule type: mRNA
A:Residues: 1-134 <YOS>
A:Cross-references: UNIPARC:UPI00001768CD
C:Genetics:
A:Map position: 14q11.2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 74.0%; Score 37; DB 2; Length 134;
Best Local Similarity 55.6%; Pred. No. 7.6;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
Db 10 FLWLQDLV 18
|:|:|:|
|:|:|:|

RESULT 5
AG1585
hypothetical protein lin1224 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
```

C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: AG1585  
 R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
 Science 294, 849-852, 2001  
 A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
 ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,  
 A;Title: Comparative genomics of *Listeria* species.  
 A;Reference number: AB1077; MUID:21537279; PMID:11679669  
 A;Accession: AG1585  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-150 <GLA>  
 A;Cross-references: UNIPROT:Q92CE8; UNIPARC:UPI00000CC4DD; GB:AL592022; PIDN:CAC96455.1;  
 A;Experimental source: strain Clip11262  
 C;Genetics:  
 A;Gene: lnl1224

Query Match 74.0%; Score 37; DB 2; Length 150;  
 Best Local Similarity 77.8%; Pred. No. 8.6;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 | | | | |  
 Db 116 FKWFEIDKV 124

RESULT 6  
 AH1231  
 hypothetical protein lml256 [imported] - *Listeria monocytogenes* (strain EGD-e)  
 C;Species: *Listeria monocytogenes*  
 C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: AH1231  
 R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
 Science 294, 849-852, 2001  
 A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
 ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,  
 A;Title: Comparative genomics of *Listeria* species.  
 A;Reference number: AB1077; MUID:21537279; PMID:11679669  
 A;Accession: AH1231  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-150 <GLA>  
 A;Cross-references: UNIPROT:Q8Y7L8; UNIPARC:UPI0000055488; GB:NC\_003210; PIDN:CAC99334.1  
 A;Experimental source: strain EGD-e  
 C;Genetics:  
 A;Gene: lml256

Query Match 74.0%; Score 37; DB 2; Length 150;  
 Best Local Similarity 77.8%; Pred. No. 8.6;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 | | | | |  
 Db 116 FKWFEIDKV 124

RESULT 7  
 B86815  
 hypothetical protein ypgD [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)  
 C;Species: *Lactococcus lactis* subsp. *lactis*  
 C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: B86815  
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli  
 Genome Res. 11, 731-753, 2001  
 A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s  
 A;Reference number: A86625; MUID:21235186; PMID:11337471  
 A;Accession: B86815  
 A;Status: preliminary  
 A;Molecule type: DNA

A;Residues: 1-529 <STO>  
 A;Cross-references: UNIPROT:Q9CFF6; UNIPARC:UPI00000CGA6E; GB:AE005176; PID:g12724521;  
 A;Experimental source: strain IL1403  
 C;Genetics:  
 A;Gene: ypgD

Query Match 74.0%; Score 37; DB 2; Length 529;  
 Best Local Similarity 66.7%; Pred. No. 33;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 | | | | |  
 Db 49 FLWLAIIDII 57

RESULT 8  
 A86641  
 hypothetical protein ybdC [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)  
 C;Species: *Lactococcus lactis* subsp. *lactis*  
 C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: A86641  
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli  
 Genome Res. 11, 731-753, 2001  
 A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s  
 A;Reference number: A86625; MUID:21235186; PMID:11337471  
 A;Accession: A86641  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-269 <STO>  
 A;Cross-references: UNIPROT:Q9CJ72; UNIPARC:UPI00000CG57F; GB:AE005176; PID:g12722977;  
 A;Experimental source: strain IL1403  
 C;Genetics:  
 A;Gene: ybdC  
 C;Superfamily: stage III sporulation protein; stage III sporulation protein homology

Query Match 72.0%; Score 36; DB 2; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEI 6  
 | | | | |  
 Db 155 FLWFEI 160

RESULT 9  
 E64815  
 ybH protein - *Escherichia coli* (strain K-12)  
 N;Alternate names: protein b0789  
 C;Species: *Escherichia coli*  
 C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
 C;Accession: E64815  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of *Escherichia coli* K-12.  
 A;Reference number: A64720; MUID:97426617; PMID:9278503  
 A;Accession: E64815  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-413 <BLAT>  
 A;Cross-references: UNIPROT:P75771; UNIPARC:UPI000013A35B; GB:AE000181; GB:U00096; NID:  
 A;Experimental source: strain K-12, substrain MG1655  
 C;Genetics:  
 A;Gene: ybhO  
 C;Superfamily: cardiolipin synthase

Query Match 72.0%; Score 36; DB 2; Length 413;  
 Best Local Similarity 62.5%; Pred. No. 39;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
 | | | | |  
 Db 40 FIWFEIDV 47

```
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: D69457
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-250 <KLE>
A:Cross-references: UNIPROT:O28612; UNIPARC:UPI0000056C57; GB:AE000989; GB:AE000782; NII

Query Match      70.0%; Score 35; DB 2; Length 250;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDI 8
Db      101 YLWFAVDV 108
      :|||:|:
      :|||:|:

RESULT 13
B82372
SpOoM-related protein VC0039 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82372
R:Heidelber, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82372
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <HEI>
A:Cross-references: UNIPROT:Q9KV00; UNIPARC:UPI00000C2BA2; GB:AE004096; GB:AE003852; NII
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0039
A:Map position: 1
C:Superfamily: Bacillus subtilis hypothetical protein ygal

Query Match      70.0%; Score 35; DB 2; Length 280;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEID 7
Db      229 LWFEVD 234
      :|||:|
      :|||:|

RESULT 14
T08856
hypothetical protein A_TM017A05.5 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08856
R:Waterston, R.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z16500
A:Accession: T08856
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-648 <WAT>
A:Cross-references: UNIPROT:Q9SLX4; UNIPARC:UPI000017AF64; EMBL:AF024504; NID:G2435510;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 47/3; 90/1; 120/1; 185/1; 208/2; 222/3; 570/3
A:Note: A_TM017A05.5

Query Match      70.0%; Score 35; DB 2; Length 648;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

probable synthetase ybho [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85587
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85587
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-413 <STO>
A:Cross-references: UNIPROT:P75771; UNIPARC:UPI000013A35B; GB:AE005174; NID:gl2513778; H
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ybho
C:Superfamily: cardiolipin synthase

Query Match      72.0%; Score 36; DB 2; Length 413;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDI 8
Db      40 FIWFEDDV 47
      :|||:|
      :|||:|

RESULT 11
C90737
cardiolipin synthetase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C90737
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C90737
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-413 <HAY>
A:Cross-references: UNIPROT:P75771; UNIPARC:UPI000013A35B; GB:BA0000007; PIDN:BA834290.1;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC80867
C:Superfamily: cardiolipin synthase

Query Match      72.0%; Score 36; DB 2; Length 413;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDI 8
Db      40 FIWFEDDV 47
      :|||:|
      :|||:|

RESULT 12
D69457
hypothetical protein AFI1661 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D69457
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uitterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
```

QY 2 LWFEID 7  
| | | | |  
Db 175 LWFEVD 180

## RESULT 15

T25325  
hypothetical protein T26H2.7 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T25325  
R;Matthews, L.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z20016  
A;Accession: T25325  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-848 <WIL>  
A;Cross-references: UNIPROT:O18139; UNIPARC:UPI000008117F; EMBL:Z82055; PIDN: CAB04848.1  
A;Experimental source: clone T26H2  
C;Genetics:  
A;Gene: CESP-T26H2.7  
A;Map position: 5  
A;Introns: 41/2; 129/3; 176/1; 254/2; 312/1; 388/1; 425/3; 466/1; 514/3; 557/3; 628/3; 6  
C;Superfamily: Caenorhabditis elegans hypothetical protein T26H2.7

Query Match 70.0%; Score 35; DB 2; Length 848;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEIDI 8  
| | | | |  
Db 699 LWFEQDI 705

## RESULT 16

T00842  
probable histidine kinase [imported] - Arabidopsis thaliana  
N;Alternate names: hypothetical protein Tl3L16.16  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: T00842; G84556  
R;de la Bastide, M.; Hameed, A.; Gnoj, L.; Jensen, K.; Shohdy, N.; Gottesman, T.; Haberm  
McCombie, W.R.  
submitted to the EMBL Data Library, January 1999  
A;Description: A. thaliana BAC Tl3L16 from chromosome IV, top arm.  
A;Reference number: Z14205  
A;Accession: T00842  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1190 <DEL>  
A;Cross-references: UNIPROT:Q7XJR4; UNIPARC:UPI0000017AFAC; EMBL:AC003952; NID:G2708736;  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84556  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1190 <STO>  
A;Cross-references: UNIPARC:UPI000017AFAC; GB:AE002093; NID:G2708752; PIDN: AAD03576.1; C  
C;Genetics:  
A;Gene: Tl3L16.16; At2g17820  
A;Map position: 2  
A;Introns: 68/3; 149/3; 407/3; 490/2; 543/3; 586/1; 616/1; 681/1; 704/2; 718/3; 764/3; 1

Query Match 70.0%; Score 35; DB 2; Length 1190;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEID 7  
| | | | |  
Db 671 LWFEVD 676

## RESULT 17

T52459  
sensory transduction histidine kinase 1 [validated] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 09-Jul-2004  
C;Accession: T52459  
R;Urao, T.; Yamaguchi-Shinozaki, K.; Hirayama, T.; Shinozaki, K.  
Plant Cell 11, 1743-1754, 1999  
A;Title: A transmembrane hybrid-type histidine kinase in Arabidopsis functions as as os  
A;Reference number: Z26082  
A;Accession: T52459  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1207 <URA>  
A;Cross-references: UNIPROT:Q9SXL4; UNIPARC:UPI000000A6640; EMBL:AB010914; PIDN: BAA32085  
C;Genetics:  
A;Gene: ATHK1  
A;Map position: 2  
C;Function:  
C;Keywords: involved in osmoregulation [validated, MUID:99418886]; probably function  
C;Keywords: transmembrane protein

Query Match 70.0%; Score 35; DB 2; Length 1207;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEID 7  
| | | | |  
Db 688 LWFEVD 693

## RESULT 18

AI2244  
dihydroneopterin aldolase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AI2244  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AI2244  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-121 <KUR>  
A;Cross-references: UNIPROT:Q9YRD6; UNIPARC:UPI000000CE7FC; GB:BA000019; PIDN: BAB75211.1  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr3512  
C;Superfamily: dihydroneopterin aldolase folA; dihydroneopterin aldolase homology

Query Match 68.0%; Score 34; DB 2; Length 121;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDI 8  
| | | | |  
Db 27 WFEVDV 32

## RESULT 19

AB0185  
probable membrane protein YPO1518 [imported] - Yersinia pestis (strain CO92)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AB0185  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AB0185  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-175 <KUR>  
A:Cross-references: UNIPROT:Q8ZG02; UNIPARC:UPI00000CD80B; GB:AL590842; PIDN:CAC90341.1;  
C:Genetics:  
A:Gene: YPO1518

Query Match 68.0%; Score 34; DB 2; Length 175;  
Best Local Similarity 57.1%; Pred. No. 38;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|||:|:  
73 FWFELD 79

Db

RESULT 20  
F71612  
Glycosyl transferase (novel euk. family) PFB0515w - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004  
C:Accession: F71612  
R: Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.  
A:Reference number: A71600; MUID:99021743; PMID:9804551  
A:Accession: F71612  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-209 <GAR>  
A:Cross-references: UNIPROT:Q96196; UNIPARC:UPI0000081DB1; GB:AE001400; GB:AE001362; NID  
A:Experimental source: clone 3D7  
C:Genetics:  
A:Gene: PFB0515w

Query Match 68.0%; Score 34; DB 2; Length 209;  
Best Local Similarity 75.0%; Pred. No. 45;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
|||:|:  
15 FLWFVINI 22

Db

RESULT 21  
AB1468  
ribosomal protein L1 [imported] - *Listeria innocua* (strain Clip11262)  
C:Species: *Listeria innocua*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AB1468  
R: Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Meok, C.; Schlatterer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A:Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AB1468  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-229 <GLA>  
A:Cross-references: UNIPROT:Q92F26; UNIPARC:UPI000000CC197; GB:AL592022; PIDN:CAC95514.1;  
A:Experimental source: strain Clip11262

C:Genetics:  
A:Gene: rplA  
C:Superfamily: ribosomal protein L1p/L10e

Query Match 68.0%; Score 34; DB 2; Length 229;  
Best Local Similarity 57.1%; Pred. No. 50;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
|||:|:  
108 WFEFDVI 114

Db

RESULT 22  
C90024  
hypothetical protein [imported] - *Staphylococcus aureus* (strain N315)  
C:Species: *Staphylococcus aureus*  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: C90024  
R: Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
A:Reference number: AB9758; MUID:21311952; PMID:11418146  
A:Accession: C90024  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-254 <KUR>  
A:Cross-references: UNIPROT:Q99508; UNIPARC:UPI00000546E8; GB:BA000018; PID:g13702064;  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA2059

Query Match 68.0%; Score 34; DB 2; Length 254;  
Best Local Similarity 71.4%; Pred. No. 56;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
|||:|:  
191 WFDMDIV 197

Db

RESULT 23  
T05592  
tyrosine transaminase homolog F9D16.70 - *Arabidopsis thaliana*  
C:Species: *Arabidopsis thaliana* (mouse-ear cross)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T05592  
R: Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15419  
A:Accession: T05592  
A:Molecule type: DNA  
A:Residues: 1-422 <BEV>  
A:Cross-references: UNIPROT:Q9SUR6; UNIPARC:UPI0000051FE7; EMBL:AL035394  
A:Experimental source: cultivar Columbia; BAC clone F9D16  
C:Genetics:  
A:Map position: 4  
A:Introns: 84/2; 197/3; 270/3; 290/3; 342/3; 374/1  
A:Note: F9D16.70  
C:Superfamily: tyrosine transaminase

Query Match 68.0%; Score 34; DB 2; Length 422;  
Best Local Similarity 62.5%; Pred. No. 96;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
|||:|:  
340 FLWTELDL 347

Db

RESULT 24

S44620  
C50C3.1 protein - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S44620  
R;Favell, A.D.  
submitted to the EMBL Data Library, May 1993  
A;Description: Sequence of the *C. elegans* cosmid C50C3.  
A;Reference number: S44620  
A;Accession: S44620  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-469 <PAV>  
A;Cross-references: UNIPROT:P34366; UNIPARC:UPI0000138831; EMBL:LI14433; NID:G289649; PID:G289649  
C;Genetics:  
A;Introns: 113/2; 125/3; 142/3; 181/1; 248/2; 355/3; 405/2

Query Match 68.0%; Score 34; DB 2; Length 469;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:|:|:  
Db 67 FIFWHD 73

RESULT 25  
S55593  
membrane protein SLS1 precursor - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: protein L3159; protein YLR139C  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
C;Accession: S55593; S59335; S64981; S72478  
R;Dufour, M.; Rouillard, J.; Mandart, E.; Lacroute, F.  
submitted to the EMBL Data Library, February 1995  
A;Description: SLS1, a new *Saccharomyces cerevisiae* gene, presenting a phenotype of synth  
A;Reference number: S55593  
A;Accession: S55593  
A;Molecule type: DNA  
A;Residues: 1-643 <DUF>  
A;Cross-references: UNIPROT:P42900; UNIPARC:UPI0000135A2E; EMBL:Z48452; NID:G683706; PID:G683706  
R;Delius, H.  
submitted to the EMBL Data Library, June 1995  
A;Description: 36.8 kb of *S. cerevisiae* chromosome XII including ACE2, CK11, PDC5, SLS1,  
A;Reference number: S59313  
A;Accession: S59335  
A;Molecule type: DNA  
A;Residues: 1-643 <DBL>  
A;Cross-references: UNIPARC:UPI0000135A2E; EMBL:X91250; NID:G995686; PID:G995709  
A;Experimental source: strain S288C  
R;Delius, H.; Hebling, U.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S64967  
A;Accession: S64981  
A;Molecule type: DNA  
A;Residues: 1-643 <DUF>  
A;Cross-references: UNIPARC:UPI0000135A2E; EMBL:Z73311; NID:G1360558; PID:e245576; PID:G1360558  
A;Experimental source: strain S288C  
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S64987  
A;Accession: S64988  
A;Molecule type: DNA  
A;Residues: 1-643 <RIE>  
A;Cross-references: UNIPARC:UPI0000135A2E; EMBL:Z73311; NID:G1360558; PID:e245576; PID:G1360558  
A;Experimental source: strain S288C  
R;Rouillard, J.M.; Dufour, M.E.; Theunissen, B.; Mandart, E.; Dujardin, G.; Lacroute, F.  
Mol. Gen. Genet. 252, 700-708, 1996  
A;Title: SLS1, a new *Saccharomyces cerevisiae* gene involved in mitochondrial metabolism,  
A;Reference number: S72478; MUID:97074886; PMID:8917313  
A;Accession: S72478  
A;Molecule type: DNA  
A;Residues: 1-643 <ROU>

A;Cross-references: UNIPARC:UPI0000135A2E; EMBL:Z48452; NID:G683706; PID:CAA88362.1; F  
C;Genetics:  
A;Gene: SGD:SLS1  
A;Cross-references: SGD:S0004129; MIPS:YLR139C  
A;Map position: 12R  
A;Genome: nuclear  
C;Keywords: mitochondrion

Query Match 68.0%; Score 34; DB 2; Length 643;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFED 7  
:|:|:|  
Db 477 IWFED 482

RESULT 26  
T49399  
hypothetical protein B1D4.140 [imported] - *Neurospora crassa*  
C;Species: *Neurospora crassa*  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C;Accession: T49399  
R;Schultze, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura  
submitted to the Protein Sequence Database, May 2000  
A;Reference number: Z25022  
A;Accession: T49399  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-912 <SCH>  
A;Cross-references: UNIPARC:UPI000017B46E; EMBL:AL355928; GSPDB:GN00116; NCSP:B1D4.140  
A;Experimental source: BAC clone B1D4; strain OR74A  
C;Genetics:  
A;Gene: NCSP:B1D4.140  
A;Map position: 6  
A;Introns: 702/1; 766/3

Query Match 68.0%; Score 34; DB 2; Length 912;  
Best Local Similarity 85.7%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWFEDI 8  
|:|:|:|  
Db 415 LWFESDI 421

RESULT 27  
T38841  
probable pre-mRNA splicing factor - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: *Schizosaccharomyces pombe*  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T38841  
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1995  
A;Reference number: Z21815  
A;Accession: T38841  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-2363 <GEN>  
A;Cross-references: UNIPROT:O14187; UNIPARC:UPI000006A413; EMBL:Z98530; PIDN:CAB11062.1  
A;Experimental source: strain 972H-; cosmid c4F8  
C;Genetics:  
A;Gene: SPDB:SPAC4F8.12c  
A;Map position: 1

Query Match 68.0%; Score 34; DB 2; Length 2363;  
Best Local Similarity 71.4%; Pred. No. 6.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
:|:|:|:|  
Db 948 YLWFEAD 954

## RESULT 28

C82565  
 hypothetical protein XP2378 [imported] - Xylella fastidiosa (strain 9a5c)  
 C:Species: Xylella fastidiosa  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: C82565  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; PMID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: C82565  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-55 <SIM>  
 A:Cross-references: UNIPROT:Q9PAW7; UNIPARC:UPI00000C2A15; GB:AE004047; GB:AE003849; NID: A82519  
 A:Experimental source: strain 9a5c  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328  
 A:Status: preliminary  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XP2378

Query Match 66.0%; Score 33; DB 2; Length 55;  
 Best Local Similarity 71.4%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
 | ||| : |  
 DB 24 FEWFELD 30

## RESULT 29

A82519  
 hypothetical protein XP2774 [imported] - Xylella fastidiosa (strain 9a5c)  
 C:Species: Xylella fastidiosa  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: A82519  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; PMID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: A82519  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-126 <SIM>  
 A:Cross-references: UNIPROT:Q9P9U7; UNIPARC:UPI00000C2B53; GB:AE004082; GB:AE003849; NID: A82519  
 A:Experimental source: strain 9a5c  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

Query Match 66.0%; Score 33; DB 2; Length 55;  
 Best Local Similarity 71.4%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
 | ||| : |  
 DB 24 FEWFELD 30

A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XP2774

Query Match 66.0%; Score 33; DB 2; Length 126;  
 Best Local Similarity 83.3%; Pred. No. 41;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEI 6  
 |||| : |  
 DB 20 FLWFPI 25

## RESULT 30

A1511  
 hypothetical protein homolog lin0633 [imported] - Listeria innocua (strain Clip11262)  
 C:Species: Listeria innocua  
 C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: A1511  
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. ; Jones, L.M.; Karst, U.  
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.  
 A:Reference number: A1077; PMID:21537279; PMID:11679669  
 A:Accession: A1511  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-143 <GLA>  
 A:Cross-references: UNIPROT:Q92E28; UNIPARC:UPI00000C2CF; GB:AL592022; PIDN:CAC95865.1;  
 A:Experimental source: strain Clip11262  
 C:Genetics:  
 A:Gene: lin0633  
 C:Superfamily: Bacillus subtilis conserved hypothetical protein ydGE

Query Match 66.0%; Score 33; DB 2; Length 143;  
 Best Local Similarity 57.1%; Pred. No. 47;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
 : ||| : |  
 DB 66 YLWFHVD 72

## RESULT 31

S76177  
 dihydronopterin aldolase (EC 4.1.2.25) - Synecocystis sp. (strain PCC 6803)  
 C:Species: Synecocystis sp.  
 A:Variety: PCC 6803  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
 C:Accession: S76177  
 R:Kansko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis s.

A:Reference number: S74322; MUID:97061201; PMID:8905231  
 A:Accession: S76177  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-150 <KAN>  
 A:Cross-references: UNIPARC:UPI0000164C69; EMBL:P09014; GB:AB001339; NID:g1653477; PIDN: A82519  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C:Superfamily: dihydronopterin aldolase folA; dihydronopterin aldolase homology  
 C:Keywords: aldehyde-lyase; carbon-carbon lyase; folate biosynthesis  
 Pf34-150/Domain: dihydronopterin aldolase homology <DHA>

Query Match 66.0%; Score 33; DB 1; Length 150;  
 Best Local Similarity 66.7%; Pred. No. 49;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



Qy 3 WFEIDI 8  
|||:  
Db 59 WFEVDL 64

RESULT 32  
A82343  
conserved hypothetical protein VC0266 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: A82343  
R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B. L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20408833; PMID:10952301  
A:Accession: A82343  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-190 <HEI>  
A:Cross-references: UNIPROT:Q9KV90; UNIPARC:UPI000000C2C4C; GB:AE004116; GB:AE003852; NID:10952301  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC0266  
A:Map position: 1

Query Match 66.0%; Score 33; DB 2; Length 190;  
Best Local Similarity 85.7%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WFEIDIV 9  
|||:  
Db 172 WFEQDIV 178

RESULT 33  
G86612  
hypothetical protein CPj0978 [imported] - Chlamydophila pneumoniae (strain J138)  
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001  
C:Accession: G86612  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise, N.  
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20330349; PMID:10871362  
A:Accession: G86612  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-218 <STO>  
A:Cross-references: UNIPARC:UPI000017A6AE; GB:BA000008; NID:g8979351; PIDN:BAA99185.1; G86612  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: CPj0978

Query Match 66.0%; Score 33; DB 2; Length 218;  
Best Local Similarity 71.4%; Pred. No. 73;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLWFEID 7  
|||:  
Db 120 FLWFEKD 126

RESULT 34  
A86316  
protein T10022.3 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: A86316  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Holt, D.F.; Bohnert, J.; Chao, M.; Chang, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A86316  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-226 <STO>  
A:Cross-references: UNIPROT:Q9LM40; UNIPARC:UPI00000988D7; GB:AE005172; NID:g8671786; C:Genetics:  
A:Gene: T10022.3  
A:Map position: 1

Query Match 66.0%; Score 33; DB 2; Length 226;  
Best Local Similarity 71.4%; Pred. No. 76;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLWFEID 7  
|||:  
Db 196 FLWFEID 202

RESULT 35  
H82616  
hypothetical protein XFI958 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: H82616  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: H82616  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-269 <SIM>  
A:Cross-references: UNIPROT:Q9PC27; UNIPARC:UPI000000C28B5; GB:AE004015; GB:AE003849; NID:10910347  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorri, H.; Pacincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laif chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawada A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XFI958

Query Match 66.0%; Score 33; DB 2; Length 269;  
Best Local Similarity 62.5%; Pred. No. 92;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LWFEIDIV 9  
|||:  
Db 242 LWFEIDLI 249

RESULT 36  
D95396  
probable polyketide synthase protein [imported] - Sinorhizobium meliloti (strain 1021)

C:Species: Sinorhizobium meliloti  
C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: D95396  
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A>Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: D95396  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-269 <KUR>  
A:Cross-references: UNIPROT:Q92Y12; UNIPARC:UPI00000CB2D1; GB:AE006469; PIDN:AAK65734.1  
A:Experimental source: strain 1021, megaplasmid pSymA  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Hubler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Sma1963  
A:Genome: plasmid

Query Match 66.0%; Score 33; DB 2; Length 269;  
Best Local Similarity 66.7%; Pred. No. 92;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDI 8  
|||:|:  
DB 107 WFEIDV 112

RESULT 37  
B71876  
probable prolipoprotein diacylglyceryl transferase - Helicobacter pylori (strain J99)  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: B71876  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A:Reference number: A71800; MUID:99120557; PMID:9923682  
A:Accession: B71876  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-283 <ARN>  
A:Cross-references: UNIPROT:Q9ZKP6; UNIPARC:UPI000012E601; GB:AE001518; GB:AE001439; NID  
A:Experimental source: strain J99  
C:Genetics:  
A:Gene: lgt  
C:Superfamily: prolipoprotein diacylglyceryl transferase

Query Match 66.0%; Score 33; DB 2; Length 283;  
Best Local Similarity 66.7%; Pred. No. 97;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDI 9  
|||:|:  
DB 63 FLWAEIGV 71

RESULT 38  
C64639  
prolipoprotein diacylglyceryl transferase (SC 2.4.99.-) - Helicobacter pylori (strain 26  
C:Species: Helicobacter pylori  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: C64639

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L  
Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: C64639  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-284 <TOM>  
A:Cross-references: UNIPROT:O25609; UNIPARC:UPI000012E602; GB:AE000604; GB:AE000511; NI  
C:Superfamily: prolipoprotein diacylglyceryl transferase  
C:Keywords: glycosyltransferase

Query Match 66.0%; Score 33; DB 1; Length 284;  
Best Local Similarity 66.7%; Pred. No. 98;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDI 9  
|||:|:  
DB 63 FLWAEIGV 71

RESULT 39  
AG2429  
delta-9 desaturase [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 05-Oct-2004  
C:Accession: AG2429  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, ;  
DNA Res. 8, 205-213, 2001  
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG2429  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-285 <KUR>  
A:Cross-references: UNIPROT:Q8YME3; UNIPARC:UPI00000CED0D; GB:BA000019; PIDN:BAB76690.1  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: desc  
C:Superfamily: acyl-CoA desaturase; stearyl-CoA desaturase homology

Query Match 66.0%; Score 33; DB 2; Length 285;  
Best Local Similarity 50.0%; Pred. No. 98;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
|||:|:  
DB 250 FQWWEVDV 257

RESULT 40  
F72011  
hypothetical protein CP0878 [imported] - Chlamydophila pneumoniae (strains CWL029 and A  
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: F72011; H81528  
R;Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.  
Nature Genet. 21, 385-389, 1999  
A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: F72011  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-343 <ARN>  
A:Cross-references: UNIPROT:Q9ZGT1; UNIPARC:UPI00000470C9; GB:AE001678; GB:AE001363; NI  
A:Experimental source: strain CWL029  
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000  
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A;Reference number: A81500; MUID:20150255; PMID:10684935  
A;Accession: H81528  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-343 <REA>  
A;Cross-references: UNIPARC:UPI00000470C8; GB:AE002246; GB:AE002161; NID:g7189785; PIDN:  
A;Experimental source: strain AR39, HL cells  
C;Genetics:  
A;Gene: CPn0978; CP0878  
C;Superfamily: Chlamydia hypothetical protein CPn0976

Query Match 66.0%; Score 33; DB 2; Length 343;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:|||||  
Db 120 FIWFEXD 126

RESULT 41  
G64206  
hexosephosphate transport protein uhpT homolog - Mycoplasma genitalium  
C;Species: Mycoplasma genitalium  
C;Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Oct-2004  
C;Accession: G64206  
R;Praser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
C.A.; Venter, J.C.  
Science 270, 397-403, 1995  
A;Title: The minimal gene complement of Mycoplasma genitalium.  
A;Reference number: A64200; MUID:96026346; PMID:7569993  
A;Accession: G64206  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-461 <TIGR>  
A;Cross-references: UNIPROT:P47307; UNIPARC:UPI00001391C6; GB:U39685; GB:I43967; NID:g38  
A;Experimental source: strain G-37  
C;Genetics:  
A;Genetic code: SGC3  
C;Superfamily: uncharacterized conserved protein

Query Match 66.0%; Score 33; DB 2; Length 461;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
|:|||||  
Db 175 FLWFESKI 182

RESULT 42  
T41409  
probable valine-pyruvate transaminase (EC 2.6.1.66) SPCC569.07 [similarity] - fission ye  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T41409  
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.  
submitted to the EMBL Data Library, May 1999  
A;Reference number: Z21992  
A;Accession: T41409  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-470 <WOO>  
A;Cross-references: UNIPROT:Q9Y7S6; UNIPARC:UPI000006B359; EMBL:AL049755; NID:g4757096;  
A;Experimental source: strain 972h-; cosmid c569  
C;Genetics:  
A;Gene: SPDB:SPCC569.07  
A;Map position: 3  
C;Superfamily: Escherichia coli valine-pyruvate transaminase  
C;Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate

F;293/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted  
Query Match 66.0%; Score 33; DB 2; Length 470;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:|||||  
Db 386 FLWVELD 392

RESULT 43  
S75961  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4.1b - Synechocystis sp. (strain PC  
N;Alternate names: protein sll10027  
C;Species: Synechocystis sp.  
A;Variety: PC 5803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S75961  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasu  
DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti  
s.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S75961  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-507 <KAN>  
A;Cross-references: UNIPROT:Q55464; UNIPARC:UPI0000003546; EMBL:D64006; GB:AB001339; NI  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Genetics:  
A;Gene: ndhD-1b  
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4  
C;Keywords: membrane-associated complex; NAD; oxidative phosphorylation; oxidoreductase

Query Match 66.0%; Score 33; DB 2; Length 507;  
Best Local Similarity 55.6%; Pred. No. 1.8e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
|:|||||  
Db 133 FLFFELEII 141

RESULT 44  
S42093  
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Neurospora crassa  
C;Species: Neurospora crassa  
C;Date: 20-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S42093  
R;Taleb, F.; Radford, A.  
submitted to the EMBL Data Library, February 1994  
A;Description: Cloning sequencing and homologies of the CBH-1 (exocellobiohydrolase) ge  
A;Reference number: S42093  
A;Accession: S42093  
A;Molecule type: DNA  
A;Residues: 1-516 <TAL>  
A;Cross-references: UNIPROT:P38676; UNIPARC:UPI000011D714; EMBL:X77778; NID:g456657; PI  
C;Genetics:  
A;Introns: 227/3  
C;Superfamily: cellulose 1,4-beta-cellobiosidase I; fungal cellulose-binding domain hom  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;485-516/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 66.0%; Score 33; DB 2; Length 516;  
Best Local Similarity 57.1%; Pred. No. 1.9e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEIDI 8  
|:|||||  
Db 139 LWFDVDM 145

RESULT 45

A69484

hypothetical protein AF1874 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C:Accession: A69484

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
A:Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea  
A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: A69484

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-546 <KLE>

A:Cross-references: UNIPROT:O29405; UNIPARC:UPI0000056869; GB:AE000973; GB:AE000782; NID:  
C:Superfamily: Pyrococcus horikoshii probable heliCase PH0917

Query Match 66.0%; Score 33; DB 2; Length 546;  
Best Local Similarity 42.9%; Pred. No. 2e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLWFEID 7  
Db 368 YIWYVD 374  
:::|:

RESULT 46

A85042

hypothetical protein AT4g03310 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C:Accession: A85042

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: A85042

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-562 <STO>

A:Cross-references: UNIPROT:Q9ZR00; UNIPARC:UPI000009541F; GB:NC\_001268; NID:g7270201; B:  
C:Genetics:

A:Gene: AT4g03310

A:Map position: 4

C:Superfamily: Arabidopsis hypothetical protein F7N22.18

Query Match 66.0%; Score 33; DB 2; Length 562;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LWFEID 7  
Db 101 LWFID 106  
|||:|

RESULT 47

T48539

probable potassium transport protein - Arabidopsis thaliana

N:Alternate names: protein T2P22.190

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C:Accession: T48539

R:Byvan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,  
submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24490

A:Accession: T48539

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-601 <BEV>  
A:Cross-references: UNIPROT:Q9LYF1; UNIPARC:UPI0000048B11; EMBL:AL163814  
A:Experimental source: cultivar Columbia; BAC clone T2P22  
C:Genetics:  
A:Map position: 5  
A:Introns: 94/1; 108/3; 145/2; 205/2; 230/3; 255/3; 279/3; 302/3; 328/3; 357/3; 390/1;  
A:Note: T2P22.190

Query Match 66.0%; Score 33; DB 2; Length 601;  
Best Local Similarity 55.6%; Pred. No. 2.2e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
DB 467 FLWTHVDIL 475

RESULT 48  
AG0155  
probable substrate-binding transport protein YP01273 [imported] - Yersinia pestis (strain  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AG0155  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AG0155  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-602 <KUR>  
A:Cross-references: UNIPROT:Q8ZGL6; UNIPARC:UPI000000DCB6; GB:AL590842; PIDN:CAC90106.1.  
C:Genetics:  
A:Gene: YP01273  
C:Superfamily: periplasmic oligopeptide-binding protein

Query Match 66.0%; Score 33; DB 2; Length 602;  
Best Local Similarity 62.5%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
DB 113 FSWIEVDI 120

RESULT 49  
F82442  
probable peptide ABC transporter, periplasmic peptide-binding protein VCA0591 [imported]  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: F82442  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.  
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: F82442  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-611 <HEI>  
A:Cross-references: UNIPROT:Q9KL28; UNIPARC:UPI000000C359B; GB:AE004389; GB:AE003853; NID  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VCA0591  
A:Map position: 2  
C:Superfamily: periplasmic oligopeptide-binding protein

Qy 1 PLWFEIDI 8  
| | | | |  
Db 120 FTWLEIDL 127

## RESULT 50

Tl3579  
hypothetical protein 52C10.1 - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 05-Oct-2004  
C;Accession: Tl3579  
R;Benos, P.  
submitted to the EMBL Data Library, February 1999  
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
A;Reference number: Z17690  
A;Accession: Tl3579  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-784 <BN>  
A;Cross-references: UNIPROT:O96841; UNIPARC:UPI000007C4A7; EMBL:AL035311; NID:e1373062;  
C;Genetics:  
A;Cross-references: FlyBase:FBgn0026309  
A;Map position: X  
A;Introns: 34/3; 473/1; 635/3; 734/2  
A;Note: EG:52C10.1

Query Match 66.0%; Score 33; DB 2; Length 784;  
Best Local Similarity 57.1%; Pred. No. 2.9e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LWFEIDI 8  
| | | | |  
Db 683 LWFDL 689

Search completed: May 9, 2006, 02:25:27  
Job time : 26.4 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 02:06:12 ; Search time 99.6 Seconds  
(without alignments)  
63.753 Million cell updates/sec

Title: US-09-870-216C-7

Perfect score: 50

Sequence: 1 FLWFEIDIV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	80.0	634	Q5FWJ4_MOUSE	Q5fwj4 mus musculus
2	39	78.0	266	Q6D9R7_ERWCT	Q6d9r7 erwinnia car
3	39	78.0	267	Q5DZJ4_VIBF1	Q5dzj4 vibrio fisc
4	39	78.0	474	O14192_SCHPO	O14192 schizosacch
5	39	78.0	587	Q8ZG34_YERPE	Q8zg34 yerinnia pe
6	39	78.0	587	Q66CA4_YERPS	Q66ca4 yerinnia ps
7	39	78.0	596	Q8IIA6_PLAF7	Q8iia6 plasmodium
8	39	78.0	1714	Q6IZ03_OSTNU	Q6iz03 ostinnia nu
9	38	76.0	588	Q7M2S2_PHOLL	Q7m2s2 photorhabdu
10	38	76.0	667	Q4WM85_ASPTU	Q4wm85 aspergillus
11	37	74.0	64	Q4XVT5_PLACH	Q4xvt5 plasmodium
12	37	74.0	150	Q8Y7L8_LISMO	Q8y7l8 listeria mo
13	37	74.0	150	Q92CE8_LISIN	Q92ce8 listeria in
14	37	74.0	198	Q7RSS9_PLAYO	Q7rss9 plasmodium
15	37	74.0	322	Q7UJ06_RHOBA	Q7uj06 rhodopirell
16	37	74.0	522	Q4XM13_PLACH	Q4xm13 plasmodium
17	37	74.0	523	Q4Z4D7_PLABE	Q4z4d7 plasmodium
18	37	74.0	529	Q9CFP6_LACLA	Q9cfp6 lactococcus
19	37	74.0	586	Q7N267_PHOLL	Q7n267 photorhabdu
20	37	74.0	587	Q6B3A0_9PROT	Q6b3a0 uncultured
21	37	74.0	713	Q7RVS4_NEUCR	Q7rvs4 neurospora
22	37	74.0	731	Q74693_NEUCR	Q74693 neurospora
23	36	72.0	129	Q8DKV4_SYNEL	Q8dkv4 synecococc
24	36	72.0	186	Q4GG68_9CNID	Q4gg68 montastraea
25	36	72.0	186	Q4GGF5_9CNID	Q4ggf5 montastraea
26	36	72.0	186	Q4GGC9_9CNID	Q4ggc9 montastraea
27	36	72.0	228	Q5QJN7_SALTY	Q5qjn7 salmonella
28	36	72.0	257	Q573H4_9BACT	Q573h4 vibrio fisc
29	36	72.0	262	Q5BIQ2_VIBF1	Q5biq2 vibrio fisc
30	36	72.0	264	Q8DDE9_VIBVU	Q8dde9 vibrio vuln
31	36	72.0	266	Q7MGK0_VIBVY	Q7mgk0 vibrio vuln

32	36	72.0	269	1	OXAAL_LACLA	Q9cj72 lactococcus
33	36	72.0	270	2	Q87KC8_VIBPA	Q87kc8 vibrio para
34	36	72.0	273	2	Q4WIX2_ASPTU	Q4wix2 aspergillus
35	36	72.0	331	2	Q93X27_9ROSI	Q93x27 populus eur
36	36	72.0	338	2	Q65BM9_HUMAN	Q65bm9 homo sapien
37	36	72.0	411	2	Q55T92_CRYNE	Q55t92 cryptococcu
38	36	72.0	413	1	YBHO_ECOLI6	Q8fj99 escherichia
39	36	72.0	413	1	YBHO_ECOLI	P75771 escherichia
40	36	72.0	413	2	Q5KJ49_CRYNE	Q5kja9 cryptococcu
41	36	72.0	445	2	Q70XS6_SCUCO	Q70xs6 scutigera c
42	36	72.0	590	1	SYD_PHOLL	Q7mb41 photorhabdu
43	36	72.0	667	1	HPSI_MACPA	Q80h13 macaca fasc
44	36	72.0	699	2	Q5R612_PONPY	Q5r612 pongo pygma
45	36	72.0	700	1	HPSI_HUMAN	Q92902 homo sapien
46	36	72.0	700	2	Q8WXS5_HUMAN	Q8wxs5 homo sapien
47	36	72.0	704	1	HPSI_MOUSE	Q89983 mus musculu
48	36	72.0	706	2	Q99MK7_RAT	Q99mk7 rattus norv
49	36	72.0	995	2	Q5CS74_CRYPV	Q5cs74 cryptospori
50	36	72.0	996	2	Q5CIE1_CRYHO	Q5cie1 cryptospori
51	36	72.0	1249	2	Q571R6_POPCA	Q571r6 populus can
52	36	72.0	1352	2	Q5B9T9_EMENI	Q5b9t9 aspergillus
53	35	70.0	21	2	Q4X877_PLACH	Q4x877 plasmodium
54	35	70.0	76	2	Q935T6_STRTR	Q935t6 streptococ
55	35	70.0	112	2	Q9WU87_MOUSE	Q9wu87 mus musculu
56	35	70.0	177	2	Q5YYS9_NOCPA	Q5yys9 nocardia fa
57	35	70.0	194	2	Q8VEN8_MOUSE	Q8ven8 mus musculu
58	35	70.0	205	2	Q83AZ7_COXBU	Q83az7 coxiella bu
59	35	70.0	232	2	Q8IXE0_HUMAN	Q8ixe0 homo sapien
60	35	70.0	250	1	Y1661_ARCFU	Q28612 archaeoglob
61	35	70.0	261	2	Q8ES40_OCEIH	Q8es40 oceanobacil
62	35	70.0	280	2	Q9KVV0_VIBCH	Q9kvv0 vibrio chol
63	35	70.0	284	1	FPG_COREF	Q8fp17 corynebacte
64	35	70.0	287	2	Q4NRR3_9DELT	Q4nrr3 anaeromyxob
65	35	70.0	309	2	Q7TRM3_MOUSE	Q7trm3 mus musculu
66	35	70.0	309	2	Q8VFT9_MOUSE	Q8vft9 mus musculu
67	35	70.0	311	2	Q7TRM1_MOUSE	Q7trm1 mus musculu
68	35	70.0	311	2	Q7TRM2_MOUSE	Q7trm2 mus musculu
69	35	70.0	311	2	Q8VF70_MOUSE	Q8vf70 mus musculu
70	35	70.0	311	2	Q8VFT7_MOUSE	Q8vft7 mus musculu
71	35	70.0	311	2	Q8VFT8_MOUSE	Q8vft8 mus musculu
72	35	70.0	314	2	Q4JXH7_CORJK	Q4jxh7 corynebacte
73	35	70.0	315	1	OL1H1_HUMAN	Q8ng94 homo sapien
74	35	70.0	322	2	Q758Z7_ASHGO	Q758z7 ashbya goss
75	35	70.0	323	2	Q7TRM0_MOUSE	Q7trm0 mus musculu
76	35	70.0	326	2	Q6IEX0_HUMAN	Q6iex0 homo sapien
77	35	70.0	326	2	Q8NH07_HUMAN	Q8nh07 homo sapien
78	35	70.0	332	2	Q4NGS0_9MCC	Q4ngs0 arthrobacte
79	35	70.0	358	2	Q74A18_GEOSL	Q74a18 geobacter s
80	35	70.0	392	2	Q89LF0_BRAJA	Q89lf0 bradyrhizob
81	35	70.0	495	2	Q6C551_YARLI	Q6c551 yarrowia li
82	35	70.0	518	2	Q8D8K8_VIBVU	Q8d8k8 vibrio vuln
83	35	70.0	535	2	Q7MJP6_VIBVY	Q7mjp6 vibrio vuln
84	35	70.0	647	2	Q73P12_TREDE	Q73p12 treponema d
85	35	70.0	667	2	Q5B359_EMENI	Q5b359 aspergillus
86	35	70.0	673	2	Q9SQ77_ARATH	Q9sq77 arabidopsis
87	35	70.0	765	2	Q4SA73_TETNG	Q4sa73 tetradodon n
88	35	70.0	766	2	Q4TNP1_9SPHN	Q4tnp1 erythrobact
89	35	70.0	848	2	O18139_CAEEL	O18139 caenorhadi
90	35	70.0	953	2	Q6FCX8_ACTAD	Q6fcx8 acinetobact
91	35	70.0	1190	2	Q7XJ44_ARATH	Q7xj44 arabidopsis
92	35	70.0	1207	2	Q9SXL4_ARATH	Q9sxl4 arabidopsis
93	35	70.0	2728	2	Q583U1_9TRYP	Q583u1 trypanosoma
94	34	68.0	64	2	Q6Z393_ORYSA	Q6z393 oryza sativ
95	34	68.0	90	2	Q6DS56_ARATH	Q6ds56 arabidopsis
96	34	68.0	91	2	Q6DS55_ARATH	Q6ds55 arabidopsis
97	34	68.0	92	2	Q6DS57_ARATH	Q6ds57 arabidopsis
98	34	68.0	106	2	Q4YFE0_PLABE	Q4yfe0 plasmodium
99	34	68.0	112	2	Q8D5K6_VIBVU	Q8d5k6 vibrio vuln
100	34	68.0	121	2	Q8YRD6_ANASP	Q8yrd6 anabaena ep
101	34	68.0	175	2	Q8ZG02_YERPE	Q8zg02 versinia pe
102	34	68.0	205	2	Q4R896_MACPA	Q4r896 macaca fasc
103	34	68.0	219	2	Q96196_PLAF7	Q96196 plasmodium
104	34	68.0	219	2	Q8KED3_CHLTE	Q8ked3 chlorobium

105	34	68.0	220	2	Q8CKX8_YERPE	Q8ckx8_yersinia pe	178	33	66.0	205	2	Q759N2_ASHGO	Q759n2_ashbya goss
106	34	68.0	227	1	RL1_MSFL	Q6f0k8_mesoplasma	179	33	66.0	206	2	Q7MJH0_VTBVY	Q7mjh0_vibrio vuln
107	34	68.0	229	1	RL1_LISIN	Q92f26_listeria in	180	33	66.0	208	2	Q9Z5S4_ZYMMO	Q9z5s4_zymomonas m
108	34	68.0	229	1	RL1_LISMF	Q92f26_listeria mo	181	33	66.0	215	2	Q7VIK2_HELHP	Q7vik2_helicobacte
109	34	68.0	230	1	RL1_OCEIH	Q8et22_oceanobacil	182	33	66.0	220	2	Q6SL21_9MAXI	Q6sl21_argulus ame
110	34	68.0	254	2	Q8KYA6_STAAU	Q8kya6_staphylococ	183	33	66.0	225	2	Q5BCS9_EMENI	Q5bcs9_aspergillus
111	34	68.0	254	2	Q6G758_STAAS	Q6g758_staphylococ	184	33	66.0	225	2	Q9LMS8_ARATH	Q9lms8_arabidopsis
112	34	68.0	254	2	Q6GEH0_STAAR	Q6geh0_staphylococ	185	33	66.0	226	2	Q9LM40_ARATH	Q9lm40_arabidopsis
113	34	68.0	254	2	Q5HDUS_STAAC	Q5hdus_staphylococ	186	33	66.0	226	2	Q6A7U6_PSONC	Q6a7u6_propionibac
114	34	68.0	254	2	Q7AA45_STAAN	Q7aa45_staphylococ	187	33	66.0	239	2	Q70LP5_PASMO	Q70lp5_pasteurella
115	34	68.0	254	2	Q8NVA7_STAAM	Q8nva7_staphylococ	188	33	66.0	239	2	Q9CP50_PASMO	Q9cp50_pasteurella
116	34	68.0	254	2	Q99S08_STAAM	Q99s08_staphylococ	189	33	66.0	247	2	Q6MPM4_BDEBA	Q6mpm4_bdellovibri
117	34	68.0	262	2	Q6LLI7_PHOPR	Q6lli7_photobacter	190	33	66.0	248	2	Q605K8_METCA	Q605k8_methylococ
118	34	68.0	273	2	Q75FX9_LEPIC	Q75fx9_leptospira	191	33	66.0	250	2	Q5NFT8_FRATT	Q5nft8_franciaella
119	34	68.0	276	2	Q8EXI9_LEFIN	Q8exy9_leptospira	192	33	66.0	257	2	Q73T63_WCPA	Q73t63_mycobacteri
120	34	68.0	276	2	Q66C73_YERPS	Q66c73_yersinia ps	193	33	66.0	265	2	Q940D2_LYCES	Q940d2_lycoperisio
121	34	68.0	287	2	Q5UQ00_MIMIV	Q5uq00_mimivirus	194	33	66.0	269	2	Q19703_CAEBL	Q19703_caenorhabdi
122	34	68.0	296	2	Q5UQ00_MIMIV	Q5uq00_corynebacte	195	33	66.0	269	2	Q87D44_XYLFT	Q87d44_xyllaella fas
123	34	68.0	311	1	FMT_RHME	Q92sh5_rhizobium m	196	33	66.0	269	2	Q9PC27_XYLFA	Q9pc27_xyllaella fas
124	34	68.0	364	2	Q8U0I0_PYRFU	Q8u0i0_pyrococcus	197	33	66.0	269	2	Q92Y12_RHIME	Q92y12_rhizobium m
125	34	68.0	375	2	Q9LGSJ4_ARATH	Q9lgsj4_arabidopsis	198	33	66.0	273	2	Q7NNS2_GLOVI	Q7nnr2_gloeobacter
126	34	68.0	378	2	Q8GMH1_STRGL	Q8gmh1_streptomyce	199	33	66.0	283	1	LGT_HELPY	Q9xcp6_helicobacte
127	34	68.0	390	2	Q57MM0_9TRYP	Q57mm0_trypanosoma	200	33	66.0	283	2	Q5CBA2_9THEM	Q5cba2_thermotoga
128	34	68.0	390	2	Q57WML_9TRYP	Q57wml_trypanosoma	201	33	66.0	284	1	Q6FB11_ACTAD	Q6fb11_acinetobact
129	34	68.0	401	2	Q87PS5_VIBPA	Q87ps5_vibrio para	202	33	66.0	284	1	LGT_HELPY	Q25609_helicobacte
130	34	68.0	416	2	Q64W68_BACFR	Q64w68_bacteroides	203	33	66.0	285	2	Q5M8I6_RAT	Q5m8i6_rattus norv
131	34	68.0	422	2	Q9S0R6_ARATH	Q9sur6_arabidopsis	204	33	66.0	285	2	Q8YME3_ANASP	Q8yme3_anabaena sp
132	34	68.0	430	2	Q4N418_THEPA	Q4n418_thailleria p	205	33	66.0	309	1	S39A2_HUMAN	Q9np94_homo sapien
133	34	68.0	441	2	Q6BHI0_DEBHA	Q6bhi0_debaryomyce	206	33	66.0	309	2	Q9UD20_HUMAN	Q9ud20_homo sapien
134	34	68.0	455	2	Q6CB41_YARLI	Q6cb41_yarrowia li	207	33	66.0	309	2	Q4QQJ1_HUMAN	Q4qqj1_homo sapien
135	34	68.0	469	1	YLJ1_CAEEL	P34366_caenorhabdi	208	33	66.0	309	2	Q4V9S4_HUMAN	Q4v9s4_homo sapien
136	34	68.0	505	2	Q6FPE9_CANGA	Q6fpe9_candida gla	209	33	66.0	309	2	Q4R9D0_MACFA	Q4r9d0_macaca fasc
137	34	68.0	523	2	Q5LPM8_SILPO	Q5lpm8_silicibacte	210	33	66.0	311	1	O1LIG2_HUMAN	Q8ngcl_homo sapien
138	34	68.0	529	2	Q8PYV7_METMA	Q8pyv7_methanosarc	211	33	66.0	312	2	Q8VFT6_MOUSE	Q8vft6_mus musculu
139	34	68.0	620	2	Q76E43_POEGU	Q76e43_poephila gu	212	33	66.0	313	2	Q8ET33_OCEIH	Q8et33_oceanobacil
140	34	68.0	632	2	Q96KV2_HUMAN	Q96kv2_homo sapien	213	33	66.0	314	2	Q5FP76_GLUOX	Q5fp76_gluconobact
141	34	68.0	635	2	Q9Y3H6_HUMAN	Q9y3h6_homo sapien	214	33	66.0	316	2	O24847_ACTAD	O24847_acinetobact
142	34	68.0	638	2	Q98V18_PBCV1	Q98vi8_paramecium	215	33	66.0	323	2	Q6FBT8_ACTAD	Q6fbt8_acinetobact
143	34	68.0	643	1	SLS1_YEAST	P42900_saccharomyc	216	33	66.0	324	2	Q9Z4K0_STRGR	Q9z4k0_streptomyce
144	34	68.0	651	2	Q6ZV26_HUMAN	Q6zv26_homo sapien	217	33	66.0	333	2	Q4WVY5_ASPFU	Q4wvy5_aspergillus
145	34	68.0	702	2	Q4RHQ0_TETNG	Q4rhq0_tetraodon n	218	33	66.0	343	2	Q926T1_CHLPN	Q926t1_chlamydia p
146	34	68.0	705	2	Q7RIS0_PLAYO	Q7ris0_plasmodium	219	33	66.0	345	2	Q61F09_HUMAN	Q61f09_homo sapien
147	34	68.0	711	2	Q6RJO3_CANGA	Q6rj03_candida gla	220	33	66.0	353	2	Q6FDH8_ACTAD	Q6fdh8_acinetobact
148	34	68.0	713	2	Q73ZV1_MYCPA	Q73zv1_mycobacteri	221	33	66.0	354	2	Q95429_PONPY	Q95429_pongo pygma
149	34	68.0	741	2	Q9C6V7_ARATH	Q9c6v7_arabidopsis	222	33	66.0	357	2	Q30222_AREBE	Q30222_ateles beiz
150	34	68.0	889	2	Q4F917_USTMA	Q4f917_ustilago ma	223	33	66.0	357	2	Q6AIR2_ORYSA	Q6air2_oryza sativ
151	34	68.0	915	2	Q4FUP5_9GAMM	Q4fup5_psychrobact	224	33	66.0	381	2	Q6YRC3_ONYPE	Q6yrc3_onion yello
152	34	68.0	944	2	Q5IVC1_MAGGR	Q5ivc1_magnaporthe	225	33	66.0	384	2	Q57Y29_9TRYP	Q57y29_trypanosoma
153	34	68.0	1010	2	Q6C961_YARLI	Q6c961_yarrowia li	226	33	66.0	384	2	Q57Y31_9TRYP	Q57y31_trypanosoma
154	34	68.0	1077	2	Q51E17_ENTHI	Q51e17_entamoeba h	227	33	66.0	385	2	Q57Y33_9TRYP	Q57y33_trypanosoma
155	34	68.0	1146	2	Q9F668_NEUCR	Q9f668_neurospora	228	33	66.0	403	2	Q9CXZ5_MOUSE	Q9cxz5_mus musculu
156	34	68.0	1561	2	Q675X9_9UROC	Q675x9_oikopleura	229	33	66.0	411	2	Q8C963_MOUSE	Q8c963_mus musculu
157	34	68.0	2363	2	O14187_SCHPO	O14187_schizosacch	230	33	66.0	430	2	O17697_CAEEL	O17697_caenorhabdi
158	34	68.0	2532	2	Q560W1_CRYNE	Q560w1_cryptococcu	231	33	66.0	441	2	Q9CNR2_PASMO	Q9cnr2_pasteurella
159	34	68.0	2532	2	Q5KPW2_CRYNE	Q5kpw2_cryptococcu	232	33	66.0	445	2	Q658G6_ORYSA	Q658g6_oryza sativ
160	33	66.0	44	2	Q6W215_RHLSN	Q6w215_rhizobium s	233	33	66.0	451	2	Q87JQ0_VIBPA	Q87jq0_vibrio para
161	33	66.0	55	2	Q9FAW7_XYLFA	Q9faw7_xyllaella fas	234	33	66.0	454	2	Q9XF16_FORIN	Q9xf16_forasythia i
162	33	66.0	83	2	Q4QGS1_RHTLO	Q4qgs1_rhizobium l	235	33	66.0	461	1	Y061_WTCGB	Y061_mycoplasma
163	33	66.0	85	2	Q4QQ13_HUMAN	Q4qq13_homo sapien	236	33	66.0	470	2	Q9Y7S6_SCHPO	Q9y7s6_schizosacch
164	33	66.0	85	2	Q4RC97_TETNG	Q4rc97_tetraodon n	237	33	66.0	473	2	Q8Q500_BRAJA	Q8q500_bradyrhizob
165	33	66.0	118	1	FOLB_SINY3	P74342_synechocyst	238	33	66.0	479	2	Q84M81_ORYSA	Q84m81_oryza sativ
166	33	66.0	120	2	Q7P637_FUSNV	Q7p637_fusobacteri	239	33	66.0	481	1	AMPA_CLOTE	AMPA_clostridium
167	33	66.0	125	2	Q5N221_SYNP6	Q5n221_synechococc	240	33	66.0	484	2	Q61W36_CAEER	Q61w36_caenorhabdi
168	33	66.0	126	2	Q879T7_XYLFT	Q879t7_xyllaella fas	241	33	66.0	491	2	Q39152_ARATH	Q39152_arabidopsis
169	33	66.0	126	2	Q9P9U7_XYLFA	Q9p9u7_xyllaella fas	242	33	66.0	501	2	Q4PDC0_USTMA	Q4pdc0_ustilago ma
170	33	66.0	143	2	Q92E28_LISIN	Q92e28_listeria in	243	33	66.0	501	2	Q51YN8_MAGGR	Q51yn8_magnaporthe
171	33	66.0	153	2	Q720G6_LISMF	Q720g6_listeria mo	244	33	66.0	503	2	Q9RK46_STRCO	Q9rk46_streptomyce
172	33	66.0	156	2	Q75KU3_ORYSA	Q75ku3_oryza sativ	245	33	66.0	507	2	Q55464_SYNY3	Q55464_synechocyst
173	33	66.0	160	2	Q615G4_ORYSA	Q615g4_oryza sativ	246	33	66.0	513	2	Q76CE9_CHICK	Q76ce9_gallus gall
174	33	66.0	186	2	Q6LRR0_PHOPR	Q6lrr0_photobacter	247	33	66.0	513	2	Q5I1H2_CHICK	Q5i1h2_gallus gall
175	33	66.0	190	2	Q9KV90_VIBCH	Q9kv90_vibrio chol	248	33	66.0	516	1	GUX1_NEUCR	P38676_neurospora
176	33	66.0	194	2	Q6CEH3_YARLI	Q6ceh3_yarrowia li	249	33	66.0	543	2	O2SLY4_SILPO	O2sls4_silicibacte
177	33	66.0	196	2	Q8A7F5_BACTN	Q8a7f5_bacteroides	250	33	66.0	546	2	O28405_ARCFU	O28405_archaeoglob



251	33	66.0	562	2	Q9ZR00_ARATH	Q9ZR00 arabisopsis	324	163	2	Q4HM54_CAMLA	Q4hm54 campylobact
252	33	66.0	588	2	Q413M5_GIBZE	Q413m5 gibberella	325	165	2	Q4LH93_9BURK	Q4lh93 burkholderi
253	33	66.0	598	1	VG9_BP03	Q37890 bacterioph	326	170	2	Q6E7U4_GVAO	Q6e7u4 adoxophyes
254	33	66.0	601	2	Q9LYF1_ARATH	Q9lyf1 arabisopsis	327	170	2	Q6E7V6_9BACU	Q6e7v6 pandemia li
255	33	66.0	602	2	Q8ZG16_YERPE	Q8zgi16 yerainia pe	328	170	2	Q6E7Z5_9BACU	Q6e7z5 amelia pall
256	33	66.0	602	2	Q66CU5_YERPS	Q66cus yerainia ps	329	178	2	Q51TP9_MAGGR	Q51tp9 magnaporthe
257	33	66.0	608	2	Q5ZRD3_LEGPH	Q5zrd3 legionella	330	183	1	Q6K7Q4_ORYSA	Q6k7q4 oryza sativ
258	33	66.0	611	2	Q9KLZ8_VIBCH	Q9klz8 vibrio chol	331	183	1	Y2092_SHIFL	F37789 shigella fl
259	33	66.0	617	2	Q8MLG6_DROME	Q8mlg6 drosophila	332	189	2	Q767F6_9ACTO	Q767f6 actinoptane
260	33	66.0	620	2	Q93R69_9MICO	Q93r69 microbacter	333	191	2	Q9AKB0_RICTY	Q9akb0 rickettsia
261	33	66.0	621	2	Q4WBG7_ASPFU	Q4wb77 aspergillus	334	194	2	Q8L9Q7_ARATH	Q8l9q7 arabisopsis
262	33	66.0	625	2	Q9MCK8_9CAUD	Q9mck8 streptococc	335	194	2	Q8PGR4_XYLPA	Q8pg44 xylella fas
263	33	66.0	629	2	Q6G030_BARQU	Q6g030 bartonella	336	197	2	Q6LLW7_PHOPR	Q6llw7 photobacter
264	33	66.0	631	2	Q7S272_NEUCR	Q7s272 neurospora	337	197	2	Q8RE64_FUSNN	Q8re64 fusobacteri
265	33	66.0	635	2	Q84GD0_CORGL	Q84gd0 corynebacte	338	198	1	FA18_DICDI	Q84195 dictyosteli
266	33	66.0	636	2	Q51OD1_MAGGR	Q51od1 magnaporthe	339	198	2	Q551W6_DICDI	Q551w6 dictyosteli
267	33	66.0	702	2	Q41EA2_GIBZE	Q41ea2 gibberella	340	204	2	Q586H6_9TRYP	Q586h6 trypanosoma
268	33	66.0	702	2	Q5ZIL0_CHICK	Q5zilo gallus gall	341	204	2	Q6UU03_ORYSA	Q6uu03 oryza sativ
269	33	66.0	707	2	Q6S761_CICAR	Q6s761 ciccer ariet	342	206	2	Q4KDQ0_PSEFP	Q4kdq0 pseudomonas
270	33	66.0	712	2	Q4INQ8_GIBZE	Q4inq8 gibberella	343	207	2	Q9WJD7_9HYME	Q9wj77 protaphidiu
271	33	66.0	712	2	Q6C6E3_YARLI	Q6c6e3 yarrowia li	344	214	2	Q83HC1_TROW8	Q83hc1 tropheryma
272	33	66.0	771	2	Q73PT9_TREDE	Q73pt9 treponema d	345	220	2	Q5LKL2_SILPO	Q5lkl2 silicibacte
273	33	66.0	784	2	Q96841_DROME	Q96841 drosophila	346	224	2	Q98MJ2_RHILO	Q98mj2 rhizobium l
274	33	66.0	790	2	Q6CJL8_KLUJA	Q6cjl8 kluyveromyc	347	226	1	RL1_MYCMS	Q6mry7 mycoplasma
275	33	66.0	816	2	Q09396_CAENRABDI	Q09396 caenorhabdi	348	226	1	RL1_TBEP4	Q83266 treponema p
276	33	66.0	875	2	Q9M2L2_ARATH	Q9m2l2 arabisopsis	349	227	2	Q65U79_MANSM	Q65u79 mantheimia
277	33	66.0	884	2	Q8X006_NEUCR	Q8x006 neurospora	350	229	1	RL1_CLOAB	Q97eg6 clostridium
278	33	66.0	897	1	SV1_FERPE	Q9xdb4 feryidobact	351	229	1	RL1_ENTFA	Q830q6 enterococcu
279	33	66.0	1015	2	Q5L7M5_BACFN	Q5l7m5 bacteroides	352	229	1	RL1_STAAR	Q69jd0 staphylococ
280	33	66.0	1015	2	Q64MU2_BACFR	Q64mu2 bacteroides	353	229	2	Q9LK42_ARATH	Q9lk42 arabisopsis
281	33	66.0	1024	2	Q8CCF7_MOUSE	Q8ccf7 mus musculus	354	230	1	RL1_BACAN	Q81vu2 bacillus an
282	33	66.0	1182	2	Q8QVF2_9REOV	Q8qvf2 eyach virus	355	230	1	RL1_BACC1	Q73fa8 bacillus ce
283	33	66.0	1182	2	Q9ENL3_9REOV	Q9enl3 colorado ti	356	230	1	RL1_BACC2	Q63ha2 bacillus ce
284	33	66.0	1194	2	Q4ILN4_GIBZE	Q4iln4 gibberella	357	230	1	RL1_BACHK	Q6hps0 bacillus th
285	33	66.0	1230	2	Q53R90_HUMAN	Q53r90 homo sapien	358	230	1	RL1_STAAM	Q66091 staphylococ
286	33	66.0	1374	1	DCRL_SCHPO	Q09884 schizosacch	359	230	1	RL1_STAAN	Q99w68 staphylococ
287	33	66.0	1420	2	Q55HQ4_CRYNE	Q55hq4 cryptococcu	360	230	1	RL1_STAAS	Q99w68 staphylococ
288	33	66.0	1420	2	Q5K790_CRYNE	Q5k790 cryptococcu	361	230	1	RL1_STAAM	Q66092 staphylococ
289	33	66.0	1608	2	Q54VR7_DICDI	Q54vr7 dictyosteli	362	230	2	Q6CVH7_KLUJA	Q6cvh7 kluyveromyc
290	33	66.0	1931	2	Q4REK5_TETNG	Q4rek5 tetraodon n	363	230	2	Q5HID7_STAAC	Q5hid7 staphylococ
291	33	66.0	1931	2	Q4S6W0_TETNG	Q4s6w0 tetraodon n	364	231	1	RL1_STREP	Q8ctt4 staphylococ
292	33	66.0	1982	2	Q5SPC5_BRARE	Q5spc5 brachydanio	365	231	2	Q4L3J7_STAHL	Q4l3j7 staphylococ
293	33	66.0	1997	1	OTOF_MOUSE	Q9hcl0 homo sapien	366	231	2	Q5HRL4_STAAB	Q5hrl4 staphylococ
294	33	66.0	1997	1	OTOF_MOUSE	Q9esf1 mus musculus	367	232	1	RL1_BACCR	Q81j52 bacillus ce
295	33	66.0	2122	2	Q54EA3_DICDI	Q54ea3 dictyosteli	368	232	1	RL1_BACST	P04447 bacillus st
296	33	66.0	2182	2	Q815E3_PLAP7	Q815e3 plasmodium	369	233	1	RL1_GEOKA	Q51420 geobacillus
297	33	66.0	2318	2	Q4RRM6_TETNG	Q4rrm6 tetraodon n	370	234	2	Q51J19_MAGGR	Q51j19 magnaporthe
298	32.5	65.0	328	2	Q8FW15_BRUSU	Q8fw15 bruceella su	371	237	2	Q41JV3_GIBZE	Q41jv3 gibberella
299	32.5	65.0	335	2	Q8U7D2_AGR75	Q8u7d2 agrobacteri	372	237	2	Q83FM9_TROWT	Q83fm9 tropheryma
300	32.5	65.0	586	2	Q5MKL8_BRARE	Q5mkl8 brachydanio	373	247	2	Q8A2E1_BACTN	Q8a2e1 bacteroides
301	32.5	65.0	586	2	Q7ZWK8_BRARE	Q7zwk8 brachydanio	374	248	1	GRAN_GVAO	Q91b74 adoxophyes
302	32.5	65.0	586	2	Q5XJ61_BRARE	Q5xj61 brachydanio	375	248	1	GRAN_GVCF	O18559 choristoneu
303	32.5	65.0	593	2	Q7M555_FUGRU	Q7m555 fugu rubrip	376	248	2	Q77C18_GVAO	Q77c18 adoxophyes
304	32	64.0	50	2	Q73PU9_TREDE	Q73pu9 treponema d	377	248	2	Q4LIP4_9BACU	Q4lip4 andraca bip
305	32	64.0	62	2	Q4H8U9_9DEIO	Q4h8u9 deinococcus	378	249	2	Q4W900_ASPFU	Q4w900 aspergillus
306	32	64.0	69	2	Q8L906_ARATH	Q8l906 arabisopsis	379	252	2	Q5WV04_LEGFL	Q5wv04 legionella
307	32	64.0	76	2	Q70CA6_STRTR	Q70ca6 streptococc	380	252	2	Q5X3L6_LEGPA	Q5x3l6 legionella
308	32	64.0	79	2	Q9RSV6_DEIRA	Q9rsv6 deinococcus	381	252	2	Q5XTX3_LEGPH	O5zt33 legionella
309	32	64.0	85	2	Q82SJ4_NITEU	Q82sj4 nitrosomona	382	252	2	Q92X70_RHIME	Q92x70 rhizobium m
310	32	64.0	101	1	RS6_THET2	P62666 thermus the	383	258	2	Q9V071_PYROCCU	Q9v071 pyrococcus
311	32	64.0	101	1	RS6_THET8	Q5slp8 thermus the	384	261	2	Q5G694_GOSHI	Q5g694 gossypium h
312	32	64.0	101	1	RS6_THETH	P23370 thermus the	385	263	2	Q67NE2_SYMTN	Q67ne2 symbiobacte
313	32	64.0	106	2	Q5L1N6_GEOKA	Q5l1n6 geobacillus	386	267	2	Q63KU4_BURPS	Q63ku4 burkholderi
314	32	64.0	109	2	Q7NC24_MYCCA	Q7nc24 mycoplasma	387	267	2	Q62C89_BURMA	Q62c89 burkholderi
315	32	64.0	123	2	Q7S8K9_ASHGO	Q7s8k9 ashbya goss	388	270	2	Q6GJ71_KLUJA	Q6cj71 kluyveromyc
316	32	64.0	140	2	Q6D6B9_ERWCT	Q6d6b9 erwinia car	389	270	2	Q982D9_RHILO	Q982d9 rhizobium l
317	32	64.0	143	2	Q6IJS8_DROME	Q6ijs8 drosophila	390	271	1	LGT_CAMJR	Q9pi98 campylobact
318	32	64.0	143	2	Q9KAJ9_BACHD	Q9kaj9 bacillus ha	391	271	1	LGT_CAMJR	Q5hw60 campylobact
319	32	64.0	144	2	Q63307_RAT	Q63307 rattus norv	392	271	2	Q4HFU2_CAMCO	Q4hfu2 campylobact
320	32	64.0	148	2	Q5P999_ANAMM	Q5p999 anaplasma m	393	271	2	Q4HLI8_CAMLA	Q4hli8 campylobact
321	32	64.0	152	2	Q4IIM2_GIBZE	Q4iim2 gibberella	394	272	1	Y415_MYCGE	P47655 mycoplasma
322	32	64.0	153	1	YXIK_BACSU	P42302 bacillus su	395	280	2	Q6FT41_CANGA	Q6ft41 candida gla
323	32	64.0	153	2	Q4PLV3_9RICK	Q4plv3 candidatus	396	284	1	ST2A1_HUMAN	Q06520 homo sapien

397	32	64.0	284	1	ST2A1_MACFA	P52842	macaca fasc	470	32	64.0	465	2	Q9KTG8_VIBCH	Q9ktg8	vibrio chol
398	32	64.0	287	1	ERMD_BACLI	Q03986	bacillus li	471	32	64.0	467	2	Q721D5_LISMF	Q721d5	listeria mo
399	32	64.0	287	1	ERMJ_BACAN	Q04720	bacillus an	472	32	64.0	467	2	Q8Y886_LISMO	Q8y886	listeria mo
400	32	64.0	287	1	ERMK_BACLI	P45438	bacillus li	473	32	64.0	468	2	Q4Q8W6_LEIMA	Q4q8w6	leishmania
401	32	64.0	287	2	Q9FT95_ARATH	Q9ft95	arabidopsis	474	32	64.0	472	2	Q4ZRV3_PSESY	Q4zrv3	pseudomonas
402	32	64.0	291	2	Q4WCH6_ASFPF	Q4wch6	aspergillus	475	32	64.0	480	2	Q7Q7B2_ANOGA	Q7q7b2	anopheles g
403	32	64.0	292	1	LGT_HELHP	Q7v1u4	bellolibacte	476	32	64.0	493	2	Q9LXN3_ARATH	Q9lxn3	arabidopsis
404	32	64.0	294	2	Q6MX3_BDEBA	Q6mx3	bdellovibri	477	32	64.0	493	2	Q9XG77_SIMCH	Q9xg77	simmondsia
405	32	64.0	295	2	Q65KW1_BACLD	Q65kw1	bacillus li	478	32	64.0	493	2	Q8KX50_SNP2	Q8kx50	synechococc
406	32	64.0	298	2	Q8A3E0_BACTN	Q8a3e0	bacteroides	479	32	64.0	494	2	Q874V7_PODAN	Q874v7	podospira a
407	32	64.0	301	2	Q54PH3_DICDI	Q54ph3	dictyosteli	480	32	64.0	499	2	Q6LT82_POHPR	Q6lt82	photobacter
408	32	64.0	301	2	Q5DNB3_9BILA	Q5dnb3	leptorhynch	481	32	64.0	501	2	Q9L9P6_LEGPN	Q9l9p6	legionella
409	32	64.0	306	2	Q61I76_CABBR	Q61i76	caenorhabdi	482	32	64.0	502	2	Q5WYF3_LEGPL	Q5wyf3	legionella
410	32	64.0	306	2	Q7V4O9_PROMM	Q7v4o9	prochloroco	483	32	64.0	502	2	Q5X701_LRGPA	Q5x701	legionella
411	32	64.0	309	1	Y4386_EHILLO	Q78666	rhizobium l	484	32	64.0	502	2	Q5ZX15_LEGPH	Q5zx15	legionella
412	32	64.0	309	2	Q6LT13_PHOPR	Q6lt13	photobacter	485	32	64.0	506	2	Q56V88_9ROSI	Q56v88	leptopus co
413	32	64.0	309	2	Q8DBM9_VIBVU	Q8dbm9	vibrio vuln	486	32	64.0	508	2	Q6NZW2_BRARE	Q6nzw2	brachydanio
414	32	64.0	309	2	Q7MI90_VIBVU	Q7mi90	vibrio vuln	487	32	64.0	510	2	Q4TB82_TETNG	Q4tb82	tetradodon n
415	32	64.0	310	2	Q4SV84_TETNG	Q4sv84	tetradodon n	488	32	64.0	511	1	VGLC_HHV11	P10228	human herpe
416	32	64.0	315	2	Q8Y107_RALSO	Q8y107	raistonia s	489	32	64.0	511	2	Q8UYA4_HHV1	Q8uya4	human herpe
417	32	64.0	327	2	Q5MOV5_STRT1	Q5mov5	streptococc	490	32	64.0	511	2	Q8UYE2_HHV1	Q8uye2	human herpe
418	32	64.0	328	1	Y084_STRR6	Q5m5el	streptococc	491	32	64.0	511	2	Q8UYF2_HHV1	Q8uyf2	human herpe
419	32	64.0	328	1	Y095_STRPN	P67331	streptococc	492	32	64.0	511	2	Q8UZ62_HHV1	Q8uz62	human herpe
420	32	64.0	328	1	Y1434_STRAS	P67330	streptococc	493	32	64.0	511	2	Q8UZ63_HHV1	Q8uz63	human herpe
421	32	64.0	328	1	Y1504_STRAS	P67329	streptococc	494	32	64.0	511	2	Q8UZ65_HHV1	Q8uz65	human herpe
422	32	64.0	328	1	Y630_STRP3	P67328	streptococc	495	32	64.0	511	2	Q8UZ66_HHV1	Q8uz66	human herpe
423	32	64.0	328	1	Y743_STRP6	Q8krv2	streptococc	496	32	64.0	511	2	Q8UZ68_HHV1	Q8uz68	human herpe
424	32	64.0	328	1	Y915_STRPY	Q5xcu5	streptococc	497	32	64.0	511	2	Q8UZ69_HHV1	Q8uz69	human herpe
425	32	64.0	328	1	Y973_STRP8	P67332	streptococc	498	32	64.0	511	2	Q8UZ70_HHV1	Q8uz70	human herpe
426	32	64.0	328	1	Q6VZD1_ARATH	P67331	streptococc	499	32	64.0	511	2	Q8UZ71_HHV1	Q8uz71	human herpe
427	32	64.0	333	2	Q6HB61_BACHK	Q8vzd1	arabidopsis	500	32	64.0	511	2	Q9WIW3_HHV1	Q9wiw3	human herpe
428	32	64.0	341	2	Q63IC9_BACCC	Q6hb61	bacillus th	501	32	64.0	512	2	Q95K28_MACFA	Q95k28	macaca fasc
429	32	64.0	341	2	Q63IC9_BACCC	Q6hb61	bacillus th	502	32	64.0	526	2	Q7NP39_GLOVI	Q7np39	gloeobacter
430	32	64.0	344	2	Q27247_METTH	Q27247	methanobact	503	32	64.0	530	2	Q8Z372_ORISA	Q8z372	oryza sativ
431	32	64.0	356	2	Q9M634_CVACA	Q9m634	cyanidulim c	504	32	64.0	537	2	Q8S5V1_ORISA	Q8s5v1	oryza sativ
432	32	64.0	357	2	Q97YW8_SULSO	Q97yw8	pyrococcus	505	32	64.0	555	2	Q54ER7_DICDI	Q54er7	dictyosteli
433	32	64.0	359	2	Q5JG10_PVRKO	Q5jg10	pyrococcus	506	32	64.0	560	2	Q4J6H9_SULAC	Q4j6h9	sulfolobus
434	32	64.0	360	2	Q07866_STRPN	O07866	streptococc	507	32	64.0	562	2	Q9FLI8_ARATH	Q9fli8	arabidopsis
435	32	64.0	361	2	Q4KXO0_STRPN	Q4kxo0	streptococc	508	32	64.0	568	2	Q8VYR9_ARATH	Q8vyr9	arabidopsis
436	32	64.0	362	2	Q23864_DICDI	Q23864	dictyosteli	509	32	64.0	574	2	Q9YRZ3_ARATH	Q9yrz3	arabidopsis
437	32	64.0	364	2	Q4LAD4_STAHH	Q4lad4	staphylococ	510	32	64.0	580	2	Q6MUH7_MYCMS	Q6muh7	mycoplasma
438	32	64.0	377	2	Q76653_CABEL	O76653	caenorhabdi	511	32	64.0	592	2	Q52BS2_MAGGR	Q52bs2	magnaporthe
439	32	64.0	390	2	Q8LEQ6_ARATH	Q8leq6	arabidopsis	512	32	64.0	593	1	MUTL_LEPIN	Q72pf7	leptosira
440	32	64.0	392	2	Q8FVC5_LILLO	Q8fvc5	lilium long	513	32	64.0	593	1	MUTL_LEPIN	Q8f6x4	leptosira
441	32	64.0	392	2	Q6DAK5_ERWCT	Q6dak2	erwinia car	514	32	64.0	594	2	Q7QHJ4_ANOGA	Q7qhj4	anopheles g
442	32	64.0	393	2	Q4LI15_9BURL	Q4li15	burkholderi	515	32	64.0	596	2	Q5BE16_EMENI	Q5be16	aspergillus
443	32	64.0	394	2	Q739L7_BACCL	Q739l7	bacillus ce	516	32	64.0	596	2	Q9V766_DROME	Q9v766	drosophila
444	32	64.0	395	2	Q63V02_BURPS	Q63v02	burkholderi	517	32	64.0	614	2	Q8HAK4_9CAUD	Q8hak4	burkholderi
445	32	64.0	395	2	Q62JP5_BURMA	Q62jp5	burkholderi	518	32	64.0	614	2	Q6UK93_9CAUD	Q6uk93	burkholderi
446	32	64.0	396	2	Q7XBT8_ORYSA	O7xbt8	oryza sativ	519	32	64.0	614	2	Q6UIX2_9CAUD	Q6uix2	burkholderi
447	32	64.0	396	2	Q9FRQ3_ORYSA	Q9frq3	oryza sativ	520	32	64.0	615	1	LQWT2_MOUSE	Q8byr1	mus musculu
448	32	64.0	399	2	Q623M9_CABBR	Q623m9	caenorhabdi	521	32	64.0	622	2	Q61FD5_CABBR	Q61fd9	caenorhabdi
449	32	64.0	400	2	Q9KDT4_BACHD	Q9kdt4	bacillus ha	522	32	64.0	627	2	Q5Z8T1_ORYSA	Q5z8t1	oryza sativ
450	32	64.0	403	2	Q59LL2_CANAL	Q59ll2	candida alb	523	32	64.0	628	2	Q57D00_BRUAB	Q57d00	bruceella ab
451	32	64.0	414	2	Q5LEZ6_BACFN	Q5lez6	bacteroides	524	32	64.0	628	2	Q8GOF6_BRUSE	Q8gof6	bruceella su
452	32	64.0	415	2	Q5EN01_MAGGR	Q5en01	magnaporthe	525	32	64.0	628	2	Q8VHP6_BRUME	Q8vhp6	bruceella me
453	32	64.0	415	2	Q51Z99_MAGGR	Q51z99	magnaporthe	526	32	64.0	633	2	Q8B8K3_GRATL	Q8b8k3	gracilaria
454	32	64.0	416	2	Q4UFF8_THEAN	Q4uff8	theileria a	527	32	64.0	637	2	Q91909_ABRPE	Q919y9	aeropyrum p
455	32	64.0	418	2	Q8VZ82_ARATH	Q8vz82	arabidopsis	528	32	64.0	639	2	Q9LEV5_ARATH	Q9lev5	arabidopsis
456	32	64.0	420	1	ECTB_STRCH	Q6cuy9	streptomyce	529	32	64.0	644	2	Q9C5N2_ARATH	Q9c5n2	arabidopsis
457	32	64.0	420	1	ECTB_STRCH	Q82914	streptomyce	530	32	64.0	656	2	Q59G95_HUMAN	Q59g95	homo sapien
458	32	64.0	423	1	ECTB_STRCH	Q82914	streptomyce	531	32	64.0	664	2	Q81KC7_PLAF7	Q81kc7	plasmodium
459	32	64.0	424	2	Q84UD0_BRAOL	Q84ud0	brassica ol	532	32	64.0	664	2	Q4N5M4_THEPA	Q4n5m4	theileria p
460	32	64.0	425	2	Q5WBPO_BACSK	Q5wbpo	bacillus cl	533	32	64.0	669	2	Q6DJSC_XENTR	Q6djs6	xenopus tro
461	32	64.0	435	2	Q64VY8_BACFR	Q64vy8	bacteroides	534	32	64.0	676	2	Q5GH66_MOUSE	Q5gh66	mus musculu
462	32	64.0	439	2	Q8BJZ3_SHEON	Q8bjz3	shewanella	535	32	64.0	694	2	Q4WY80_ASFPF	Q4wy80	aspergillus
463	32	64.0	447	2	O04114_PPRFR	O04114	perilla fru	536	32	64.0	703	2	Q6A048_MOUSE	Q6a048	mus musculu
464	32	64.0	448	2	Q9SUR7_ARATH	Q9sur7	arabidopsis	537	32	64.0	706	2	Q4P8Y5_USTMA	Q4p8y5	ustilago ma
465	32	64.0	457	2	Q4J737_SULAC	Q4j737	sulfolobus	538	32	64.0	707	2	Q55JR7_MACFA	Q55jr7	macaca fasc
466	32	64.0	458	2	Q96XT8_SULTO	Q96xt8	sulfolobus	539	32	64.0	720	1	VF19_BPAPF	Q9fci9	bacterioph
467	32	64.0	464	2	Q57MQ1_SALCH	Q57mq1	salmonella	540	32	64.0	732	2	Q75003_GRIFR	Q75003	grifolia fro
468	32	64.0	464	2	Q8Z5H5_SALTI	Q8z5h5	salmonella	541	32	64.0	734	2	Q4QD77_LEIMA	Q4qd77	leishmania
469	32	64.0	464	2	Q9F799_SALTY	Q9f799	salmonella	542	32	64.0	747	1	Y4928_PSEAE	Q9hun6	pseudomonas

543	32	64.0	750	2	Q4N0G3_THEPA	Q4n0g3 theileria p	616	31	62.0	113	2	Q6LYJ7_METMP	O6lyj7 methanococ
544	32	64.0	751	2	Q9UV63_PLESA	Q9uv63 pleurotus s	617	31	62.0	113	2	Q4KNV9_FRANO	O4knv9 francisella
545	32	64.0	782	1	SYMC_SCHPO	Q9uuf2 schizosacch	618	31	62.0	113	2	Q4KNV3_GGAMM	O4knv3 francisella
546	32	64.0	799	1	TMP66_MOUSE	Q9dbi0 mus musculus	619	31	62.0	113	2	Q4KNV1_9PROT	O4knv1 uncultured
547	32	64.0	799	2	O6PP94_MOUSE	O6pp94 mus musculus	620	31	62.0	113	2	Q4KNV9_9PROT	O4knv9 uncultured
548	32	64.0	802	1	SYEB_BUCBP	P59505 buchnera ap	621	31	62.0	113	2	Q4KNV5_GGAMM	O4knv5 francisella
549	32	64.0	805	2	Q59LM6_CANAL	Q59lme candida alb	622	31	62.0	113	2	Q4KNV2_FRATT	O4knv2 francisella
550	32	64.0	820	2	Q73RP0_TREDE	Q73rf0 treponema d	623	31	62.0	113	2	Q4KNX7_FRATT	O4knx7 francisella
551	32	64.0	848	1	DRL32_ARATH	O22224 arabidopsis	624	31	62.0	113	2	Q4KNW2_FRATU	O4knw2 francisella
552	32	64.0	861	1	Y2162_ARATH	O22224 arabidopsis	625	31	62.0	113	2	Q4KNW8_FRATU	O4knw8 francisella
553	32	64.0	867	2	O6BTY1_DEBHA	O6bty1 debaryomyce	626	31	62.0	113	2	Q4KNV2_9PROT	O4knv2 uncultured
554	32	64.0	870	2	Q750Q5_ASHGO	Q750q5 ashbya goss	627	31	62.0	114	2	Q5RLC0_MOUSE	O5rlc0 mus musculu
555	32	64.0	872	2	Q72916_DESVH	Q72916 desulfovibr	628	31	62.0	114	2	Q5RLP6_MOUSE	O5rlp6 mus musculu
556	32	64.0	878	1	SYV_METUA	Q58413 methanococc	629	31	62.0	115	2	Q9XSE6_ZYMMO	O9xse6 zymomonas m
557	32	64.0	884	2	O629E6_CAEBR	O629e6 caenorhabdi	630	31	62.0	121	2	Q677V4_9VIRU	O677v4 cyprinus ca
558	32	64.0	885	1	TRPC2_RAT	Q9r283 rattus norv	631	31	62.0	122	2	Q9LXW2_ARATH	O9lwx2 arabidopsis
559	32	64.0	886	2	O7YRE3_PITIR	Q7yre3 pithecia ir	632	31	62.0	129	2	Q9LR39_ARATH	O9lr39 arabidopsis
560	32	64.0	889	2	O7YRE4_AOTTR	Q7yre4 aotus trivi	633	31	62.0	133	2	Q9PBB6_XYLFA	Q9pbb6 xyliella fas
561	32	64.0	890	2	O6S7D9_ALOPE	Q6s7d9 alouatta se	634	31	62.0	140	2	Q82LD4_STRAW	O82ld4 streptomyce
562	32	64.0	890	2	O6S7E0_ALOPA	Q6s7e0 alouatta pa	635	31	62.0	144	2	Q72QC1_LEPIC	Q72qc1 leptospira
563	32	64.0	890	2	O6S7E1_ALOPE	O6s7e1 alouatta be	636	31	62.0	144	2	O8PFS8_LEPIN	O8pfs8 leptospira
564	32	64.0	890	2	O7YRE0_SAGOB	Q7yre0 saguinus oe	637	31	62.0	145	2	O4NS74_9DELT	O4ns74 anaeromyxob
565	32	64.0	890	2	O7YRE1_SALSC	Q7yre1 saimiri sci	638	31	62.0	145	2	Q7N2Y4_PHOLL	Q7n2y4 photorhabdu
566	32	64.0	890	2	O7YRE2_ATEGE	Q7yre2 ateles geof	639	31	62.0	145	2	Q8CEQ2_MOUSE	Q8ceq2 mus musculu
567	32	64.0	905	2	O5WRQ0_CAEBL	Q5wrq0 caenorhabdi	640	31	62.0	145	2	Q73814_CYPCA	Q73814 cyprinus ca
568	32	64.0	906	2	O8NFS2_HUMAN	Q8nfs2 homo sapien	641	31	62.0	146	2	Q7VOC2_PROMP	Q7voc2 prochloroco
569	32	64.0	911	2	O8NFS3_HUMAN	Q8nfs3 homo sapien	642	31	62.0	147	2	Q8Y9A8_LISMO	O8y9a8 listeria mo
570	32	64.0	912	2	O9LDK6_ARATH	Q9ldk6 arabidopsis	643	31	62.0	147	2	Q722S6_LISMP	Q722s6 listeria mo
571	32	64.0	915	1	MGR7_HUMAN	Q14831 homo sapien	644	31	62.0	155	2	Q5HC79_EHRRG	Q5hc79 ehrlichia r
572	32	64.0	915	1	MGR7_MOUSE	Q68ed2 mus musculu	645	31	62.0	157	2	Q7Y2J3_9CAUD	Q7y2j3 stx2 conver
573	32	64.0	915	1	MGR7_RAT	P35400 rattus norv	646	31	62.0	157	2	Q8SC37_9CAUD	Q8sc37 stx2 conver
574	32	64.0	920	1	Q41WD0_AZOVI	Q4iwd0 azotobacter	647	31	62.0	157	2	Q9KXE0_ECO57	Q9kxe0 escherichia
575	32	64.0	921	2	O22515_CAEBL	O22515 caenorhabdi	648	31	62.0	158	2	Q9YXS6_ANASP	Q9yxs6 anabaena sp
576	32	64.0	922	2	O5RDQ8_PONPY	O5rdq8 pongo pygma	649	31	62.0	159	2	Q9EX27_STRCO	Q9ex27 streptomyce
577	32	64.0	924	2	O8NFS4_HUMAN	Q8nfs4 homo sapien	650	31	62.0	162	2	Q5FP97_EHRRG	Q5fp97 ehrlichia r
578	32	64.0	950	1	GYP2_YEAST	P53258 saccharomyc	651	31	62.0	162	2	Q6ACV1_LEIXX	Q6acv1 leifsonia x
579	32	64.0	951	2	Q60W90_CAEBR	Q60w90 caenorhabdi	652	31	62.0	166	2	Q8U8R3_AGR75	Q8u8r3 agrobacteri
580	32	64.0	991	2	O89HF0_BRAJA	Q89hf0 bradyrhizob	653	31	62.0	173	1	RPA4_SCHPO	Q43036 schizosacch
581	32	64.0	993	2	Q4T361_TETNG	Q4t361 tetraodon n	654	31	62.0	176	2	Q5TNU3_ANOGA	O5tnu3 anopheles g
582	32	64.0	1001	1	Q4PNF6_9BACT	O4pnf6 uncultured	655	31	62.0	178	2	O6C4X8_YARLI	O6c4x8 yarrowia li
583	32	64.0	1021	1	PEX5_ASHGO	Q74213 ashbya goss	656	31	62.0	180	2	O805A7_CHICK	O805a7 gallus gall
584	32	64.0	1047	2	Q7UJA2_RHOBA	Q7uja2 rhodopirell	657	31	62.0	181	2	Q605F7_METCA	Q605f7 methylococc
585	32	64.0	1076	2	Q4UDW9_THEAN	Q4udw9 theileria a	658	31	62.0	184	2	O5FCQ6_EHRRW	O5fcq6 ehrlichia r
586	32	64.0	1092	2	Q4P714_USITWA	Q4p714 ustilago ma	659	31	62.0	189	2	Q4WDM1_ASPPU	Q4wdm1 aspergillus
587	32	64.0	1119	2	O5F0M4_MOUSE	O5f0m4 mus musculu	660	31	62.0	191	2	Q9CBS1_MYCLE	O9cbn1 mycobacteri
588	32	64.0	1136	2	O50NK1_ENTHI	O50nk1 entamoeba h	661	31	62.0	192	2	O5LSX2_SILPO	O5lsx2 silicibacte
589	32	64.0	1156	2	Q4RWK3_TETNG	Q4rwk3 tetraodon n	662	31	62.0	197	2	Q8YT77_ANASP	Q8yt77 anabaena sp
590	32	64.0	1172	1	TRPC2_MOUSE	Q9r244 mus musculu	663	31	62.0	198	2	Q63RB9_BURPS	Q63rb9 burkholderi
591	32	64.0	1176	2	O6F749_ACIAD	O6f749 acinetobact	664	31	62.0	200	2	Q678B0_9VIRU	Q678b0 lymphocysti
592	32	64.0	1186	2	Q8JH78_BRARE	O8jh78 brachydanio	665	31	62.0	201	2	Q601G5_AVIMR	O601g5 mycoplasma
593	32	64.0	1317	2	Q7PQ15_ANOGA	O7pq15 anopheles g	666	31	62.0	202	2	Q9PPD1_AVIMR	O9fpd1 avicennia m
594	32	64.0	1342	1	RPOB_BUCAP	P41184 buchnera ap	667	31	62.0	204	2	Q83111_ENTFA	Q83111 enterococcu
595	32	64.0	1370	1	DP2L_HALSA	Q9hm88 halobacteri	668	31	62.0	206	2	Q816T5_PLAP7	Q816t5 plasmodium
596	32	64.0	1391	1	Q5AVS1_EMENI	Q5avs1 aspergillus	669	31	62.0	211	2	Q859C2_9CAUD	Q859c2 bacterioph
597	32	64.0	1551	2	Q4S523_TETNG	Q4s523 tetraodon n	670	31	62.0	213	2	Q9ZXB1_BPHCN	O9zxb1 bacterioph
598	32	64.0	1586	2	Q8TWJ3_METKA	O8twj3 methanopyru	671	31	62.0	213	2	Q8EAH8_SHEON	O8eah8 shewanella
599	32	64.0	1786	1	YCF1_ARATH	P56785 arabidopsis	672	31	62.0	213	2	Q7UTF7_RHOBA	Q7utf7 rhodopirell
600	32	64.0	1838	2	O861V6_DICDI	O861v6 dicystosteli	673	31	62.0	218	2	O5E015_VIBF1	O5e015 vibrio fisc
601	32	64.0	2024	2	Q7NUT7_CHRVO	Q7nut7 chromobacte	674	31	62.0	220	2	Q9VR65_DROME	Q9vr65 drosophila
602	32	64.0	3498	2	Q20497_CAEBL	Q20497 caenorhabdi	675	31	62.0	222	2	Q6SNB8_TRAAU	Q6snb8 trachypithe
603	32	64.0	3779	2	O5GQB9_9CAUD	O5gqb9 bacterioph	676	31	62.0	223	2	O5XCZ6_STRP6	O5xcz6 streptococc
604	32	64.0	6973	2	Q7QXR7_GIALA	Q7qxr7 giardia lam	677	31	62.0	223	2	Q9AOK2_STRPY	O9aok2 streptococc
605	31.5	63.0	259	1	Y039_THEMA	Q9wxp6 thermotoga	678	31	62.0	223	2	Q8PIL8_STRP8	O8pil8 streptococc
606	31.5	63.0	527	2	Q8JU08_ASPNG	Q8ju08 aspergillus	679	31	62.0	223	2	Q8K837_STRP3	O8k837 streptococc
607	31	62.0	58	2	Q7MBP1_VIBVY	Q7mbp1 vibrio vuln	680	31	62.0	225	2	Q6Z4D6_ORISA	Q6z4d6 oryza sativ
608	31	62.0	63	2	Q69234_BHV4	Q69234 bovine herp	681	31	62.0	229	1	RL1_CLOPE	Q8xhfs clostridium
609	31	62.0	64	2	Q92H47_RICCN	Q92h47 rickettsia	682	31	62.0	229	1	RL1_CLOTE	Q89on2 clostridium
610	31	62.0	67	2	Q8VAK4_WSSV	Q8vak4 white spot	683	31	62.0	229	1	RL1_LISMO	O8yaa4 listeria mo
611	31	62.0	69	2	Q92X94_RHIME	Q92x94 rhizobium m	684	31	62.0	231	1	RL1_BACHD	O6fcf7 acinetobact
612	31	62.0	83	2	P72638_SYNY3	P72638 synchocyst	685	31	62.0	231	1	RL1_BACSK	O9kgs5 bacillus ha
613	31	62.0	93	2	Q5CM09_CRYHO	Q5cm09 cryptospori	686	31	62.0	231	1	RL1_BACSU	O5w184 bacillus cl
614	31	62.0	94	2	Q9FYV5_ARATH	Q9fyv5 arabidopsis	687	31	62.0	231	1	RL1_THETN	Q6r797 bacillus su
615	31	62.0	111	2	Q8YPY4_ANASP	O8ypy4 anabaena sp	688	31	62.0	231	1		Q8r7u3 thermoanaer

689	31	62.0	231	2	Q4V6Q1_DROME	Q4v6q1 drosophila	762	31	62.0	322	2	Q920S2_MOUSE	Q920s2 mus musculu
690	31	62.0	232	2	Q6SPB9_BACLD	Q6spb9 bacillus li	763	31	62.0	332	2	Q8M61_TYCR	Q8m61 trypanosoma
691	31	62.0	233	2	Q8UJZ6_PYRWO	Q8ujz6 pyrococcus	764	31	62.0	332	2	Q45397_CABE	Q45397 caenorhabdi
692	31	62.0	233	2	Q8TH28_PYRFU	Q8th28 pyrococcus	765	31	62.0	340	2	Q41AD0_GIBZE	Q41ad0 gibberella
693	31	62.0	233	2	Q8U2P8_PYRFU	Q8u2p8 pyrococcus	766	31	62.0	344	2	Q8AU03_BACTN	Q8au03 bacteroides
694	31	62.0	234	2	Q75TJ3_BACST	Q75tj3 bacillus st	767	31	62.0	344	2	Q8YQ35_ANASP	Q8yq35 anabaena sp
695	31	62.0	235	2	Q5W130_BACSK	Q5w130 bacillus cl	768	31	62.0	347	2	Q8U9B2_AGRT5	Q8u9b2 agrobacteri
696	31	62.0	236	2	Q67934_AQUAE	Q67934 aquifex aeo	769	31	62.0	357	2	Q7CTD8_AGRT5	Q7ctd8 agrobacteri
697	31	62.0	246	2	Q4MLF4_BACCCE	Q4mlf4 bacillus ce	770	31	62.0	358	2	Q63547_9RUGL	Q63547 bodo saltan
698	31	62.0	247	1	GRAN_GVPB	Q4mlf4 bacillus ce	771	31	62.0	360	2	Q82ND9_STRAW	Q82nd9 streptomyc
699	31	62.0	248	2	Q8J558_9BACU	P06502 pteris bras	772	31	62.0	361	2	Q603X2_METCA	Q603x2 methylococ
700	31	62.0	251	1	Q52002_HALSA	Q8j558 phthorimaea	773	31	62.0	363	2	Q7XJN2_ARATH	Q7xjn2 arabidopsis
701	31	62.0	252	1	Q5A0_OCEIH	Q8ekui oceanobacil	774	31	62.0	365	2	Q603T0_METCA	Q603t0 methylococ
702	31	62.0	252	2	Q9FV00_ARATH	Q9fv00 arabidopsis	775	31	62.0	365	2	Q5QU42_IDILO	Q5qu42 idiomarina
703	31	62.0	252	2	Q41W62_AZOV1	Q41w62 azotobacter	776	31	62.0	366	1	5HT1P_EAT	Q5QU42 idiomarina
704	31	62.0	254	2	Q9LGP4_ORYSA	Q9lgp4 oryza sativ	777	31	62.0	367	2	P71056_BACSU	P71056 bacillus su
705	31	62.0	254	2	Q5KU55_GEOKA	Q5ku55 geobacillus	778	31	62.0	374	1	HGF5_ARATH	Q897u5 arabidopsis
706	31	62.0	255	1	Q5K001_BACAN	Q81jh1 bacillus an	779	31	62.0	375	2	Q895E1_CLOTE	Q895e1 clostridium
707	31	62.0	255	2	Q41GQ3_9BURK	Q41gq3 burkholderi	780	31	62.0	376	1	TGFB1_CYPCA	Q9ptq2 cyprinus ca
708	31	62.0	255	2	Q630B6_BACCK	Q630b6 bacillus ce	781	31	62.0	378	2	P96072_STRVP	P96072 streptomyc
709	31	62.0	255	2	Q6HAF0_BACHK	Q6haf0 bacillus th	782	31	62.0	380	1	NTG2_YEAST	Q8214 saccharomyc
710	31	62.0	255	2	Q72WU1_BACC1	Q72wu1 bacillus ce	783	31	62.0	380	2	Q52AH4_MAGGR	Q52ah4 magnaporthe
711	31	62.0	257	2	Q5K9Q1_CRYNE	Q5k9q1 cryptococcu	784	31	62.0	384	2	Q59Q13_CANAL	Q59q13 candida alb
712	31	62.0	258	1	Q5A41_BACCR	Q814f4 bacillus ce	785	31	62.0	384	2	Q6CS84_KIULA	Q6cs84 kluyveromyc
713	31	62.0	258	2	Q02483_BHV4	Q02483 bovine herp	786	31	62.0	385	2	Q61EN9_CABER	Q61en9 caenorhabdi
714	31	62.0	261	1	QXAA1_EACSU	Q01625 bacillus su	787	31	62.0	385	2	Q44887_CABEL	Q44887 caenorhabdi
715	31	62.0	261	2	Q7YSM4_BRANA	Q7ysm4 brassica na	788	31	62.0	385	2	Q8A7P9_BACTN	Q8a7p9 bacteroides
716	31	62.0	262	2	Q7SBB1_NEUPOR	Q7sbb1 neurospora	789	31	62.0	388	2	Q57VH7_9TRYP	Q57vh7 trypanosoma
717	31	62.0	262	2	Q9M1H9_ARATH	Q9m1h9 arabidopsis	790	31	62.0	391	2	Q41088_GIBZE	Q41088 gibberella
718	31	62.0	263	2	Q7NNT4_CHRVO	Q7nnt4 chromobacte	791	31	62.0	391	2	Q7XKC0_ORYSA	Q7xkc0 oryza sativ
719	31	62.0	264	2	Q6W281_RHLSN	Q6w281 rhizobium s	792	31	62.0	392	2	Q6FUS8_CANGA	Q6fus8 candida gla
720	31	62.0	264	2	Q62N58_BACLD	Q62n58 bacillus li	793	31	62.0	396	2	Q82D46_STRAW	Q82d46 streptomyc
721	31	62.0	264	2	Q6ADX0_LEIXX	Q6adx0 leifsonia x	794	31	62.0	398	2	Q7U5Y4_SYNPX	Q7u5y4 synechococ
722	31	62.0	265	2	Q6SCM9_BACLD	Q6scm9 bacillus li	795	31	62.0	400	2	Q8X0T3_NEUCR	Q8x0t3 neurospora
723	31	62.0	270	2	Q4NYB1_9DELT	Q4nyb1 anaeromyxob	796	31	62.0	401	2	Q5QMJ7_IDILO	Q5qwj7 idiomarina
724	31	62.0	270	2	Q8YKZ7_ANASP	Q8y kz7 anabaena sp	797	31	62.0	402	2	Q7VXJ9_BORPE	Q7vxj9 bordetella
725	31	62.0	272	1	LGT_WOLSU	Q7m7s6 wolinnella s	798	31	62.0	402	2	Q7W8Y7_BORPE	Q7w8y7 bordetella
726	31	62.0	273	2	Q92CA0_LISIN	Q92ca0 listeria in	799	31	62.0	402	1	Q7WKD0_BORBR	Q7wkd0 bordetella
727	31	62.0	274	2	Q94FT2_ARATH	Q94ft2 arabidopsis	800	31	62.0	406	1	HUT1_YERPE	Q9ac74 yersinia pe
728	31	62.0	276	2	Q937L7_9CVAN	Q937l7 uncultured	801	31	62.0	406	2	Q5C1L1_CRYHO	Q5c1l1 cryptospori
729	31	62.0	276	2	Q937L8_9CVAN	Q937l8 uncultured	802	31	62.0	406	2	Q66B14_YERPS	Q66b14 yersinia ps
730	31	62.0	277	2	Q6VPB5_PROHO	Q6vpb5 prochloroth	803	31	62.0	413	1	YBHO_SHIFL	P59715 shigella fl
731	31	62.0	278	1	QXAA1_STAEP	Q8cmk4 staphylococ	804	31	62.0	416	2	Q5CPN1_CRYPV	Q5cpn1 cryptospori
732	31	62.0	278	2	Q5HLG3_STAEP	Q5hlg6 staphylococ	805	31	62.0	416	2	Q5CPN1_CRYPV	Q5cpn1 cryptospori
733	31	62.0	280	1	QXAA2_BACHD	Q9k0p2 bacillus ha	806	31	62.0	416	2	Q5YZJ6_NOCFA	Q5yzj6 nocardia fa
734	31	62.0	280	2	Q7PMX9_ANOGA	Q7pmx9 anopheles g	807	31	62.0	419	2	Q97HW3_CLOAB	Q97hw3 clostridium
735	31	62.0	280	2	Q8KL78_RHIET	Q8kl78 rhizobium e	808	31	62.0	422	2	Q523W6_MAGGR	Q523w6 magnaporthe
736	31	62.0	282	2	Q9D413_MOUSE	Q9d413 mus musculu	809	31	62.0	422	2	Q8H7T3_ORYSA	Q8h7t3 oryza sativ
737	31	62.0	283	2	Q89M01_BRAJA	Q89mq1 bradyrhizob	810	31	62.0	428	2	Q9FRL4_ARATH	Q9frl4 arabidopsis
738	31	62.0	287	2	Q9KZ06_STRCO	Q9kz06 streptomyc	811	31	62.0	433	2	Q4XPA8_PLACH	Q4xpa8 plasmodium
739	31	62.0	287	2	Q9YVNG_MSEPV	Q9yvng melanoplus	812	31	62.0	433	2	Q62254_CABEL	Q62254 caenorhabdi
740	31	62.0	288	2	Q79354_9TRYP	Q79354 herpetomona	813	31	62.0	435	2	Q9FB05_9PSED	Q9fb05 pseudomonas
741	31	62.0	289	2	Q9K8J1_BACHD	Q9k8j1 bacillus ha	814	31	62.0	439	2	Q52E78_MAGGR	Q52e78 magnaporthe
742	31	62.0	290	1	QXAA1_STAAM	P65628 staphylococ	815	31	62.0	439	2	Q6YWE7_ORYSA	Q6ywe7 oryza sativ
743	31	62.0	290	1	QXAA1_STAAR	P65629 staphylococ	816	31	62.0	440	2	Q4HUP4_TETNG	Q4hup4 tetraodon n
744	31	62.0	290	1	QXAA1_STAAR	Q6g9y5 staphylococ	817	31	62.0	441	2	Q4HVE2_GIBZE	Q4hve2 gibberella
745	31	62.0	290	1	QXAA1_STAAS	Q6g9m0 staphylococ	818	31	62.0	441	2	Q626C5_CABER	Q626c5 caenorhabdi
746	31	62.0	290	1	QXAA1_STAAS	P65630 staphylococ	819	31	62.0	443	2	Q5B6E2_EMENI	Q5b6e2 aspergillus
747	31	62.0	290	1	Q5HEA9_STAAC	Q5hea9 staphylococ	820	31	62.0	445	2	Q5D1Y0_9GAMM	Q5d1y0 halomonas m
748	31	62.0	291	2	Q9LN77_ARATH	Q9ln77 arabidopsis	821	31	62.0	447	2	Q64787_ARATH	Q64787 arabidopsis
749	31	62.0	291	2	Q821K8_SALTI	Q821k8 salmonella	822	31	62.0	448	2	Q6BEV2_CABEL	Q6bev2 caenorhabdi
750	31	62.0	299	2	Q5A972_CANAL	Q5a972 candida alb	823	31	62.0	450	1	Q8MYL8_CABEL	Q8myl8 caenorhabdi
751	31	62.0	299	2	Q99CZ1_BHV4	Q99cz1 bovine herp	824	31	62.0	452	1	NUAM_LUMTE	Q3a949 lumbricus t
752	31	62.0	300	2	Q96169_PLAPF7	Q96169 plasmodium	825	31	62.0	452	2	Q76G21_ARACO	Q76g21 aralia cord
753	31	62.0	300	2	Q91F92_ARATH	Q91f92 arabidopsis	826	31	62.0	453	1	FORT_ARATH	Q9sp96 arabidopsis
754	31	62.0	302	2	P73974_SYNV3	P73974 synechocyst	827	31	62.0	453	1	UFQG_GENTR	Q96493 gentiana tr
755	31	62.0	304	2	Q6L3R9_SOLDE	Q6l3r9 solanum dem	828	31	62.0	453	2	Q7NJZ5_GLOVI	Q7njz5 gloeobacter
756	31	62.0	309	2	Q8PYI5_METWA	Q8pyi5 methanosarc	829	31	62.0	456	2	Q4ST57_TETNG	Q4st57 tetraodon n
757	31	62.0	310	2	Q6FEX8_ACTIAD	Q6fex8 acinetobact	830	31	62.0	459	2	Q64788_ARATH	Q64788 arabidopsis
758	31	62.0	311	1	PRWA_CLOAB	P45558 clostridium	831	31	62.0	462	2	Q7XUE9_ORYSA	Q7xue9 oryza sativ
759	31	62.0	314	2	Q5V2S8_HALMA	Q5v2s8 haloarcula	832	31	62.0	464	1	WCJAJ_ECOLI	P71241 escherichia
760	31	62.0	315	2	Q4UCD8_THEAN	Q4ucd8 theileria a	833	31	62.0	464	2	Q7UCB5_SHIFL	Q7ucb5 shigella fl
761	31	62.0	315	2	Q732Y3_MYCPA	Q732y3 mycobacteri	834	31	62.0	464	2	Q8FG28_ECOLD	Q8fg28 escherichia

835	31	62.0	464	2	Q83R01_SHIFL	Q83R01 shigella fl	908	31	62.0	599	2	Q9FJG5_ARATH	Q9fjg5 arabidopsis
836	31	62.0	464	2	Q8X7P2_ECO57	Q8x7p2 escherichia	909	31	62.0	601	2	Q51GZ5_ENTHI	Q51gz5 entamoeba h
837	31	62.0	474	2	Q4N050_THEPA	Q4n050 theileria p	910	31	62.0	607	2	Q57X14_9TRYP	Q57x14 trypanosoma
838	31	62.0	475	2	Q60M62_CAEBR	Q60m62 caenorhabdi	911	31	62.0	608	2	Q51MF9_MAGGR	Q51mf9 magnaporthe
839	31	62.0	475	2	Q9D6C8_MOUSE	Q9d6c8 mus musculus	912	31	62.0	608	2	Q51912_ENTHI	Q51912 entamoeba h
840	31	62.0	478	2	Q8SVU7_ARATH	Q8svu7 arabidopsis	913	31	62.0	609	2	Q8GRA6_VIBFA	Q8gra6 vibrio para
841	31	62.0	479	2	Q9VVK2_DROME	Q9vvk2 drosophila	914	31	62.0	609	2	Q87FL8_VIBPA	Q87fl8 vibrio para
842	31	62.0	481	2	Q09658_CAEBR	Q09658 caenorhabdi	915	31	62.0	610	2	Q82W91_RHIME	Q82w91 rhizobium m
843	31	62.0	484	2	Q23173_CAEBL	Q23173 caenorhabdi	916	31	62.0	615	2	Q86T96_HUMAN	Q86t96 homo sapien
844	31	62.0	486	1	VPS773_YEAST	P53142 saccharomyc	917	31	62.0	616	2	Q64UY7_BACFR	Q64uy7 bacteroides
845	31	62.0	497	2	Q6CBP5_YARLI	Q6cbp5 yarrowia li	918	31	62.0	620	2	Q96ZH5_SULTO	Q96zh5 sulfolobus
846	31	62.0	497	2	Q6WC04_IXOSC	Q6wcq4 ixodes scap	919	31	62.0	622	2	Q5JDQ6_PYROCO	Q5jdq6 pyrococcus
847	31	62.0	498	2	Q9KN11_VIBCH	Q9kn11 vibrio chol	920	31	62.0	624	2	Q91271_PSEAE	Q91271 pseudomonas
848	31	62.0	499	2	Q83BC6_COXBU	Q83bc6 coxiella bu	921	31	62.0	627	2	Q97W70_SULSO	Q97w70 sulfolob
849	31	62.0	500	2	Q5LLQ4_SILPO	Q5llq4 silicibacte	922	31	62.0	630	2	Q4RE54_TETNG	Q4re54 tetraodon n
850	31	62.0	501	2	Q814A9_CAEBL	Q814a9 caenorhabdi	923	31	62.0	638	1	NUSM_PARLI	Q4re54 tetraodon n
851	31	62.0	504	2	Q74AL2_GEOSL	Q74al2 geobacter s	924	31	62.0	640	2	Q6BU28_DEBHA	P12776 paracentrot
852	31	62.0	505	2	Q94Z19_SCHCO	Q94z19 schizophyll	925	31	62.0	645	2	Q7PTC5_ANOGA	Q8buc28 debaryomyce
853	31	62.0	510	2	Q62RF3_BACLD	Q62rf3 bacillus li	926	31	62.0	663	1	TFBI_NEUCR	Q7ptcs anopheles g
854	31	62.0	511	2	Q8EBB6_SHEON	Q8ebb6 shewanella	927	31	62.0	666	2	Q9N2T3_CAEBL	Q9n2t3 neuropept
855	31	62.0	512	1	OPUD_BACSU	P54117 bacillus su	928	31	62.0	668	2	Q7R8J8_PLAYO	Q7r8j8 plasmodium
856	31	62.0	512	2	Q65FZ6_BACLD	Q65fz6 bacillus li	929	31	62.0	668	2	Q4YQ07_PLABE	Q4yq07 plasmodium
857	31	62.0	514	2	Q59Q10_CANAL	Q59q10 candida alb	930	31	62.0	669	2	Q4Y017_PLACH	Q4y017 plasmodium
858	31	62.0	514	2	Q4WQ21_ASPTU	Q4wq21 aspergillus	931	31	62.0	679	2	Q9FY53_ARATH	Q9fy53 arabidopsis
859	31	62.0	515	2	Q7SBU0_NEUCR	Q7sbu0 neuropept	932	31	62.0	680	2	Q8NR20_CORGL	Q8nr20 corynebacte
860	31	62.0	520	2	Q600P5_MYCHY	Q600p5 mycoplasma	933	31	62.0	686	1	LCMT2_HUMAN	Q8nr20 corynebacte
861	31	62.0	523	2	Q7PYW0_ANOGA	Q7pyw0 anopheles g	934	31	62.0	690	2	Q4KF38_PSEPF	Q4kf38 pseudomonas
862	31	62.0	524	2	Q814B1_CAEBL	Q814b1 caenorhabdi	935	31	62.0	691	2	Q88P10_PSEPK	Q88p10 pseudomonas
863	31	62.0	525	2	Q98QK0_MYCPU	Q98qk0 mycoplasma	936	31	62.0	692	2	Q571W1_SALCH	Q571w1 salmonella
864	31	62.0	528	2	Q5E4C1_VIBFI	Q5e4c1 vibrio fisc	937	31	62.0	692	2	Q5PM02_SALPA	Q5pm02 salmonella
865	31	62.0	530	2	Q51KC3_MAGGR	Q51kc3 magnaporthe	938	31	62.0	692	2	Q8ZLI5_SALTY	Q8zli5 salmonella
866	31	62.0	531	2	Q6FXZ7_CANGA	Q6fxz7 candida gla	939	31	62.0	693	2	Q8Z225_SALTY	Q8z225 salmonella
867	31	62.0	531	2	Q42582_ARATH	Q42582 arabidopsis	940	31	62.0	698	2	Q9U404_9TRYP	Q9u404 trypanosoma
868	31	62.0	531	2	Q9STZ3_ARATH	Q9stz3 arabidopsis	941	31	62.0	700	2	Q988W5_RHILO	Q988w5 rhizobium l
869	31	62.0	531	2	Q4RUA0_TETNG	Q4rua0 tetraodon n	942	31	62.0	713	2	Q4WQ75_ASPTU	Q4wq75 aspergillus
870	31	62.0	531	2	Q4SUV8_TETNG	Q4suv8 tetraodon n	943	31	62.0	713	2	Q9ZAE1_THETH	Q9zael thermus the
871	31	62.0	532	2	Q7ZVU4_BRARE	Q7zvuv4 brachydanio	944	31	62.0	713	2	Q5SJ75_THETH	Q5sej75 thermus the
872	31	62.0	533	2	Q6CG10_YARLI	Q6cg10 yarrowia ae	945	31	62.0	713	2	Q72J38_THETH	Q72j38 thermus the
873	31	62.0	533	2	Q5CC72_WHEAT	Q5cc72 triticum li	946	31	62.0	719	2	Q5LX86_SILPO	Q5lxe86 silicibacte
874	31	62.0	533	2	Q6Y3A2_HORVD	Q6y3a2 hordeum vul	947	31	62.0	719	2	Q92Z49_RHIME	Q92z49 rhizobium m
875	31	62.0	533	2	Q9KSX5_VIBCH	Q9ksx5 vibrio chol	948	31	62.0	728	2	Q65408_ARATH	Q65408 arabidopsis
876	31	62.0	534	2	Q5A117_CANAL	Q5a117 candida alb	949	31	62.0	731	1	BGAL_DIACA	Q00662 dianthus ca
877	31	62.0	534	2	Q5A1S5_CANAL	Q5a1s5 candida alb	950	31	62.0	747	2	Q59YC7_CANAL	Q59yc7 candida alb
878	31	62.0	535	2	Q5A116_CANAL	Q5a116 candida alb	951	31	62.0	750	2	Q88G74_PSEPK	Q88g74 pseudomonas
879	31	62.0	536	2	Q814B0_CAEBL	Q814b0 caenorhabdi	952	31	62.0	752	2	Q55F07_DICDI	Q55f07 dictyosteli
880	31	62.0	537	2	Q6BS95_DEBHA	Q6bs95 debaryomyce	953	31	62.0	754	2	Q6WC05_IXOSC	Q6wc05 ixodes scap
881	31	62.0	550	2	Q8SUC2_ENCCU	Q8suc2 encephalito	954	31	62.0	772	2	Q89YG2_BACTN	Q89yg2 bacteroides
882	31	62.0	552	1	Y1292_METJA	Q58688 methanococc	955	31	62.0	772	2	Q6A7A2_PROAC	Q6a7a2 propionibac
883	31	62.0	554	2	Q57RQ4_SALCH	Q57rq4 salmonella	956	31	62.0	779	2	Q5CJ55_CRYHO	Q5cjj55 cryptospori
884	31	62.0	554	2	Q8ZQY0_SALTY	Q8zqy0 salmonella	957	31	62.0	780	2	Q5TML9_ANOGA	Q5tml9 anopheles g
885	31	62.0	557	1	CPNE4_HUMAN	Q96a23 homo sapien	958	31	62.0	796	2	Q23992_DROME	Q23992 drosophila
886	31	62.0	557	1	CPNE4_MOUSE	Q8blr2 mus musculus	959	31	62.0	807	2	Q7WY48_PSEAE	Q7wy48 pseudomonas
887	31	62.0	557	2	Q6MUA7_MYCMS	Q6muu7 mycoplasma	960	31	62.0	811	2	Q8YX29_ANASP	Q8yx29 anabaena sp
888	31	62.0	559	2	Q5AL37_CANAL	Q5al37 candida alb	961	31	62.0	818	2	Q61UR0_CAEBR	Q61ur0 caenorhabdi
889	31	62.0	559	2	Q7QDV2_ANOGA	Q7qdv2 anopheles g	962	31	62.0	841	2	Q75K09_DICDI	Q75k09 dictyosteli
890	31	62.0	559	2	Q5TJ10_ADE09	Q5tj10 human adeno	963	31	62.0	856	2	Q7MWC9_FORGI	Q7mwc9 porphyromon
891	31	62.0	560	2	Q76X34_CAUD	Q76x34 enterobacte	964	31	62.0	861	2	Q5A7T6_CANAL	Q5a7t6 candida alb
892	31	62.0	561	2	Q97W21_SULSO	Q97w21 sulfolobus	965	31	62.0	874	2	Q4QDV2_LEIMA	Q4qdv2 leishmania
893	31	62.0	562	2	Q974V8_SULTO	Q974v8 sulfolobus	966	31	62.0	875	2	Q6BQ66_DEBHA	Q6bq66 debaryomyce
894	31	62.0	562	2	Q81503_ARATH	Q81503 arabidopsis	967	31	62.0	887	2	Q8P6G7_XANCP	Q8p6g7 xanthomonas
895	31	62.0	564	2	Q73HF0_WOLPM	Q73hf0 wolbachia p	968	31	62.0	888	2	Q4IA59_GIBZE	Q4ia59 gibberella
896	31	62.0	566	2	Q97W79_SULSO	Q97w79 sulfolobus	969	31	62.0	889	2	Q8DLX6_SYNEL	Q8dlx6 synecococc
897	31	62.0	569	1	GCL_DROME	Q01820 drosophila	970	31	62.0	890	1	WFS1_HUMAN	Q76024 homo sapien
898	31	62.0	574	2	Q8RG73_FUSNN	Q8rg73 fusobacteri	971	31	62.0	890	2	WFS1_MOUSE	P56695 mus musculus
899	31	62.0	575	2	Q974Z0_SULTO	Q974z0 sulfolobus	972	31	62.0	890	2	Q5RSY5_PONPY	Q5rsy5 pongo pygma
900	31	62.0	579	2	Q51D76_ENTHI	Q51d76 entamoeba h	973	31	62.0	890	2	Q8PNB4_XANAC	Q8pnb4 xanthomonas
901	31	62.0	583	2	Q9SPT6_SOLTU	Q9spt6 solanum tub	974	31	62.0	890	2	Q5JLT5_RAT	Q5jlt5 rattus norv
902	31	62.0	585	2	Q9XFP4_ORYSA	Q9xfp4 oryza sativ	975	31	62.0	890	2	Q80UI9_MOUSE	Q80ui9 mus musculus
903	31	62.0	591	2	Q80ZK1_MOUSE	Q80zk1 mus musculus	976	31	62.0	894	2	Q5ANK9_CANAL	Q5ank9 candida alb
904	31	62.0	592	2	Q5RAK3_PONPY	Q5rak3 pongo pygma	977	31	62.0	904	1	PPRI_YEAST	P07272 saccharomyc
905	31	62.0	593	2	Q5ZZM7_MYCHY	Q5zzm7 mycoplasma	978	31	62.0	905	2	Q52LH9_MAGGR	Q52lh9 magnaporthe
906	31	62.0	594	2	Q5M3F8_STRT2	Q5m3f8 streptococc	979	31	62.0	908	1	MGR8_HUMAN	Q00222 homo sapien
907	31	62.0	597	2	Q5NIJ3_FRATT	Q5nij3 francisella	980	31	62.0	908	1	MGR8_MOUSE	P47743 mus musculus

981 31 62.0 908 1 MGR8 RAT P70579 rattus norv  
 982 31 62.0 908 2 Q6J165 HUMAN Q6J165 homo sapien  
 983 31 62.0 908 2 Q52M02 HUMAN Q52M02 homo sapien  
 984 31 62.0 908 2 Q6B964 MOUSE Q6B964 mus musculus  
 985 31 62.0 923 1 NRPIA BRARE Q8GTX6 brachydanio  
 986 31 62.0 923 2 Q69DB8 BRARE Q69DB8 brachydanio  
 987 31 62.0 924 1 DPOL BFSP1 P30314 bacteriophag  
 988 31 62.0 927 2 Q8H1E7 ARATH Q8H1E7 arabidopsis  
 989 31 62.0 938 2 Q8FPZ7 COREF Q8FPZ7 corynebacte  
 990 31 62.0 951 2 Q54ZQ4 DICDI Q54ZQ4 dictyosteli  
 991 31 62.0 954 2 Q414W2 GIBZE Q414W2 gibberella  
 992 31 62.0 956 2 Q6BZD7 DEBHA Q6BZD7 debaryomyce  
 993 31 62.0 970 2 Q02222 CAEL Q02222 caenorhabdi  
 994 31 62.0 972 2 Q72261 CAEL Q72261 caenorhabdi  
 995 31 62.0 1003 2 Q53PD8 ORYSA Q53PD8 oryza sativ  
 996 31 62.0 1013 2 Q6XM69 PHYC Q6XM69 feldmannia  
 997 31 62.0 1019 1 LFC CARRO Q26422 carinoscor  
 998 31 62.0 1042 2 Q6ABV1 PROAC Q6ABV1 propionibac  
 999 31 62.0 1053 2 Q7WTU5 9MCC Q7WTU5 arthrobacte  
 1000 31 62.0 1083 2 Q26423 CARRO Q26423 carinoscor

## ALIGNMENTS

RESULT 1  
 ID Q5FWJ4\_MOUSE PRELIMINARY; PRT; 634 AA.  
 AC Q5FWJ4;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DE Hps1 protein.  
 GN Name=Hps1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Faxner A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchan J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Director MGC Project;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC089331; AAH89331.1; -; mRNA.  
 DR GO; GO:0030318; P:melanocyte differentiation; IMP.  
 DR GO; GO:0006996; P:organelle organization and biogenesis; IMP.  
 SQ SEQUENCE 634 AA; 71918 MW; 4D116F40608E25E7 CRC64;

Query Match 80.0%; Score 40; DB 2; Length 634;  
 Best Local Similarity 77.8%; Pred. No. 78;  
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 DB 616 FLWFENDMV 624  
 ||||| |

## RESULT 2

Q6D9R7\_ERWCT PRELIMINARY; PRT; 266 AA.  
 ID Q6D9R7\_ERWCT  
 AC Q6D9R7;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DE Putative plasmid transfer protein.  
 GN Name=traE; OrderedLocusNames=ECA0548;  
 OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Pectobacterium.  
 OX NCBI\_TaxID=29471;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=SCRI 1043 / ATCC BAA-672;  
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;  
 RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,  
 RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,  
 RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,  
 RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,  
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,  
 RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;  
 RT "Genome sequence of the enterobacterial phytopathogen Erwinia  
 RT carotovora subsp. atroseptica and characterization of virulence  
 RT factors.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).  
 DR EMBL; BX950851; CAG73463.1; -; Genomic DNA.  
 DR GO; GO:0003677; P:DNA binding; IEA.  
 DR GO; GO:0006276; P:plasmid maintenance; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 KW Complete proteome.  
 SQ SEQUENCE 266 AA; 30560 MW; 8D7628F313223FBE CRC64;

Query Match 78.0%; Score 39; DB 2; Length 266;  
 Best Local Similarity 85.7%; Pred. No. 51;  
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 2 LWFEIDI 8  
 DB 134 LWFEIDV 140  
 ||||| |

## RESULT 3

Q5DZJ4\_VIBF1 PRELIMINARY; PRT; 267 AA.  
 ID Q5DZJ4\_VIBF1  
 AC Q5DZJ4;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DE Transcriptional regulator.  
 GN OrderedLocusNames=VPA0732;  
 OS Vibrio fischeri (strain ATCC 700601 / ES114).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=312309;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX PubMed=15703294; DOI=10.1073/pnas.0409900102;  
 RA Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R.,  
 RA Losroth P., Lupp C., McCann J., Mallikan D., Schaefer A., Stabb E.,  
 RA Stevens A., Visick K., Whistler C., Greenberg E.P.;  
 RT "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium  
 RT with pathogenic congeners.";

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RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; CP000021; AAW87802.1; -; Genomic_DNA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0000156; P:two-component response regulator activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR007492; LYTTR DNA bind.
DR InterPro; IPR001789; Response reg.
DR InterPro; IPR008246; RR_LYTTR_AlgR.
DR Pfam; PF04397; LYTTR; 1.
DR Pfam; PF00072; Response reg; 1.
DR PRSF; PRSF006198; RR_LYTTR_AlgR; 1.
DR PRODOM; PD000039; Response reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50930; HTH_LYTTR; 1.
DR PROSITE; PS50110; RESPONSE REGULATORY; 1.
KW Complete proteome; DNA-binding; Sensory transduction; Transcription;
Transcription regulation; Two-component regulatory system.
SQ SEQUENCE 267 AA; 30302 MW; 7C8CC2DB825570B CRC64;

Query Match 78.0%; Score 39; DB 2; Length 267;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFPEIDIV 9
|:|:|:|
DB 27 LWFPEIDIV 34

RESULT 4
O14192 SCHPO PRELIMINARY; PRT; 474 AA.
AC O14192;
DT 01-JAN-1999 (TrEMBLrel. 09, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DR SPAC56E4.03 protein (BC 2.6.1.-).
GN ORFNames=SPAC56E4.03;
OS Schizosaccharomyces pombe (Pission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., William R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouras J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K.M., Rutter S., Saunders D., Quail M.A., Rabinowitsch E.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.J., Warren T., Whitehead S.,
RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltyjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoef A., Fritzc C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Leirach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe.";
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RL Nature 415:871-880(2002).
DR EMBL; Z99261; CAB16394.1; -; Genomic_DNA.
DR PIR; T38905; T38905.
DR GeneDB Spombe; SPAC56E4.03; -.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004839; Aminotrans_I/II.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00155; Aminotran_1_2; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 474 AA; 53166 MW; E546EABC7E884623 CRC64;

Query Match 78.0%; Score 39; DB 2; Length 474;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7
|:|:|:|
DB 390 FLWFEID 396

RESULT 5
Q8ZG34_YERPE PRELIMINARY; PRT; 587 AA.
ID Q8ZG34_YERPE PRELIMINARY;
AC Q8ZG34; Q74VD6; Q7CHPO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein YPO1485.
GN OrderedLocustNames=YPI375, YPO1485, Y2684;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Ferna N.T., Rose D.J., Mau B., Zhou S., Zhau S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=91001;
RX PubMed=15368893;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
avirulent to humans.";
RL DNA Res. 11:179-197(2004).
DR EMBL; AJ414148; CAC90308.1; -; Genomic_DNA.
DR EMBL; AB013870; AAM86237.1; -; Genomic_DNA.
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DR EMBL; AB017132; AAS61616.1; -; Genomic_DNA.
DR PIR; A10180; A10180. DUF979_bac.
DR InterPro; IPR010272; DUF979_bac.
DR Pfam; PF05947; DUF879; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 587 AA; 67418 MW; 389A200B93753764 CRC64;

Query Match          78.0%; Score 39; DB 2; Length 587;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9
    |||||
Db 272 WFEIDVV 278

RESULT 6
Q66CA4 YERPS
ID Q66CA4_YERPS PRELIMINARY; PRT; 587 AA.
AC Q66CA4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
DE OrderedLocNames-vpTB1502;
GN Versinia pseudotuberculosis.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I;
RX PubMed=15338858; DOI=10.1073/pnas.04040120101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RA "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH20741.1; -; Genomic_DNA.
DR InterPro; IPR010272; DUF979_bac.
DR Pfam; PF05947; DUF879; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 587 AA; 67502 MW; 34B32E4F8CE74E83 CRC64;

Query Match          78.0%; Score 39; DB 2; Length 587;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9
    |||||
Db 272 WFEIDVV 278

RESULT 7
Q8IIA6 PLAF7
ID Q8IIA6_PLAF7 PRELIMINARY; PRT; 596 AA.
AC Q8IIA6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF11_0268;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.G.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
RL EMBL; AE014839; AAN35852.1; -; Genomic_DNA.
DR InterPro; IPR011498; Kelch_2.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF01344; Kelch_1; 2.
DR Pfam; PF07646; Kelch_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 596 AA; 68046 MW; B07DCS8441A754AF CRC64;

Query Match          78.0%; Score 39; DB 2; Length 596;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8
    |||||
Db 433 FSWFEVDI 440

RESULT 8
Q6IZ03 OSTNU
ID Q6IZ03 OSTNU PRELIMINARY; PRT; 1714 AA.
AC Q6IZ03;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cadherin A1.
OS Ostrinia nubilalis (European corn borer).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Crambidae; Pyraustinae; Ostrinia.
OX NCBI_TaxID=29057;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15681223; DOI=10.1016/j.ibmb.2004.10.008;
RA Coates B.S., Sumnerford D.V., Hellmich R.L., Lewis L.C.;
RT "Sequence variation in the cadherin gene of Ostrinia nubilalis: a tool
RT for field monitoring."
RL Insect Biochem. Mol. Biol. 35:129-139(2005).
DR EMBL; AY612336; AAT37678.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; Cadherin; 5.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 10.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS00268; CADHERIN_2; 11.
KW Calcium.
SQ SEQUENCE 1714 AA; 191902 MW; 89E3CAE0614654DE CRC64;

Query Match          78.0%; Score 39; DB 2; Length 1714;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7
    :|||||
Db 650 YLWFEID 656

RESULT 9
Q7MZS2 PHOLL
ID Q7MZS2_PHOLL PRELIMINARY; PRT; 588 AA.
AC Q7MZS2;

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RT  Aperegillus fumigatus.";
CC  Submitted (MAY-2005) to the EMBL/GenBank/DBDJ databases.
CC  -1- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBDJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; AAHF01000003; EAL91141.1; -; Genomic DNA.
SQ  SEQUENCE 667 AA; 75550 MW; 76CF8A8D65402C98 CRC64;

Query Match 76.0%; Score 38; DB 2; Length 667;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFPEIDIV 9
Db 115 LWFPEIDIV 122

RESULT 11
Q4XVT5 PLACH
ID Q4XVT5_PLACH PRELIMINARY; PRT; 64 AA.
AC Q4XVT5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC000009.03.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OC NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolj T.W.A.,
RA Britman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.K., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBDJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01002753; CAH78976.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 64 64
SQ SEQUENCE 64 AA; 7269 MW; C9C671BCA98C4DE0 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 64;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWPEIDI 8
Db 10 FSWYEIDI 17

RESULT 12
Q8Y7L8 LISMO
ID Q8Y7L8_LISMO PRELIMINARY; PRT; 150 AA.
AC Q8Y7L8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE lmo1256 protein.
GN OrderedLocusNames=lmo1256;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGD-e / Serovar 1/2a;

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RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,
RA Madsen E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- SIMILARITY: Belongs to the Nudix hydrolase family.
DR EMBL; AL591978; CAC93934.1; -; Genomic_DNA.
DR PIR; AH1231; AH1231.
DR ListiList; LM01256; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00893; NUDIX; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 150 AA; 17795 MW; D72C70989525E5B0 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 150;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
DB 116 FKWFIDKV 124
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| | | | |

RESULT 13
Q92CE8 LISIN PRELIMINARY; PRT; 150 AA.
AC Q92CE8_
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lin1224 protein.
GN OrderedLocusNames=lin1224;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,
RA Madsen E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- SIMILARITY: Belongs to the Nudix hydrolase family.
DR EMBL; AL596168; CAC96455.1; -; Genomic_DNA.
DR PIR; AG1585; AG1585.
DR ListiList; LIN1224; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00893; NUDIX; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 150 AA; 17636 MW; 205F376076CB8CE7 CRC64;

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Query Match 74.0%; Score 37; DB 2; Length 150;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
DB 116 FKWFIDKV 124
| | | | |
| | | | |

RESULT 14
Q7RSS9 PLAYO PRELIMINARY; PRT; 198 AA.
AC Q7RSS9_
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY00274;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteaux M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.B.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL0100077; EAA22282.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 198 AA; 22441 MW; 50A2D7E56AB5E236 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 198;
Best Local Similarity 75.0%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8
DB 33 FSWYEIDI 40
| | | | |
| | | | |

RESULT 15
Q7UJ06 RHOB PRELIMINARY; PRT; 322 AA.
AC Q7UJ06_
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB12213;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Fireillula.
OX NCBI_TaxID=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,

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RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlessner H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL: BX294154; CA077454.1; -: Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 322 AA; 35597 MW; 9790D69F2C0EB08B CRC64;

Query Match 74.0%; Score 37; DB 2; Length 322;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7
Db 79 FFWFID 85

RESULT 16
Q4XM13 PLACH
ID Q4XM13 PLACH PRELIMINARY; PRT; 522 AA.
AC Q4XM13;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PC000149.05.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CAJ01004748; CAH82049.1; -: Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 522 AA; 59879 MW; C8BICE7A93F619C0 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 522;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8
Db 398 FSWYEIDI 405

RESULT 17
Q4Z4D7 PLABE
ID Q4Z4D7 PLABE PRELIMINARY; PRT; 523 AA.
AC Q4Z4D7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PB000887.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

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RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CAJ01000661; CAH94846.1; -: Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 523 AA; 59694 MW; 369F47ABB1475D83 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 523;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8
Db 360 FSWYEIDI 367

RESULT 18
Q9CFF6 LACIA
ID Q9CFF6 LACIA PRELIMINARY; PRT; 529 AA.
AC Q9CFF6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter ATP binding and permease protein.
GN Namesyppd; OrderedLocNames=Lli522;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=LI1403;
RC MEDLINE=21325186; PubMed=11337471; DOI=10.1101/gr-1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malmgren K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis LI1403.";
RL Genome Res. 11:731-753 (2001).
DR EMBL: AB006383; AAK05620.1; -: Genomic_DNA.
DR PIR: B86815; B86815.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0016887; F: ATPase activity; IEA.
DR GO: GO:0042626; F: ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0000166; F: nucleotide binding; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR011527; ABC_membrane_1.
DR InterPro: IPR003439; ABC_transp_like.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA_1.
DR PROSITE: PS00929; ABC_TM1F; 1.
DR PROSITE: PS00893; ABC_TRANSPORTER_2; 1.
KW Complete proteome.
SQ SEQUENCE 529 AA; 59763 MW; 7838906A4D09E0C5 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 529;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
Db 49 FLWLAIIDII 57

RESULT 19

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Q7N267 PHOLL
ID Q7N267_PHOLL PRELIMINARY; PRT; 586 AA.
AC Q7N267;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to unknown protein.
DE OrderedLocNames=plu3225;
GN Photorhabdus luminescens (subsp. laumondii).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusnok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguiet P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.,
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571869; CAE15599.1; -; Genomic_DNA.
DR PhotoList; plu3225; -;
DR InterPro; IPR010272; DUF879_bac.
DR Pfam; PF05947; DUF879; 1.
KW Complete proteome.
SQ SEQUENCE 586 AA; 67513 MW; AA8AB383C031F30F CRC64;

Query Match 74.0%; Score 37; DB 2; Length 586;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9
|||:|:|
Db 272 WFEIDVV 278

RESULT 20
Q6B3A0 9PROT
ID Q6B3A0_9PROT PRELIMINARY; PRT; 587 AA.
AC Q6B3A0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=q8107;
OS uncultured proteobacterium Q81.
OC Bacteria; Proteobacteria; environmental samples.
OX NCBI_TaxID=288647;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Williamson L.L., Borlee B.R., Schloss P.D., Guan C., Handelsman J.;
RT "Quorum Sensing Genes from Uncultured Bacteria in Alaskan Soil.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY688432; AAT90770.1; -; Genomic_DNA.
DR InterPro; IPR010272; DUF879_bac.
DR Pfam; PF05947; DUF879; 1.
KW Hypothetical protein.
SQ SEQUENCE 587 AA; 67046 MW; D02029DCECA36304 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 587;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9
|||:|:|
Db 272 WFEIDVV 278

RESULT 21

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Q7RVS4 NEUCR
ID Q7RVS4_NEUCR PRELIMINARY; PRT; 713 AA.
AC Q7RVS4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (AF088906) clock-controlled gene-9
DE protein).
GN Name=NCU09559.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass I., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RT Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000379; EAA30248.1; -; Genomic_DNA.
DR GO; GO:0009058; P:biocynthesis; IEA.
DR InterPro; IPR001296; Glyco_trans_1.
DR Pfam; PF00534; Glyco_transf_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 713 AA; 79717 MW; DA651BA0E524DBEC CRC64;

Query Match 74.0%; Score 37; DB 2; Length 713;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9
|||:|:|
Db 124 LWLEVDIV 131

RESULT 22
Q74693 NEUCR
ID Q74693_NEUCR PRELIMINARY; PRT; 731 AA.
AC Q74693; Q01308;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Clock-controlled gene-9 protein.
GN Name=ccg-9;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97075124; PubMed=8917550; DOI=10.1073/pnas.93.23.13096;
RA Bell-Pedersen D., Shinohara M.L., Loros J.J., Dunlap J.C.;
RT "Circadian clock-controlled genes isolated from Neurospora crassa are
RT late night- to early morning-specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13096-13101(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RA Shinohara M.L., Bell-Pedersen D., Loros J.J., Dunlap J.C.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF088906; AAC64285.1; -; Genomic\_DNA.  
 DR PIR; T47213; T47213.  
 DR GO; GO:0009058; P:biosynthesis; IEA.  
 DR InterPro; IPR001296; Glyco\_transf\_1.  
 DR Pfam; PF00534; Glycosyl\_transf\_1; 1.  
 SQ SEQUENCE 731 AA; 81834 MW; DAF9484FFDF773A2 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 731;  
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LWFEDIV 9  
 ||| |||  
 Db 124 LWFEDIV 131

RESULT 23  
 Q8DKV4 SYNEL  
 ID Q8DKV4 SYNEL PRELIMINARY; PRT; 129 AA.  
 AC Q8DKV4;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Dihydroneopterin aldolase.  
 GN OrderedLocustNames=t110747;  
 OS Synechococcus elongatus (Thermosynechococcus elongatus).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OX NCBI\_TaxID=32046;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=BP-1;  
 RC MEDLINE=2225144; PubMed=12240834;  
 RX Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,  
 RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,  
 RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the thermophilic cyanobacterium  
 Thermosynechococcus elongatus BP-1";  
 RL DNA Res. 9:123-130(2002).  
 DR EMBL; BA00039; BAC08298.1; -; Genomic\_DNA.  
 DR HSP; P56740; 1DNH.  
 DR GO; GO:0004150; F:dihydroneopterin aldolase activity; IEA.  
 DR GO; GO:0006760; P:folic acid and derivative metabolism; IEA.  
 DR InterPro; IPR006157; FolB  
 DR InterPro; IPR006156; FolB\_fam.  
 DR Pfam; PF02152; FolB; 1.  
 DR TIGRFAMs; TIGR00525; folB; 1.  
 DR TIGRFAMs; TIGR00526; folB\_dom; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 129 AA; 14567 MW; 689CC2E1C5BEC20 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDI 8  
 |||||  
 Db 34 WFEIDI 39

RESULT 24  
 Q4G6G8\_9CNID  
 ID Q4G6G8\_9CNID PRELIMINARY; PRT; 186 AA.  
 AC Q4G6G8;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE NADH dehydrogenase subunit 6.  
 GN Name=nad6;  
 OS Montastraea annularis (boulder star coral).  
 OG Mitochondrion.

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;  
 OC Faviina; Faviidae; Montastraea.  
 OX NCBI\_TaxID=48500;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=M01-4, and Pa01-23;  
 RA Fukami H., Knowlton N.;  
 RT "Analysis of complete mitochondrial DNA sequences of three members of  
 the Montastraea annularis coral species complex (Cnidaria, Anthozoa,  
 Scleractinia)";  
 RL Coral Reefs 0:0-0(2005).  
 DR EMBL; AP008974; BAE16194.1; -; Genomic\_DNA.  
 DR EMBL; AP008973; BAE16181.1; -; Genomic\_DNA.  
 KW Mitochondrion.  
 SQ SEQUENCE 186 AA; 21235 MW; E7D85E11D764A494 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 186;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 ||| |||  
 Db 43 FLWFEIDIV 51

RESULT 25  
 Q4G6F5\_9CNID  
 ID Q4G6F5\_9CNID PRELIMINARY; PRT; 186 AA.  
 AC Q4G6F5;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE NADH dehydrogenase subunit 6.  
 GN Name=nad6;  
 OS Montastraea franki.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;  
 OC Faviina; Faviidae; Montastraea.  
 OX NCBI\_TaxID=48499;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Pa00-3, and Pa01-5;  
 RA Fukami H., Knowlton N.;  
 RT "Analysis of complete mitochondrial DNA sequences of three members of  
 the Montastraea annularis coral species complex (Cnidaria, Anthozoa,  
 Scleractinia)";  
 RL Coral Reefs 0:0-0(2005).  
 DR EMBL; AP008975; BAE16207.1; -; Genomic\_DNA.  
 DR EMBL; AP008976; BAE16220.1; -; Genomic\_DNA.  
 KW Mitochondrion.  
 SQ SEQUENCE 186 AA; 21235 MW; E7D85E11D764A494 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 186;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
 ||| |||  
 Db 43 FLWFEIDIV 51

RESULT 26  
 Q4G6C9\_9CNID  
 ID Q4G6C9\_9CNID PRELIMINARY; PRT; 186 AA.  
 AC Q4G6C9;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE NADH dehydrogenase subunit 6.  
 GN Name=nad6;  
 OS Montastraea faveolata.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;

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OC Favina; Faviidae; Montastraea.
OX NCBI_TaxID=48498;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Pa00-9, and Pa01-28;
RA Fukami H., Knowlton N.;
RT "Analysis of complete mitochondrial DNA sequences of three members of
RT the Montastraea annularis coral species complex (Chidaria, Anthozoa,
RT Scleractinia).";
RL Coral Reefs 0:0-0(2005).
DR EMBL; AF008977; BAE16233.1; -; Genomic DNA.
DR EMBL; AF008978; BAE16246.1; -; Genomic_DNA.
KW Mitochondrion.
SQ SEQUENCE 186 AA; 21235 MW; E7D85E11D764A494 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 186;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9
DB 43 FLWLEVDLF 51

RESULT 27
QSQUN7_SALTY
ID Q5QUN7_SALTY PRELIMINARY; PRT; 228 AA.
AC Q5QUN7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
OS Salmonella typhimurium.
OG Plasmid pU302L.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G8430;
RA Chen C.-Y., Nace G.W., Briggs C., Solow B., Fraticchio P.;
RT "Complete sequence of two plasmids that possess antibiotic resistance
RT genes in Salmonella enterica Serovar Typhimurium U302 MR strain
RT G8430."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY334334; AAR05720.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 228 AA; 25823 MW; 8858491B3ECD8B1B CRC64;

Query Match 72.0%; Score 36; DB 2; Length 228;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9
DB 168 VWFEADIV 175

RESULT 28
ID Q573H4_9BACT PRELIMINARY; PRT; 257 AA.
AC Q573H4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS uncultured bacterium.
OG Plasmid pRSB107.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Szczepanowski R., Braun S., Riedel V., Schneider S., Krahn I.,

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RA Puehler A., Schlueter A.;
RT "The 120 592 bp IncF plasmid pRSB107 isolated from a sewage-treatment
RT plant encodes nine different antibiotic-resistance determinants,
RT two iron-acquisition systems and other putative virulence-associated
RT functions.";
RL Microbiol. 151:1095-1111(2005).
DR EMBL; AJ851089; CAH64830.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 257 AA; 28909 MW; 427743434C1476CC CRC64;

Query Match 72.0%; Score 36; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9
DB 197 VWFEADIV 204

RESULT 29
QSEIQ2_VIBF1
ID QSEIQ2_VIBF1 PRELIMINARY; PRT; 262 AA.
AC QSEIQ2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Sporulation-control protein.
GN OrderedLocusNames=VF2549;
OS Vibrio fischeri (strain ATCC 700601 / ES114).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Vibrio.
OX NCBI_TaxID=312309;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15703234; DOI=10.1073/pnas.0409900102;
RA Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R.,
RA Lostroh P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
RA Stevens A., Visick K., Whistler C., Greenberg E.P.;
RT "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
RT with pathogenic congeners.";
RT Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
DR EMBL; CP000020; AAW87044.1; -; Genomic_DNA.
DR InterPro; IPR009776; Spo0M.
DR Pfam; PF07070; Spo0M; 1.
KW Complete proteome.
SQ SEQUENCE 262 AA; 29524 MW; B7F68274D642F19E CRC64;

Query Match 72.0%; Score 36; DB 2; Length 262;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEID 7
DB 210 LWFEID 215

RESULT 30
Q8DDE9_VIBVU
ID Q8DDE9_VIBVU PRELIMINARY; PRT; 264 AA.
AC Q8DDE9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Spo0M-related protein.
GN OrderedLocusNames=VW11041;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,

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RA Choy H.E.;
RT *Complete genome sequence of Vibrio vulnificus CMCP6."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016800; AAO09529.1; -; Genomic_DNA.
DR InterPro; IPR009776; SpoOM.
DR Pfam; PF07070; SpoOM; 1.
KW Complete proteome.
SQ SEQUENCE 264 AA; 29616 MW; 3CC45B870F25938C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 264;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LWFEID 7
Db 213 LWFEID 218

RESULT 31
Q7MGK0_VIBVY
ID Q7MGK0_VIBVY PRELIMINARY; PRT; 266 AA.
AC Q7MGK0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SpoOM-related protein.
GN OrderedLocusNames=VV3231;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu X.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
pathogen."
RL Genome Res. 13:2577-2587(2003).
DR EMBL; BA000037; BAC95995.1; -; Genomic_DNA.
DR InterPro; IPR009776; SpoOM.
DR Pfam; PF07070; SpoOM; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 29875 MW; 2C6DC41A32C8FBDC CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 266;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LWFEID 7
Db 215 LWFEID 220

RESULT 32
OXA01_LACLA
ID OXA01_LACLA STANDARD; PRT; 269 AA.
AC Q9CJ72;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Membrane protein oxaA 1 precursor.
GN Name=oxaA1; OrderedLocusNames=LL0129;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=111403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.169701;
RA Bolotin A., Wincker P., Mauer S., Jaillon O., Malmgren K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;

RT The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis I11403."
RL Genome Res. 11:731-753(2001).
CC -I- FUNCTION: Required for the insertion of integral membrane proteins
CC into the membrane. May also be involved in protein secretion
CC processes (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the OXA1/oxaA family. Type 2 subfamily.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AE006251; AAK04227.1; -; Genomic_DNA.
DR PIR; A86641; A86641.
DR HAMAP; MF_01811; -; 1.
DR InterPro; IPR001708; Innermemb_insert.
DR Pfam; PF02096; 60KD IMP; 1.
DR PRINTS; PR00701; 60KDINNERMP.
DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
KW Complete proteome; Lipoprotein; Palmitate; Signal; Transmembrane.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 269 Membrane protein oxaA 1.
FT TRANSMEM 47 69 Potential.
FT TRANSMEM 166 185 Potential.
FT TRANSMEM 200 222 Potential.
FT LIPID 21 21 N-palmitoyl cysteine (Potential).
FT LIPID 21 21 S-diacylglycerol cysteine (Potential).
SQ SEQUENCE 269 AA; 30294 MW; B57A158CB264F0DF CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 269;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLWFEI 6
Db 155 FLWFEI 160

RESULT 33
Q87KC8_VIBPA
ID Q87KC8_VIBPA PRELIMINARY; PRT; 270 AA.
AC Q87KC8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SpoOM-related protein.
GN OrderedLocusNames=VP3049;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; BA000031; BAC61312.1; -; Genomic_DNA.
DR InterPro; IPR009776; SpoOM.
DR Pfam; PF07070; SpoOM; 1.
KW Complete proteome.
SQ SEQUENCE 270 AA; 30310 MW; DFE66C307A0F062D CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 270;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 LWFIED 7
DB      214 LWFIED 219

RESULT 34
Q4WIX2_ASPFU
ID Q4WIX2_ASPFU PRELIMINARY; PRT; 273 AA.
AC Q4WIX2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Acetylornithine deacetylase (ArgE), putative.
GN AFNames=AF2900350;
OS Aspergillus fumigatus AF293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AF293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.B., Garcia M.J., Goble A.,
RA Goldman N.G., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohammed Y., Molina M., Monod M.,
RA Mouny I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penava M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekaita F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.B., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF0100008; EAL87133.1; -; Genomic DNA.
SQ SEQUENCE 273 AA; 29877 MW; 401E12DC022E02CA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 273;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
DB      71 FVWVEVDIL 79

RESULT 35
Q93X27_9ROSI
ID Q93X27_9ROSI PRELIMINARY; PRT; 331 AA.
AC Q93X27;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative osmosensor histidine Kinase (Fragment).
GN Name=uhk1;
OS Populus euramericana.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
OX NCBI_TaxID=106131;

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RN      [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RA Caruso A.M.;
RL Thesis (2001), Department of Laboratoire de Biologie des Ligneux,
RL Universite des Sciences d Orlean, Orleans, France.
RN      [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaves;
RA Caruso A.M., Morabito D., Martin A., Chefedor F., Depierreux C.,
RA Kahlem G., Carpin S.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ319875; CAC42409.1; -; mRNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0001055; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATP_bd_ATPase.
DR InterPro; IPR004358; His_kin_like_C.
DR InterPro; IPR003661; His_kinA_N.
DR InterPro; IPR005467; His_kinase.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HisKA; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; HisKA; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
KW Kinase; Transferase.
FT NON_TER 1
FT NON_TER 331
SQ SEQUENCE 331 AA; 37258 MW; 2E3CA26ABD5023C4 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFIED 7
DB      181 LWFIED 186

RESULT 36
Q658M5_HUMAN
ID Q658M5_HUMAN PRELIMINARY; PRT; 338 AA.
AC Q658M5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp666K145 (Fragment).
GN Name=DKFZp666K145;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Stomach;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL833734; CAH56230.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 338 AA; 38870 MW; 4EB05E84C68F929B CRC64;

Query Match 72.0%; Score 36; DB 2; Length 338;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 FLWFEIDI 8
DB      250 FLWFPENDM 257

RESULT 37
Q55T92 CRYNE
ID      Q55T92 CRYNE PRELIMINARY; PRT; 411 AA.
AC      Q55T92;
DT      13-SEP-2005 (TREMELrel. 31, Created)
DT      13-SEP-2005 (TREMELrel. 31, Last sequence update)
DT      13-SEP-2005 (TREMELrel. 31, Last annotation update)
DE      Hypothetical protein.
GN      ORFNames=CNB05600;
OS      Cryptococcus neoformans var. neoformans B-3501A.
OC      Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC      Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX      NCBI_TaxID=283643;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=B-3501A;
RA      Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA      Wickes B.L., Fu J., Davis R.W.;
RA      "Cryptococcus neoformans serotype D sequencing.";
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
CC      EMBL; AA01000022; EAL20959.1; -; Genomic_DNA.
DR      InterPro; IPR001680; WD40.
DR      Pfam; PF00400; WD40; 3.
DR      SMART; SM00320; WD40; 5.
KW      Hypothetical protein; Transport.
SQ      SEQUENCE 411 AA; 45087 MW; F291ADB1207B4C6F CRC64;

Query Match 72.0%; Score 36; DB 2; Length 411;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEIDI 8
DB      288 LWFPDIDV 294

RESULT 38
YBHO_ECOLI
ID      YBHO_ECOLI STANDARD; PRT; 413 AA.
AC      Q8FJN9;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Putative cardiolipin synthetase ybho (EC 2.7.8.-) (Cardiolipin
DE      synthase) (CL synthase).
GN      Name=ybho; OrderedLocNames=c0872;
OS      Escherichia coli O6.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=217992;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX      MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA      Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA      Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA      Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA      Mobley H.B.T., Donnenberg M.S., Blattner F.R.;
RT      "Extensive mosaic structure revealed by the complete genome sequence
RT      of uropathogenic Escherichia coli.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC      -!- FUNCTION: Catalyzes, in vitro, the phosphatidyl group transfer
CC      from one phosphatidylglycerol molecule to another to form
CC      cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By
CC      similarity).

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CC      -!- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol =
CC      diphosphatidylglycerol + glycerol.
CC      -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC      -!- SIMILARITY: Belongs to the phospholipase D family. Cardiolipin
CC      synthase subfamily.
CC      -!- SIMILARITY: Contains 2 PLD phosphodiesterase domains.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AE016757; AAN79345.1; -; Genomic_DNA.
DR      InterPro; IPR001736; PLD.
DR      Pfam; PF00614; PLDE; 2.
DR      SMART; SM00155; PLDE; 2.
DR      PROSITE; PS00035; PLD; 2.
KW      Complete proteome; Phospholipid biosynthesis; Repeat; Transferase.
FT      DOMAIN 108 135 PLD phosphodiesterase 1.
FT      DOMAIN 285 312 PLD phosphodiesterase 2.
FT      ACT_SITE 113 113 Potential.
FT      ACT_SITE 290 290 Potential.
SQ      SEQUENCE 413 AA; 47552 MW; 21F9ED2C7CD24CA3 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 413;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDI 8
DB      40 FLWFPEDDV 47

RESULT 39
YBHO_ECOLI
ID      YBHO_ECOLI STANDARD; PRT; 413 AA.
AC      P75771;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Putative cardiolipin synthetase ybho (EC 2.7.8.-) (Cardiolipin
DE      synthase) (CL synthase).
GN      Name=ybho; OrderedLocNames=b0789, z1008, ECs0867;
OS      Escherichia coli, and
OS      Escherichia coli O157:H7.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=562, 83334;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=K12 / MG1655;
RX      MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA      Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,
RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA      Mau B., Shao Y.;
RT      "The complete genome sequence of Escherichia coli K-12.";
RL      Science 277:1453-1474(1997).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=K12;
RX      MEDLINE=97061202; PubMed=8905232;
RA      Oshima T., Aiba H., Baba T., Fujita K., Hayaishi K., Honjo A.,
RA      Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA      Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA      Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA      Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA      Yano M., Horiuchi T.;
RT      "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT      corresponding to the 12.7-28.0 min region on the linkage map.";
RL      DNA Res. 3:137-155(1996).
RN      [3]

```

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC.  
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;  
RA Ferra N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";  
RL Nature 409:529-533 (2001).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=0157:H7 / Sakai / RMD 050952 / EHEC;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayaishi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*  
O157:H7 and genomic comparison with a laboratory strain K-12.";  
RL DNA Res. 8:11-22 (2001).  
RN [5]  
RP CHARACTERIZATION.  
RC STRAIN=HB101;  
RX MEDLINE=20102623; PubMed=10634942; DOI=10.1016/S1388-1981(99)00193-6;  
RA Guo D., Tropp B.E.;  
RT "A second *Escherichia coli* protein with CL synthase activity.";  
RL Biochim. Biophys. Acta 1483:263-274 (2000).  
CC -!- FUNCTION: Catalyzes, in vitro, the phosphatidyl group transfer  
from one phosphatidylglycerol molecule to another to form  
cardiolipin (CL) (diphosphatidylglycerol) and glycerol. Can also  
catalyze phosphatidyl group transfer to water to form  
phosphatidate. Catalyzes little, if any, cardiolipin synthesis in  
vivo, even when the expression level is very high.  
CC -!- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol =  
diphosphatidylglycerol + glycerol  
CC -!- ENZYME REGULATION: Activated by phosphate. Inhibited by  
cardiolipin and phosphatidate.  
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Probable).  
CC -!- SIMILARITY: Belongs to the phospholipase D family. Cardiolipin  
synthase subfamily.  
CC -!- SIMILARITY: Contains 2 PLD phosphodiesterase domains.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC  
CC EMBL; U00096; AAC73876.1; -; Genomic DNA.  
DR EMBL; D90716; BAA35448.1; -; Genomic DNA.  
DR EMBL; AB005174; AAG55160.1; -; Genomic DNA.  
CC EMBL; BA000007; BAB34290.1; -; Genomic DNA.  
DR PIR; C90737; C90737.  
DR PIR; D85587; D85587.  
DR PIR; D84815; E84815.  
DR EchoBASE; EB3435; -.  
DR EcoGene; EG13671; ybho.  
DR InterPro; IPR001736; PLD.  
DR Pfam; PF00614; PLDC; 2.  
DR SMART; SM00155; PLDC; 2.  
DR PROSITE; PS00035; PLD; 2.  
KW Complete proteome; Phospholipid biosynthesis; Repeat; Transferase.  
FT DOMAIN 108 135 PLD phosphodiesterase 1.  
FT DOMAIN 285 312 PLD phosphodiesterase 2.  
FT ACT\_SITE 113 113 Potential.  
FT ACT\_SITE 290 290 Potential.  
SQ SEQUENCE 413 AA; 47634 MW; 74998B2A1AD24A11 CRC64;  
Query Match 72.0%; Score 36; DB 1; Length 413;  
Best Local Similarity 62.5%; Pred. No. 3e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LWFEBIDI 8  
DB 40 FIWFEDDV 47  
RESULT 40  
Q5KJ49\_CRYNE PRELIMINARY; PRT; 413 AA.  
ID Q5KJ49;  
AC Q5KJ49;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Guanylnucleotide binding protein, putative.  
GN ORFNames=CND00670;  
OS *Cryptococcus neoformans* var. *neoformans* JEC21.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=214684;  
RN [1]\_TaxID=214684;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JEC21;  
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,  
RA Van Aken S., Fraser C.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=JEC21;  
RX PubMed=15653466; DOI=10.1126/science.1103773;  
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,  
RA Huang J.C., Janbon G., Jones S.J.W., Koo H.L., Krzywinski M.I.,  
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,  
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,  
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
RA Fraser C.M., Hyman R.W.;  
RT "The genome of the basidiomycetous yeast and human pathogen  
RT *Cryptococcus neoformans*."  
RL Science 307:1321-1324 (2005).  
DR EMBL; AB017344; BAA43078.1; -; Genomic DNA.  
DR InterPro; IPR001680; WD40.  
DR Pfam; PF00400; WD40; 4.  
DR SMART; SM00320; WD40; 6.  
DR PROSITE; PS00294; WD\_REPEATS\_REGION; 1.  
KW Complete proteome; Repeat; WD repeat.  
SQ SEQUENCE 413 AA; 45281 MW; CD6AFC2C86F8C9B1 CRC64;  
Query Match 72.0%; Score 36; DB 2; Length 413;  
Best Local Similarity 71.4%; Pred. No. 3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LWFEBIDI 8  
DB 288 LWFEDDV 294  
RESULT 41  
Q70XS6\_SCUCO PRELIMINARY; PRT; 445 AA.  
ID Q70XS6;  
AC Q70XS6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).  
GN Name=nad4;  
OS *Scutigera coleoptrata* (House centipede).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda; Notostigmophora;  
OC Scutigermorpha; Scutigeridae; Scutigera.

```

OX NCBI_TaxID=29022;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14963096; DOI=10.1093/molbev/msh078;
RA Negrisolo E., Minelli A., Valle G.;
RT "The mitochondrial genome of the house centipede Scutigera and
RL myriapod monophyly vs. paraphyly.";
RM Mol. Biol. Evol. 21:770-780(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=15114420; DOI=10.1007/s00239-003-2563-x;
RA Negrisolo E., Minelli A., Valle G.;
RT "Extensive gene order rearrangement in the mitochondrial genome of the
RL centipede Scutigera coleoptrata.";
RM J. Mol. Evol. 58:413-423(2004).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
DR EMBL; AJ507061; CAD45022.2; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR003918; NADH_oxred4.
DR InterPro; IPR001750; Oxidored_q1.
DR InterPro; IPR000260; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1; 1.
DR Pfam; PF01059; Oxidored_q5_N; 1.
DR PRINTS; PR01437; NUOXDRDTASE4.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 445 AA; 50974 MW; D44FF59D0A72D6DB CRC64;

Query Match 72.0%; Score 36; DB 2; Length 445;
Best Local Similarity 44.4%; Pred. No. 3.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLWFEIDIV 9
Db 114 YIWFEISLI 122

RESULT 42
SYD_PHOLL
ID -SYD_PHOLL STANDARD; PRT; 590 AA.
AC Q7MB41;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Aspartyl-tRNA synthetase [EC 6.1.1.12] (Aspartate--tRNA ligase)
DE (AspRS).
GN Name=asps; OrderedLocusNames=plu2107;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01.
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Kusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taurat S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-P.,
RA Dassa E., Derose R., Deruelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boenare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RL luminescens.";
RM Nat. Biotechnol. 21:1307-1313(2003).
CC -1- CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) = AMP +
CC diphosphate + L-aspartyl-tRNA(Asp).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
family.
-----
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
EMBL; BX571866; CAB14400.1; -; Genomic_DNA.
DR SMR; Q7MB41; 1-584.
DR PhotoList; plu2107; -.
DR HAMAP; MF_00044; -; 1.
DR InterPro; IPR004524; Asps_bact.
DR InterPro; IPR004115; GAD.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR004365; OB_TRNA_NA_bd.
DR InterPro; IPR004364; tRNA-synt_2.
DR InterPro; IPR002312; tRNA-synt_asp.
DR InterPro; IPR006195; tRNA_ligase_II.
DR PANTHER; PTHR10218:SF2; Asps_bact; 2.
DR Pfam; PF02938; GAD; 1.
DR Pfam; PF00152; tRNA-synt_2; 1.
DR Pfam; PF01336; tRNA anti; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR TIGRFAMs; TIGR00459; asps_bact; 1.
DR PROSITE; PSS0862; AA_TRNA_LIGASE_II; 1.
DR Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Nucleotide-binding; Protein biosynthesis.
SQ SEQUENCE 590 AA; 66229 MW; C64B65091522D9EF CRC64;

Query Match 72.0%; Score 36; DB 1; Length 590;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LWFEID 7
Db 255 LWFEID 260

RESULT 43
HPS1_MACFA
ID HPS1_MACFA STANDARD; PRT; 667 AA.
AC Q6OHF3;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hermansky-Pudlak syndrome 1 protein homolog.
GN Name=HPS1; ORFName=Qf1A-21346;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Frontal cortex;
RA Kusuda J., Osada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.;
RT "Isolation and characterization of cDNA for macaque neurological
RL disease genes".
RX Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Component of multiple cytoplasmic organelles. Apparently
CC crucial for their normal development and function. May be involved
CC in intracellular protein sorting.
-----
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
EMBL; AB125174; BAD51962.1; -; mRNA.
DR Repeat.
KW REPEAT. 45 51 [DE]-X(4)-L-L 1.
FT REPEAT 147 153 [DE]-X(4)-L-L 2.
FT REPEAT 483 489 [DE]-X(4)-L-L 3.

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FT REPEAT      611      617      [DE]-X(4)-L-L 4.
FT MOTIF       665      667      Melanosome targeting signal (Potential).
SQ SEQUENCE    667 AA; 75711 MW; 739492AA58601F8B CRC64;

Query Match
Best Local Similarity 72.0%; Score 36; DB 1; Length 667;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 FLWFEIDI 8
Db 579 FLWFENDM 586

RESULT 44
QSR612_PONPY
ID QSR612_PONPY PRELIMINARY; PRT; 699 AA.
AC QSR612;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypochemical protein DKF7p459M1527.
GN Name=DKF7p459M1527;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Oeang A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR860688; CAH92804.1; -; mRNA.
KW Hypochemical protein.
SQ SEQUENCE 699 AA; 79266 MW; E2EC0E8DB13B79BC CRC64;

Query Match
Best Local Similarity 72.0%; Score 36; DB 2; Length 699;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 FLWFEIDI 8
Db 611 FLWFENDM 618

RESULT 45
HPS1_HUMAN
ID HPS1_HUMAN STANDARD; PRT; 700 AA.
AC Q92902; O15402; O15502;
DT 15-DEC-1998 (Ref. 37, Created)
DT 13-SEP-2005 (Ref. 48, Last sequence update)
DT 13-SEP-2005 (Ref. 48, Last annotation update)
DE Hermansky-Pudlak syndrome 1 protein.
GN Name=HPS1; Synonyms=HPS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1];
RP NUCLEOTIDE SEQUENCE (ISOFORM I), AND VARIANTS.
RX MEDLINE=97051924; PubMed=8896559;
RA Oh J., Bailin T., Fukai K., Feng G.H., Ho L., Mao J.-I., Frenk E.,
RA Tamura N., Spritz R.A.;
RT "Positional cloning of a gene for Hermansky-Pudlak syndrome, a
RT disorder of cytoplasmic organelles.";
RL Nat. Genet. 14:300-306(1996).
[2]
RN NUCLEOTIDE SEQUENCE (ISOFORMS I; II AND IV), AND VARIANTS.
RX MEDLINE=97325811; PubMed=9182823; DOI=10.1111/1523-1747.ep12294634;
RA Bailin T., Oh J., Feng G.H., Fukai K., Spritz R.A.;

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RT "Organization and nucleotide sequence of the human Hermansky-Pudlak
RT syndrome (HPS) gene.";
RN J. Invest. Dermatol. 108:923-927(1997).
[3]
RP NUCLEOTIDE SEQUENCE (ISOFORM III).
RX MEDLINE=98239148; PubMed=9579545;
RX DOI=10.1046/j.1523-1747.1998.00183.x;
RA Wildenberg S.C., Fryer J.P., Gardner J.M., Oetting W.S.,
RA Brilliant M.H., King R.A.;
RT "Identification of a novel transcript produced by the gene responsible
RT for the Hermansky-Pudlak syndrome in Puerto Rico.";
RL J. Invest. Dermatol. 110:777-781(1998).
[4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM III).
RP TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN REVIEW ON HPS1 VARIANTS.
RP MEDLINE=99140254; PubMed=10094567;
RX DOI=10.1002/(SICI)1098-1004(1999)13:2<99::AID-HUMU2>3.3.CO;2-3;
RA Oetting W.S., King R.A.;
RT "Molecular basis of albinism: mutations and polymorphisms of
RT pigmentation genes associated with albinism.";
RL Hum. Mutat. 13:99-115(1999).
[6]
RN VARIANT HPS1 ILE-55 DEL.
RX MEDLINE=98163443; PubMed=9497254;
RA Oh J., Ho L., Ala-Mello S., Amato D., Armstrong L., Bellucci S.,
RA Carakushansky G., Ellis J.P., Fong C.-T., Green J.S., Heon E.,
RA Legius E., Levin A.V., Nieuwenhuis H.K., Pinckers A., Tamura N.,
RA Whiteford M.L., Yamasaki H., Spritz R.A.;
RT "Mutation analysis of patients with Hermansky-Pudlak syndrome: a
RT frameshift hot spot in the HPS gene and apparent locus
RT heterogeneity.";
RL Am. J. Hum. Genet. 62:593-598(1998).
CC -1- FUNCTION: Component of multiple cytoplasmic organelles. Apparently
CC crucial for their normal development and function. May be involved
CC in intracellular protein sorting.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=I;
CC IsoId=Q92902-1; Sequence=Displayed;
CC Name=II;
CC IsoId=Q92902-2; Sequence=VSP_004289;
CC Name=III;
CC IsoId=Q92902-3; Sequence=VSP_004290, VSP_004291;
CC Name=IV;
CC IsoId=Q92902-4; Sequence=VSP_004288;
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- DISEASE: Defects in HPS1 are the cause of Hermansky-Pudlak
CC syndrome 1 (HPS1) [MIM:203300]. Hermansky-Pudlak syndrome (HPS) is
CC a genetically heterogeneous, rare, autosomal recessive disorder
CC

```



OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SVJ, and BALB/c;  
RX MEDLINE=97301777; PubMed=9158155; DOI=10.1093/hmg/6.5.793;  
RA Feng G.H., Bailin T., Oh J., Spritz R.A.;  
RT "Mouse pale ear (ep) is homologous to human Hermansky-Pudlak syndrome  
and contains a rare 'AT-AC' intron.";  
RL Hum. Mol. Genet. 6:793-797(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Embryo;  
RX MEDLINE=97404379; PubMed=9256466; DOI=10.1073/pnas.94.17.9238;  
RA Gardner J.M., Wildenberg S.C., Keiper N.M., Novak E.K., Rusiniak M.E.,  
Swank R.T., Puri N., Finger J.N., Hagiwara N., Lehman A.L.,  
Gales T.L., Bayer M.E., King R.A., Brilliant M.H.;  
RT "The mouse pale ear (ep) mutation is the homologue of human Hermansky-  
Pudlak syndrome";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:9238-9243(1997).  
CC -!- FUNCTION: Component of multiple cytoplasmic organelles. Apparently  
crucial for their normal development and function. May be involved  
in intracellular protein sorting.  
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined with the  
possible exception of skeletal muscle. The highest expression was  
observed in lung, liver, kidney and spleen.  
CC -!- DISEASE: Defects in Hps1 are the cause of the pale ear (ep) mutant  
which exhibits hypopigmentation associated with defects of  
multiple cytoplasmic organelles, including melanosomes, lysosomes,  
and granular elements of platelets.  
CC -----  
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removed.  
CC -----  
DR EMBL; U78315; AAB60929.1; -; mRNA.  
DR EMBL; U78966; AAB61333.1; ALT\_INIT; Genomic DNA.  
DR EMBL; U78955; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78956; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78957; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78958; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78959; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78960; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78961; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78962; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78963; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78964; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U78965; AAB61333.1; JOINED; Genomic DNA.  
DR EMBL; U97149; AAB68792.1; -; mRNA.  
DR EMBL; AF003866; AAB68817.1; -; mRNA.  
DR EMBL; AF004352; AAB69159.1; -; Genomic DNA.  
DR EMBL; AF004353; AAB69160.1; -; Genomic DNA.  
DR Ensembl; ENSMUSG0000025188; Mus musculus.  
DR MGI; MGI:217763; Hps1.  
DR GO; GO:0030318; P:melanocyte differentiation; IMP.  
DR GO; GO:006996; P:organelle organization and biogenesis; IMP.  
KW Albinism; Polymorphism; Repeat.  
FT REPEAT 45 51  
FT REPEAT 520 526  
FT REPEAT 648 654  
FT COMPBIAS [DE]-X(4)-L-L 2.  
FT COMPBIAS [DE]-X(4)-L-L 3.  
FT COMPBIAS 34 39 Poly-Glu.  
FT COMPBIAS 252 258 Poly-Glu.  
FT VARIANT 31 31 Q -> R (in strain BALB/c).  
FT VARIANT 89 89 Y -> C (in strain BALB/c).  
FT VARIANT 258 258 Missing (in strain BALB/c).  
FT VARIANT 567 567 E -> K (in strain BALB/c).  
FT CONFLICT 62 62 L -> M (in Ref. 2).  
FT CONFLICT 689 689 S -> G (in Ref. 2; AAB69159).  
FT SEQUENCE 704 AA; 79853 MW; CFB610E3F5A7B89 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 704;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLWFEIDI 8  
DB 616 FLWPENDM 623  
RESULT 48  
Q99MK7 RAT PRELIMINARY; PRT; 706 AA.  
AC Q99MK7;  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Hermansky-Pudlak syndrome protein.  
GN Name=Hps1; Synonyms=Hps;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21251173; PubMed=11353395; DOI=10.1007/s003350020046;  
RA Oh J., Letras T.D., Spritz R.A.;  
RT "Characterization and evolutionary comparison of rat Hps cDNA and  
exclusion of red-eyed dilution (r) locus.";  
RL Mamm. Genome 12:466-468(2001).  
DR EMBL; AF333325; AAK37597.1; -; mRNA.  
DR Ensembl; ENSRNOG0000015891; Rattus norvegicus.  
DR RGD; 69193; Hps1.  
DR SEQUENCE 706 AA; 80259 MW; 8D325579CBA700E2 CRC64;  
Query Match 72.0%; Score 36; DB 2; Length 706;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLWFEIDI 8  
DB 618 FLWPENDM 625  
RESULT 49  
Q5CS74 CRYPV PRELIMINARY; PRT; 995 AA.  
AC Q5CS74;  
DT 10-MAY-2005 (TReMBLrel. 30, Created)  
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=cgdl\_3820;  
OS Cryptosporidium parvum.  
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
OC Cryptosporidiidae; Cryptosporidium.  
OX NCBI\_TaxID=5807;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Iowa type II;  
RX PubMed=15044751; DOI=10.1126/science.1094786;  
RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,  
Lancot C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,  
Bankier A.F., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,  
Anantharaman V., Aravind L., Kapur V.;  
RT "Complete genome sequence of the apicomplexan, Cryptosporidium  
parvum.";  
RL Science 304:441-445(2004).  
CC -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
CC EMBL; AABE0100006; BAK88278.1; -; Genomic\_DNA.  
DR InterPro; IPR010819; AGE/RnBP.

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DR InterPro; IPR010980; Cyt_c_b562.
DR InterPro; IPR000259; Fimbrin.
DR InterPro; IPR012292; Globin related.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001093; IMPDH/GMPRTase.
DR InterPro; IPR004103; Lyase_8_C_B12cap.
DR InterPro; IPR003759; Met_synth_B12cap.
DR InterPro; IPR011993; PH_type.
DR Pfam; PF00478; IMPDH; 1.
KW Hypothetical protein.
SQ SEQUENCE 995 AA; 113728 MW; 43462D50CB665398 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 995;
Best Local Similarity 62.5%; Pred. No. 7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9
Db 640 VWFLLDIV 647

RESULT 50
Q5CIE1.CRVHO
ID Q5CIE1_CRYHO PRELIMINARY; PRT; 996 AA.
AC Q5CIE1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Chro.10429;
OS Cryptosporidium hominis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=237895;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TV502;
RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
RA Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
RA Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S.,
RA Buck G.A.;
RT "The genome of Cryptosporidium hominis."
RL Nature 431:1107-1112(2004).
DR EMBL; AABL01000183; EAL36372.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 996 AA; 114251 MW; 8718E4FD3F7672F8 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 996;
Best Local Similarity 62.5%; Pred. No. 7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9
Db 641 VWFLLDIV 648

Search completed: May 9, 2006, 02:25:21
Job time : 131.6 secs
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:25:44 ; Search time 25.2 Seconds  
(without alignments)  
29.527 Million cell updates/sec

Title: US-09-870-216C-7  
Perfect score: 50  
Sequence: 1 PLWFRDIV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:\*  
1: /cgn2.6/prodata/1/iaa/5 COMB.pep.\*  
2: /cgn2.6/prodata/1/iaa/6 COMB.pep.\*  
3: /cgn2.6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2.6/prodata/1/iaa/PCUS COMB.pep.\*  
5: /cgn2.6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2.6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	78.0	585	2	US-09-489-039A-13868
2	36	72.0	373	2	US-09-252-991A-24034
3	36	72.0	700	2	US-09-266-225D-6
4	35	70.0	543	2	US-09-540-236-2405
5	35	70.0	599	2	US-09-228-986-117
6	35	70.0	599	2	US-10-101-464A-117
7	35	70.0	816	2	US-10-101-464A-827
8	35	70.0	951	2	US-09-328-352-4456
9	35	70.0	1240	2	US-10-101-464A-976
10	34	68.0	262	2	US-09-252-991A-23018
11	33	66.0	86	2	US-09-270-767-60013
12	33	66.0	309	2	US-08-952-736A-10
13	33	66.0	338	2	US-09-198-452A-1050
14	33	66.0	347	2	US-09-438-185A-979
15	33	66.0	363	2	US-09-328-352-5961
16	33	66.0	516	1	US-08-676-166A-2
17	32	64.0	68	2	US-09-513-999C-4712
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19	32	64.0	231	2	US-09-134-001C-4094
20	32	64.0	279	2	US-09-328-352-5581
21	32	64.0	308	2	US-09-328-352-7093
22	32	64.0	323	2	US-09-270-767-31938
23	32	64.0	328	2	US-09-583-110-4312
24	32	64.0	343	2	US-09-107-433-3112
25	32	64.0	350	1	US-08-415-751-43
26	32	64.0	419	2	US-09-489-039A-12789
27	32	64.0	480	2	US-09-107-532A-6160

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29	32	64.0	481	2	US-09-817-464-8	Sequence 8, Appli
30	32	64.0	493	2	US-08-657-749D-2	Sequence 2, Appli
31	32	64.0	511	1	US-08-220-151-17	Sequence 17, Appl
32	32	64.0	511	1	US-08-413-118-17	Sequence 17, Appl
33	32	64.0	511	2	US-08-473-448-17	Sequence 17, Appl
34	32	64.0	563	2	US-10-104-047-3625	Sequence 3625, Ap
35	32	64.0	575	2	US-09-248-796A-17643	Sequence 17643, A
36	32	64.0	754	2	US-09-252-991A-33133	Sequence 33133, A
37	32	64.0	828	2	US-10-101-464A-934	Sequence 934, App
38	32	64.0	867	2	US-08-617-785-4	Sequence 4, Appli
39	32	64.0	867	2	US-09-817-464-4	Sequence 4, Appli
40	32	64.0	915	1	US-08-453-862-2	Sequence 2, Appli
41	32	64.0	915	1	US-08-452-734A-2	Sequence 2, Appli
42	32	64.0	915	2	US-08-617-785-12	Sequence 12, Appl
43	32	64.0	915	2	US-08-176-401B-2	Sequence 2, Appli
44	32	64.0	915	2	US-09-817-464-12	Sequence 12, Appl
45	32	64.0	915	4	PCT-US94-14989-2	Sequence 2, Appli
46	32	64.0	922	2	US-08-617-785-14	Sequence 14, Appl
47	32	64.0	922	2	US-09-817-464-14	Sequence 14, Appl
48	31	62.0	63	2	US-09-248-796A-21418	Sequence 21418, A
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51	31	62.0	73	2	US-09-621-976-5981	Sequence 5981, Ap
52	31	62.0	73	2	US-09-973-278-183	Sequence 183, App
53	31	62.0	74	2	US-09-227-357-210	Sequence 210, App
54	31	62.0	139	2	US-09-134-001C-5327	Sequence 5327, Ap
55	31	62.0	151	2	US-09-270-767-62174	Sequence 62174, A
56	31	62.0	175	2	US-08-975-762-29	Sequence 29, Appl
57	31	62.0	175	2	US-08-821-324-29	Sequence 29, Appl
58	31	62.0	175	2	US-09-295-028-29	Sequence 29, Appl
59	31	62.0	175	2	US-09-106-582-29	Sequence 29, Appl
60	31	62.0	175	2	US-09-159-469-29	Sequence 29, Appl
61	31	62.0	175	2	US-09-693-543-29	Sequence 29, Appl
62	31	62.0	205	2	US-09-134-000C-4114	Sequence 4114, Ap
63	31	62.0	205	2	US-09-134-000C-6187	Sequence 6187, Ap
64	31	62.0	231	1	US-08-808-550-33	Sequence 33, Appl
65	31	62.0	259	2	US-09-328-352-7755	Sequence 7755, Ap
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67	31	62.0	313	2	US-09-248-796A-18064	Sequence 18064, A
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71	31	62.0	358	2	US-09-248-796A-18184	Sequence 18184, A
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73	31	62.0	408	2	US-09-248-796A-16068	Sequence 16068, A
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79	31	62.0	622	2	US-09-261-006-2	Sequence 2, Appli
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81	31	62.0	622	2	US-09-609-568-2	Sequence 2, Appli
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84	31	62.0	622	2	US-08-693-554-2	Sequence 2, Appli
85	31	62.0	623	2	US-08-975-762-68	Sequence 68, Appl
86	31	62.0	623	2	US-09-295-028-68	Sequence 68, Appl
87	31	62.0	623	2	US-09-106-582-68	Sequence 68, Appl
88	31	62.0	623	2	US-09-159-469-68	Sequence 68, Appl
89	31	62.0	623	2	US-09-693-542-68	Sequence 68, Appl
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93	31	62.0	811	2	US-09-199-637A-93	Sequence 93, Appl
94	31	62.0	862	2	US-09-328-352-5527	Sequence 5527, Ap
95	31	62.0	904	2	US-09-487-5588-272	Sequence 272, App
96	31	62.0	908	2	US-08-823-110-1	Sequence 1, Appli
97	31	62.0	908	2	US-08-604-298-1	Sequence 1, Appli
98	31	62.0	908	2	US-08-855-146-2	Sequence 2, Appli
99	31	62.0	1019	1	US-08-296-014A-4	Sequence 4, Appli
100	31	62.0	1019	1	US-08-596-405-4	Sequence 4, Appli

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103	31	62.0	1019	2	US-09-626-795-4	Sequence 4, Appli	176	30	60.0	576	2	US-09-134-000C-6480	Sequence 6480, Ap
104	31	62.0	1019	2	US-10-183-992-8	Sequence 8, Appli	177	30	60.0	644	2	US-09-300-909-18	Sequence 18, Appli
105	31	62.0	1083	1	US-08-296-014A-2	Sequence 2, Appli	178	30	60.0	683	2	US-09-270-767-46792	Sequence 46792, A
106	31	62.0	1083	1	US-08-596-405-2	Sequence 2, Appli	179	30	60.0	696	1	US-08-765-081-5	Sequence 5, Appli
107	31	62.0	1083	1	US-08-877-620-2	Sequence 2, Appli	180	30	60.0	696	2	US-09-098-082-5	Sequence 5, Appli
108	31	62.0	1083	2	US-09-287-368-2	Sequence 2, Appli	181	30	60.0	696	4	PCT-US95-06994-5	Sequence 5, Appli
109	31	62.0	1083	2	US-09-626-795-2	Sequence 2, Appli	182	30	60.0	697	2	US-09-248-796A-15295	Sequence 15295, A
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111	31	62.0	1172	2	US-09-328-352-6071	Sequence 6071, Ap	184	30	60.0	718	4	PCT-US95-06994-6	Sequence 6, Appli
112	31	62.0	2005	2	US-08-836-325-7	Sequence 7, Appli	185	30	60.0	989	2	US-09-252-991A-21468	Sequence 21468, A
113	31	62.0	2005	2	US-09-457-571-7	Sequence 7, Appli	186	30	60.0	1051	2	US-09-949-016-6190	Sequence 6190, Ap
114	31	62.0	2357	2	US-09-949-016-9656	Sequence 9656, Ap	187	30	60.0	1066	2	US-09-949-016-6617	Sequence 6617, Ap
115	31	62.0	2749	2	US-10-360-101-265	Sequence 265, App	188	30	60.0	1090	2	US-09-949-016-9725	Sequence 9725, Ap
116	31	62.0	4585	2	US-10-025-225-6	Sequence 6, Appli	189	30	60.0	1090	2	US-09-949-016-9726	Sequence 9726, Ap
117	31	62.0	4588	2	US-10-025-225-8	Sequence 8, Appli	190	30	60.0	1224	2	US-09-252-991A-32880	Sequence 32880, A
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119	30	60.0	46	2	US-09-270-767-60469	Sequence 60469, A	192	29	58.0	15	2	US-09-226-012-97	Sequence 97, Appli
120	30	60.0	63	2	US-09-583-110-3267	Sequence 3267, Ap	193	29	58.0	21	2	US-09-962-756-487	Sequence 487, App
121	30	60.0	67	2	US-09-248-796A-25319	Sequence 25319, A	194	29	58.0	21	2	US-09-962-756-541	Sequence 541, App
122	30	60.0	69	2	US-09-248-796A-23102	Sequence 23102, A	195	29	58.0	21	2	US-09-962-756-574	Sequence 574, App
123	30	60.0	97	2	US-09-328-352-6261	Sequence 6261, Ap	196	29	58.0	21	2	US-09-962-756-626	Sequence 626, App
124	30	60.0	114	2	US-09-270-767-35647	Sequence 35647, A	197	29	58.0	35	2	US-09-270-767-36800	Sequence 36800, A
125	30	60.0	114	2	US-09-270-767-50864	Sequence 50864, A	198	29	58.0	35	2	US-09-270-767-52017	Sequence 52017, A
126	30	60.0	155	2	US-09-270-767-44985	Sequence 44985, A	199	29	58.0	54	2	US-09-270-767-60261	Sequence 60261, A
127	30	60.0	172	2	US-09-543-681A-6316	Sequence 6316, Ap	200	29	58.0	61	2	US-09-621-976-7630	Sequence 7630, Ap
128	30	60.0	185	2	US-09-270-767-46913	Sequence 46913, A	201	29	58.0	66	2	US-09-513-999C-7094	Sequence 7094, Ap
129	30	60.0	192	2	US-09-583-110-5295	Sequence 5295, Ap	202	29	58.0	85	2	US-09-270-767-62123	Sequence 62123, A
130	30	60.0	192	2	US-09-107-433-4762	Sequence 4762, Ap	203	29	58.0	105	2	US-09-621-976-5135	Sequence 5135, Ap
131	30	60.0	198	2	US-09-543-681A-7038	Sequence 7038, Ap	204	29	58.0	111	1	US-08-111-939-23	Sequence 23, Appli
132	30	60.0	240	2	US-09-978-248A-4	Sequence 4, Appli	205	29	58.0	128	2	US-09-583-110-3340	Sequence 3340, Ap
133	30	60.0	248	2	US-09-270-767-59167	Sequence 59167, A	206	29	58.0	137	2	US-09-902-540-14779	Sequence 14779, A
134	30	60.0	249	2	US-09-248-796A-15815	Sequence 15815, A	207	29	58.0	139	2	US-09-134-000C-4690	Sequence 4690, Ap
135	30	60.0	292	2	US-09-051-755-10	Sequence 10, Appli	208	29	58.0	158	2	US-09-902-540-16662	Sequence 16662, A
136	30	60.0	305	2	US-09-634-238-320	Sequence 320, App	209	29	58.0	160	1	US-08-162-402B-14	Sequence 14, Appli
137	30	60.0	306	2	US-09-386-642-53	Sequence 53, Appli	210	29	58.0	163	2	US-09-270-767-48078	Sequence 48078, A
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139	30	60.0	310	2	US-09-248-796A-21233	Sequence 21233, A	212	29	58.0	167	2	US-09-328-352-7388	Sequence 7388, Ap
140	30	60.0	312	2	US-09-023-942A-4	Sequence 4, Appli	213	29	58.0	174	2	US-09-107-532A-5979	Sequence 5979, Ap
141	30	60.0	314	2	US-09-008-271A-3	Sequence 3, Appli	214	29	58.0	180	2	US-09-358-383C-24	Sequence 24, Appli
142	30	60.0	314	2	US-09-023-942A-6	Sequence 6, Appli	215	29	58.0	181	2	US-09-724-797-2	Sequence 2, Appli
143	30	60.0	314	2	US-09-907-794A-257	Sequence 257, App	216	29	58.0	203	2	US-09-270-767-57453	Sequence 57453, A
144	30	60.0	314	2	US-09-905-125A-257	Sequence 257, App	217	29	58.0	207	2	US-09-248-796A-24953	Sequence 24953, A
145	30	60.0	314	2	US-09-902-775A-257	Sequence 257, App	218	29	58.0	208	2	US-09-489-039A-13175	Sequence 13175, A
146	30	60.0	314	2	US-09-906-700-257	Sequence 257, App	219	29	58.0	212	2	US-09-489-039A-9647	Sequence 9647, Ap
147	30	60.0	314	2	US-09-903-603A-257	Sequence 257, App	220	29	58.0	213	1	US-08-808-550-35	Sequence 35, Appli
148	30	60.0	314	2	US-09-904-920A-257	Sequence 257, App	221	29	58.0	213	1	US-09-270-767-44798	Sequence 44798, A
149	30	60.0	314	2	US-09-909-064-257	Sequence 257, App	222	29	58.0	218	1	US-07-607-538C-4	Sequence 4, Appli
150	30	60.0	314	2	US-09-905-381A-257	Sequence 257, App	223	29	58.0	218	1	US-08-162-402B-4	Sequence 4, Appli
151	30	60.0	314	2	US-09-906-618-257	Sequence 257, App	224	29	58.0	218	2	US-09-364-185-4	Sequence 4, Appli
152	30	60.0	314	2	US-09-906-646-257	Sequence 257, App	225	29	58.0	218	2	US-08-482-596A-4	Sequence 4, Appli
153	30	60.0	314	2	US-09-968-415-3	Sequence 3, Appli	226	29	58.0	230	2	US-09-602-787A-604	Sequence 604, App
154	30	60.0	314	2	US-09-904-462-257	Sequence 257, App	227	29	58.0	230	2	US-09-605-703B-1872	Sequence 1872, Ap
155	30	60.0	314	2	US-09-902-736A-257	Sequence 257, App	228	29	58.0	232	2	US-09-328-352-4622	Sequence 4622, Ap
156	30	60.0	314	2	US-09-906-722A-257	Sequence 257, App	229	29	58.0	237	2	US-09-605-703B-1598	Sequence 1598, Ap
157	30	60.0	322	2	US-09-254-227A-7	Sequence 7, Appli	230	29	58.0	241	2	US-09-358-383C-23	Sequence 23, Appli
158	30	60.0	322	2	US-09-254-227A-9	Sequence 9, Appli	231	29	58.0	261	2	US-09-540-236-3359	Sequence 3359, Ap
159	30	60.0	322	2	US-10-314-048A-20	Sequence 20, Appli	232	29	58.0	261	2	US-09-902-540-9770	Sequence 9770, Ap
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162	30	60.0	332	2	US-09-902-540-10335	Sequence 10335, A	235	29	58.0	270	2	US-09-489-039A-12077	Sequence 12077, A
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165	30	60.0	358	2	US-09-270-767-41449	Sequence 41449, A	238	29	58.0	276	2	US-09-134-001C-6214	Sequence 6214, Ap
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167	30	60.0	425	2	US-09-634-238-321	Sequence 321, App	240	29	58.0	286	2	US-09-270-767-45162	Sequence 45162, A
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169	30	60.0	437	2	US-09-248-796A-14396	Sequence 14396, A	242	29	58.0	300	2	US-09-252-991A-20398	Sequence 20398, A
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171	30	60.0	446	2	US-09-333-696-11	Sequence 11, Appli	244	29	58.0	306	2	US-09-543-681A-5951	Sequence 5951, Ap
172	30	60.0	446	2	US-09-282-218A-19	Sequence 19, Appli	245	29	58.0	317	2	US-09-902-540-15080	Sequence 15080, A
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248	29	58.0	393	2	US-09-377-557-14	Sequence 14, Appl	321	29	58.0	1988	2	US-09-024-020B-4	Sequence 4, Appli
249	29	58.0	399	2	US-09-270-767-61903	Sequence 61903, A	322	29	58.0	1988	2	US-09-425-043-4	Sequence 4, Appli
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251	29	58.0	422	2	US-09-634-238-226	Sequence 226, App	324	29	58.0	2196	2	US-10-360-101-259	Sequence 259, App
252	29	58.0	430	2	US-09-328-352-5453	Sequence 5453, Ap	325	29	58.0	2224	2	US-09-054-272-38	Sequence 38, Appl
253	29	58.0	441	1	US-08-491-835-4	Sequence 4, Appli	326	29	58.0	2224	2	US-09-949-002-292	Sequence 252, App
254	29	58.0	441	2	US-08-946-092A-4	Sequence 4, Appli	327	29	58.0	27	2	US-08-905-223-454	Sequence 454, App
255	29	58.0	441	2	US-09-172-062-4	Sequence 4, Appli	328	28	56.0	41	2	US-09-270-767-36949	Sequence 36949, A
256	29	58.0	441	2	US-09-301-520D-4	Sequence 4, Appli	329	28	56.0	41	2	US-09-270-767-52166	Sequence 52166, A
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263	29	58.0	481	2	US-09-270-767-42183	Sequence 42183, A	336	28	56.0	70	2	US-09-208-210-3	Sequence 3, Appli
264	29	58.0	482	2	US-08-311-731A-204	Sequence 204, App	337	28	56.0	70	2	US-09-252-991A-26553	Sequence 26553, A
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266	29	58.0	551	2	US-09-068-195-24	Sequence 24, Appl	339	28	56.0	75	2	US-09-270-767-59050	Sequence 59050, A
267	29	58.0	504	2	US-09-543-681A-6521	Sequence 6521, Ap	340	28	56.0	75	2	US-09-248-796A-26211	Sequence 26211, A
268	29	58.0	530	2	US-09-270-767-41568	Sequence 41568, A	341	28	56.0	83	2	US-09-248-796A-19025	Sequence 19025, A
269	29	58.0	542	2	US-09-358-383C-5	Sequence 5, Appli	342	28	56.0	90	2	US-09-248-796A-22189	Sequence 22189, A
270	29	58.0	544	2	US-09-710-279-38	Sequence 38, Appl	343	28	56.0	102	2	US-09-107-532A-5862	Sequence 5862, Ap
271	29	58.0	551	2	US-09-543-681A-7532	Sequence 7532, Ap	344	28	56.0	102	2	US-09-107-532A-5863	Sequence 5863, Ap
272	29	58.0	554	2	US-09-489-039A-10541	Sequence 10541, A	345	28	56.0	104	2	US-09-107-532A-4385	Sequence 4385, Ap
273	29	58.0	566	2	US-09-252-991A-17799	Sequence 17799, A	346	28	56.0	104	2	US-09-489-039A-13386	Sequence 13386, A
274	29	58.0	571	1	US-08-419-009-1	Sequence 1, Appli	347	28	56.0	104	2	US-09-270-767-36902	Sequence 36902, A
275	29	58.0	587	2	US-09-328-352-8096	Sequence 8096, Ap	348	28	56.0	104	2	US-09-270-767-52119	Sequence 52119, A
276	29	58.0	596	2	US-09-248-796A-18472	Sequence 18472, A	349	28	56.0	107	2	US-09-513-999C-5517	Sequence 5517, Ap
277	29	58.0	615	2	US-09-248-796A-14606	Sequence 14606, A	350	28	56.0	109	1	US-08-111-939-20	Sequence 20, Appl
278	29	58.0	622	2	US-09-270-767-46333	Sequence 46333, A	351	28	56.0	128	2	US-09-830-807-36	Sequence 36, Appl
279	29	58.0	626	1	US-08-956-242-2	Sequence 2, Appli	352	28	56.0	129	2	US-09-270-767-40390	Sequence 40390, A
280	29	58.0	626	2	US-09-351-215-2	Sequence 2, Appli	353	28	56.0	129	2	US-09-270-767-55606	Sequence 55606, A
281	29	58.0	633	2	US-08-557-006C-43	Sequence 43, Appl	354	28	56.0	130	2	US-09-107-532A-7044	Sequence 7044, Ap
282	29	58.0	633	2	US-09-538-092-212	Sequence 212, App	355	28	56.0	133	2	US-09-621-976-5174	Sequence 5174, Ap
283	29	58.0	633	2	US-09-633-328B-3	Sequence 3, Appli	356	28	56.0	137	2	US-09-091-117-4	Sequence 4, Appli
284	29	58.0	633	2	US-09-824-735-3	Sequence 3, Appli	357	28	56.0	139	2	US-09-270-767-37702	Sequence 37702, A
285	29	58.0	633	2	US-09-487-558B-338	Sequence 338, App	358	28	56.0	139	2	US-09-270-767-52919	Sequence 52919, A
286	29	58.0	639	2	US-09-538-092-17	Sequence 17, Appl	359	28	56.0	144	2	US-09-270-767-59629	Sequence 59629, A
287	29	58.0	689	2	US-09-107-532A-3870	Sequence 3870, App	360	28	56.0	152	2	US-10-104-047-2463	Sequence 2463, Ap
288	29	58.0	691	2	US-09-252-991A-16809	Sequence 16809, A	361	28	56.0	153	2	US-09-107-532A-3888	Sequence 3888, Ap
289	29	58.0	737	2	US-09-583-110-4291	Sequence 4291, Ap	362	28	56.0	154	1	US-09-809-665A-34	Sequence 34, Appl
290	29	58.0	742	2	US-09-107-532A-4996	Sequence 4996, Ap	363	28	56.0	154	1	US-08-162-402B-17	Sequence 17, Appl
291	29	58.0	744	2	US-09-107-433-4054	Sequence 4054, Ap	364	28	56.0	164	2	US-09-270-767-35379	Sequence 35379, A
292	29	58.0	802	2	US-09-489-039A-10142	Sequence 10142, A	365	28	56.0	164	2	US-09-270-767-50596	Sequence 50596, A
293	29	58.0	838	1	US-08-696-944-19	Sequence 19, Appl	366	28	56.0	166	2	US-09-270-767-43161	Sequence 43161, A
294	29	58.0	838	2	US-09-701-868-10	Sequence 10, Appl	367	28	56.0	176	2	US-09-902-540-11324	Sequence 11324, A
295	29	58.0	884	2	US-09-252-991A-26707	Sequence 26707, A	368	28	56.0	180	2	US-09-902-540-10840	Sequence 10840, A
296	29	58.0	888	1	US-08-956-242-4	Sequence 4, Appli	369	28	56.0	185	2	US-09-252-991A-26176	Sequence 26176, A
297	29	58.0	888	2	US-09-351-215-4	Sequence 4, Appli	370	28	56.0	197	2	US-09-328-352-5731	Sequence 5731, Ap
298	29	58.0	905	2	US-10-104-047-2728	Sequence 2728, Ap	371	28	56.0	200	2	US-09-248-796A-16526	Sequence 16526, A
299	29	58.0	921	2	US-09-248-796A-15239	Sequence 441, App	372	28	56.0	203	2	US-09-270-767-62429	Sequence 62429, A
300	29	58.0	1017	2	US-09-600-776-6	Sequence 6, Appli	373	28	56.0	208	2	US-09-252-991A-17857	Sequence 17857, A
301	29	58.0	1017	2	US-09-965-830-6	Sequence 6, Appli	374	28	56.0	218	2	US-10-104-047-32B-9	Sequence 32B, Ap
302	29	58.0	1024	2	US-09-949-016-7276	Sequence 7276, Ap	375	28	56.0	224	2	US-09-268-364-2	Sequence 2, Appli
303	29	58.0	1049	2	US-09-949-002-330	Sequence 330, App	376	28	56.0	226	2	US-09-268-364-2	Sequence 2, Appli
304	29	58.0	1054	2	US-09-949-002-441	Sequence 441, App	377	28	56.0	228	2	US-09-286-690-12	Sequence 12, Appl
305	29	58.0	1102	2	US-09-358-383C-36	Sequence 36, Appl	378	28	56.0	228	2	US-09-248-796A-16477	Sequence 16477, A
306	29	58.0	1107	2	US-09-358-383C-16	Sequence 16, Appl	379	28	56.0	232	1	US-08-508-448C-19	Sequence 19, Appl
307	29	58.0	1159	1	US-08-956-242-13	Sequence 13, Appl	380	28	56.0	240	2	US-09-978-248A-5	Sequence 5, Appli
308	29	58.0	1159	2	US-09-351-215-13	Sequence 13, Appl	381	28	56.0	244	2	US-09-252-991A-20836	Sequence 20836, A
309	29	58.0	1159	2	US-09-226-012-2	Sequence 2, Appli	382	28	56.0	253	2	US-09-583-110-3420	Sequence 3420, Ap
310	29	58.0	1159	2	US-09-226-012-4	Sequence 4, Appli	383	28	56.0	253	2	US-09-270-767-41332	Sequence 41332, A
311	29	58.0	1159	2	US-09-358-383C-10	Sequence 10, Appl	384	28	56.0	253	2	US-09-270-767-56548	Sequence 56548, A
312	29	58.0	1219	2	US-09-275-252A-12	Sequence 12, Appl	385	28	56.0	255	2	US-09-270-767-46807	Sequence 46807, A
313	29	58.0	1219	2	US-09-252-991A-28840	Sequence 28840, A	386	28	56.0	255	2	US-09-248-796A-17183	Sequence 17183, A
314	29	58.0	1352	2	US-09-784-554B-4	Sequence 4, Appli	387	28	56.0	279	2	US-09-489-039A-13210	Sequence 13210, A
315	29	58.0	1352	2	US-09-784-554B-2	Sequence 2, Appli	388	28	56.0	283	2	US-09-328-352-7773	Sequence 7773, Ap
316	29	58.0	1441	2	US-09-252-991A-28143	Sequence 2, Appli	389	28	56.0	283	2	US-09-540-236-1936	Sequence 1936, Ap
317	29	58.0	1976	2	US-09-024-020B-9	Sequence 9, Appli	390	28	56.0	284	1	US-08-446-924-2	Sequence 2, Appli
318	29	58.0	1976	2	US-09-425-043-9	Sequence 9, Appli	391	28	56.0	284	1	US-08-798-665-2	Sequence 2, Appli
319	29	58.0	1978	2	US-09-024-020B-3	Sequence 3, Appli	392	28	56.0	284	2	US-08-982-987A-2	Sequence 2, Appli

393	28	56.0	285	2	US-09-248-796A-14977	Sequence 14977, A	466	28	56.0	541	2	US-09-605-703B-1600	Sequence 1600, Ap
394	28	56.0	287	2	US-09-599-360B-95	Sequence 95, Appl	467	28	56.0	555	2	US-09-252-991A-28313	Sequence 28313, A
395	28	56.0	287	2	US-09-107-433-4150	Sequence 4150, Ap	468	28	56.0	557	1	US-08-328-256-10	Sequence 10, Appl
396	28	56.0	300	2	US-09-248-796A-19889	Sequence 19889, A	469	28	56.0	557	1	US-08-471-454-2	Sequence 2, Appl
397	28	56.0	302	2	US-09-248-796A-14926	Sequence 14926, A	470	28	56.0	557	1	US-08-466-974-2	Sequence 2, Appl
398	28	56.0	303	2	US-09-489-039A-12581	Sequence 12581, A	471	28	56.0	557	1	US-08-471-453-2	Sequence 2, Appl
399	28	56.0	305	1	US-08-946-528-1	Sequence 1, Appl	472	28	56.0	557	1	US-08-307-588-4	Sequence 4, Appl
400	28	56.0	305	2	US-09-866-061-9	Sequence 9, Appl	473	28	56.0	557	2	US-07-971-834-4	Sequence 4, Appl
401	28	56.0	305	2	US-09-452-937A-44	Sequence 44, Appl	474	28	56.0	557	2	US-09-240-675-4	Sequence 4, Appl
402	28	56.0	305	2	US-09-664-840-3	Sequence 3, Appl	475	28	56.0	557	2	US-09-949-016-5972	Sequence 5972, Ap
403	28	56.0	306	2	US-09-866-061-10	Sequence 10, Appl	476	28	56.0	560	2	US-09-902-540-11574	Sequence 11574, A
404	28	56.0	318	1	US-08-309-182B-3	Sequence 3, Appl	477	28	56.0	567	2	US-09-902-540-11767	Sequence 11767, A
405	28	56.0	322	1	US-08-622-354-3	Sequence 3, Appl	478	28	56.0	575	2	US-09-949-016-8640	Sequence 8640, Ap
406	28	56.0	328	2	US-09-270-767-34880	Sequence 34880, A	479	28	56.0	586	2	US-09-691-344A-4	Sequence 4, Appl
407	28	56.0	328	2	US-09-270-767-50097	Sequence 50097, A	480	28	56.0	590	2	US-09-489-039A-10743	Sequence 10743, A
408	28	56.0	338	2	US-09-270-767-44206	Sequence 44206, A	481	28	56.0	591	2	US-09-252-991A-25977	Sequence 25977, A
409	28	56.0	357	2	US-09-248-796A-18015	Sequence 18015, A	482	28	56.0	602	2	US-09-248-796A-20214	Sequence 20214, A
410	28	56.0	363	1	US-08-845-742-2	Sequence 2, Appl	483	28	56.0	618	2	US-09-299-378-4	Sequence 4, Appl
411	28	56.0	364	1	US-08-318-831-6	Sequence 6, Appl	484	28	56.0	619	2	US-09-134-000C-6538	Sequence 6538, Ap
412	28	56.0	370	2	US-09-248-796A-20532	Sequence 20532, A	485	28	56.0	628	2	US-09-107-532A-7123	Sequence 7123, Ap
413	28	56.0	391	2	US-09-645-321-1	Sequence 1, Appl	486	28	56.0	631	2	US-09-056-461-22	Sequence 22, Appl
414	28	56.0	391	2	US-10-378-745-1	Sequence 1, Appl	487	28	56.0	652	1	US-08-318-831-8	Sequence 8, Appl
415	28	56.0	418	1	US-08-508-448C-25	Sequence 25, Appl	488	28	56.0	657	2	US-08-961-083-204	Sequence 204, Ap
416	28	56.0	418	2	US-09-370-838-62	Sequence 62, Appl	489	28	56.0	657	2	US-09-536-784-204	Sequence 204, Ap
417	28	56.0	418	2	US-09-370-838-82	Sequence 82, Appl	490	28	56.0	657	2	US-09-765-271-204	Sequence 204, Ap
418	28	56.0	418	2	US-09-370-838-83	Sequence 83, Appl	491	28	56.0	657	2	US-09-765-272A-204	Sequence 204, Ap
419	28	56.0	418	2	US-09-854-133-62	Sequence 62, Appl	492	28	56.0	667	2	US-08-959-004-11	Sequence 11, Appl
420	28	56.0	418	2	US-09-854-133-82	Sequence 82, Appl	493	28	56.0	676	2	US-09-198-452A-836	Sequence 836, Ap
421	28	56.0	423	1	US-09-854-133-83	Sequence 83, Appl	494	28	56.0	684	2	US-09-765-298A-18	Sequence 18, Appl
422	28	56.0	423	1	US-08-445-746-2	Sequence 2, Appl	495	28	56.0	702	2	US-09-328-352-8176	Sequence 8176, Ap
423	28	56.0	423	1	US-08-290-731C-10	Sequence 10, Appl	496	28	56.0	719	2	US-09-438-185A-788	Sequence 788, Ap
424	28	56.0	423	1	US-08-290-731C-11	Sequence 11, Appl	497	28	56.0	734	2	US-08-706-216-2	Sequence 2, Appl
425	28	56.0	423	2	US-09-008-722-2	Sequence 2, Appl	498	28	56.0	734	2	US-09-641-741-2	Sequence 2, Appl
426	28	56.0	426	2	US-09-134-001C-5210	Sequence 5210, Ap	499	28	56.0	734	2	US-09-650-284B-2	Sequence 2, Appl
427	28	56.0	434	2	US-09-252-991A-17427	Sequence 17427, A	500	28	56.0	798	2	US-09-583-110-3104	Sequence 3104, Ap
428	28	56.0	434	1	US-08-328-256-11	Sequence 11, Appl	501	28	56.0	804	2	US-09-067-091-2	Sequence 2, Appl
429	28	56.0	436	1	US-08-307-588-2	Sequence 2, Appl	502	28	56.0	804	2	US-09-107-433-4484	Sequence 4484, Ap
430	28	56.0	436	2	US-07-971-834-2	Sequence 2, Appl	503	28	56.0	835	2	US-09-701-868-8	Sequence 8, Appl
431	28	56.0	436	2	US-09-240-675-2	Sequence 2, Appl	504	28	56.0	855	2	US-09-949-016-6702	Sequence 6702, Ap
432	28	56.0	438	2	US-09-543-681A-8327	Sequence 8327, Ap	505	28	56.0	857	2	US-09-275-252A-11	Sequence 11, Appl
433	28	56.0	447	2	US-09-248-796A-20825	Sequence 20825, A	506	28	56.0	858	2	US-09-949-016-6702	Sequence 33, Appl
434	28	56.0	451	2	US-09-583-110-4585	Sequence 4585, Ap	507	28	56.0	868	1	US-08-162-081B-33	Sequence 33, Appl
435	28	56.0	451	2	US-09-107-433-4139	Sequence 4139, Ap	508	28	56.0	868	1	US-08-780-872-33	Sequence 33, Appl
436	28	56.0	451	2	US-10-012-231A-142	Sequence 142, App	509	28	56.0	868	2	US-09-085-957-33	Sequence 33, Appl
437	28	56.0	451	2	US-10-015-389A-142	Sequence 142, App	510	28	56.0	873	2	US-09-252-991A-31572	Sequence 31572, A
438	28	56.0	451	2	US-10-006-768A-142	Sequence 142, App	511	28	56.0	884	2	US-09-538-092-172	Sequence 172, App
439	28	56.0	451	2	US-10-015-671A-142	Sequence 142, App	512	28	56.0	884	2	US-09-538-092-172	Sequence 172, App
440	28	56.0	451	2	US-10-015-393A-142	Sequence 142, App	513	28	56.0	889	2	US-09-949-016-6036	Sequence 6036, Ap
441	28	56.0	451	2	US-10-011-833A-142	Sequence 142, App	514	28	56.0	901	2	US-09-710-279-342	Sequence 342, App
442	28	56.0	451	2	US-10-006-041A-142	Sequence 142, App	515	28	56.0	903	2	US-09-902-540-12957	Sequence 12957, A
443	28	56.0	451	2	US-10-012-064A-142	Sequence 142, App	516	28	56.0	904	2	US-09-252-991A-29119	Sequence 29119, A
444	28	56.0	458	2	US-09-902-540-12664	Sequence 12664, A	517	28	56.0	914	2	US-09-134-001C-5208	Sequence 5208, Ap
445	28	56.0	463	2	US-09-949-016-10540	Sequence 10540, A	518	28	56.0	919	2	US-09-248-796A-15156	Sequence 15156, A
446	28	56.0	469	2	US-09-328-352-4250	Sequence 4250, Ap	519	28	56.0	953	2	US-09-538-092-666	Sequence 666, App
447	28	56.0	473	2	US-09-934-899-4	Sequence 4, Appl	520	28	56.0	960	2	US-09-694-777A-21	Sequence 21, Appl
448	28	56.0	473	2	US-09-543-681A-4480	Sequence 4480, Ap	521	28	56.0	962	2	US-09-614-480-9	Sequence 9, Appl
449	28	56.0	473	2	US-09-934-868-24	Sequence 24, Appl	522	28	56.0	962	2	US-09-694-777A-3	Sequence 3, Appl
450	28	56.0	473	2	US-10-701-200-24	Sequence 24, Appl	523	28	56.0	962	2	US-09-694-777A-24	Sequence 24, Appl
451	28	56.0	481	2	US-09-134-078-15	Sequence 15, Appl	524	28	56.0	962	2	US-10-422-075-9	Sequence 9, Appl
452	28	56.0	483	2	US-09-489-039A-9824	Sequence 9824, Ap	525	28	56.0	987	2	US-09-694-777A-22	Sequence 22, Appl
453	28	56.0	487	2	US-09-691-344A-2	Sequence 2, Appl	526	28	56.0	988	2	US-09-614-480-2	Sequence 2, Appl
454	28	56.0	496	1	US-08-328-256-12	Sequence 12, Appl	527	28	56.0	988	2	US-10-162-012-5	Sequence 5, Appl
455	28	56.0	496	2	US-09-339-159B-28	Sequence 28, Appl	528	28	56.0	988	2	US-10-162-012-12	Sequence 12, Appl
456	28	56.0	504	2	US-09-086-436-33	Sequence 33, Appl	529	28	56.0	988	2	US-10-422-075-2	Sequence 2, Appl
457	28	56.0	510	2	US-09-543-681A-5654	Sequence 5654, Ap	530	28	56.0	989	2	US-09-694-777A-4	Sequence 4, Appl
458	28	56.0	514	2	US-09-252-991A-25281	Sequence 25281, A	531	28	56.0	989	2	US-09-694-777A-23	Sequence 23, Appl
459	28	56.0	523	2	US-09-323-195A-17	Sequence 17, Appl	532	28	56.0	1061	2	US-10-200-012-4	Sequence 4, Appl
460	28	56.0	525	2	US-09-773-428A-1	Sequence 1, Appl	533	28	56.0	1082	2	US-09-336-643A-20	Sequence 20, Appl
461	28	56.0	525	2	US-10-314-881-1	Sequence 1, Appl	534	28	56.0	1083	2	US-09-600-776-2	Sequence 2, Appl
462	28	56.0	528	2	US-09-495-823-1	Sequence 1, Appl	535	28	56.0	1083	2	US-09-343-494-1	Sequence 1, Appl
463	28	56.0	528	2	US-08-997-685A-4	Sequence 4, Appl	536	28	56.0	1083	2	US-09-358-383C-2	Sequence 2, Appl
464	28	56.0	535	2	US-09-248-796A-18860	Sequence 18860, A	537	28	56.0	1083	2	US-09-965-830-2	Sequence 2, Appl
465	28	56.0	539	2	US-09-691-344A-6	Sequence 6, Appl	538	28	56.0	1083	2	US-10-160-224-1	Sequence 1, Appl

539	28	56.0	1105	2	US-09-540-236-3299	Sequence 3299, Ap	612	27	54.0	53	2	US-09-165-042-7	Sequence 7, Appli
540	28	56.0	1297	1	US-08-290-731C-4	Sequence 4, Appli	613	27	54.0	53	2	US-09-311-021-112	Sequence 112, App
541	28	56.0	1319	1	US-08-290-731C-2	Sequence 2, Appli	614	27	54.0	57	2	US-07-741-453A-39	Sequence 39, Appl
542	28	56.0	1333	2	US-09-356-952-2	Sequence 2, Appli	615	27	54.0	61	2	US-09-134-001C-3104	Sequence 3104, Ap
543	28	56.0	1333	2	US-09-976-594-312	Sequence 312, App	616	27	54.0	63	2	US-09-188-930-176	Sequence 176, App
544	28	56.0	1336	1	US-08-290-731C-6	Sequence 6, Appli	617	27	54.0	63	2	US-09-328-352-5101	Sequence 5101, Ap
545	28	56.0	1346	2	US-09-949-016-9959	Sequence 959, Ap	618	27	54.0	63	2	US-09-312-283C-176	Sequence 176, App
546	28	56.0	1357	2	US-09-252-991A-21308	Sequence 21308, A	619	27	54.0	66	2	US-09-134-001C-5081	Sequence 5081, App
547	28	56.0	1438	2	US-09-209-916-1	Sequence 1, Appli	620	27	54.0	66	2	US-09-270-767-61597	Sequence 61597, A
548	28	56.0	1445	2	US-09-407-605-3	Sequence 3, Appli	621	27	54.0	68	2	US-09-248-796A-22145	Sequence 22145, A
549	28	56.0	1447	2	US-09-407-605-4	Sequence 4, Appli	622	27	54.0	68	2	US-09-248-796A-26072	Sequence 26072, A
550	28	56.0	1457	2	US-09-001-039B-47	Sequence 47, Appli	623	27	54.0	69	2	US-09-540-236-2584	Sequence 2584, Ap
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552	28	56.0	1548	1	US-08-463-092B-7	Sequence 7, Appli	625	27	54.0	70	2	US-09-208-210-6	Sequence 6, Appli
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844	27	54.0	382	2	US-09-614-912-6	Sequence 6, Appli	917	27	54.0	472	2	US-09-004-838-48	Sequence 48, Appl
845	27	54.0	385	2	US-09-540-236-3736	Sequence 3736, Ap	918	27	54.0	472	2	US-09-004-838-103	Sequence 103, App
846	27	54.0	387	2	US-09-457-302-1	Sequence 1, Appli	919	27	54.0	478	2	US-09-004-838-105	Sequence 105, App
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848	27	54.0	393	2	US-09-387-418A-10	Sequence 10, Appl	921	27	54.0	480	3	US-09-041-075A-5	Sequence 5, Appli
849	27	54.0	393	2	US-09-134-000C-4238	Sequence 4238, Ap	922	27	54.0	485	2	US-09-252-991A-25855	Sequence 25855, A
850	27	54.0	393	2	US-10-090-185-10	Sequence 10, Appl	923	27	54.0	485	2	US-09-540-236-2336	Sequence 2336, Ap
851	27	54.0	395	2	US-09-270-767-34718	Sequence 34718, A	924	27	54.0	494	2	US-09-252-991A-28022	Sequence 28022, A
852	27	54.0	395	2	US-09-270-767-49935	Sequence 49935, A	925	27	54.0	495	2	US-09-107-532A-6687	Sequence 6687, Ap
853	27	54.0	398	2	US-10-104-047-2010	Sequence 2010, Ap	926	27	54.0	495	2	US-09-275-252A-5	Sequence 5, Appli
854	27	54.0	402	2	US-09-025-578-2	Sequence 2, Appli	927	27	54.0	497	2	US-09-058-947A-4	Sequence 4, Appli
855	27	54.0	402	2	US-09-330-235-2	Sequence 2, Appli	928	27	54.0	498	2	US-10-183-992-2	Sequence 2, Appli
856	27	54.0	402	2	US-10-104-339-2	Sequence 2, Appli	929	27	54.0	499	2	US-09-487-558B-194	Sequence 194, App
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858	27	54.0	411	1	US-08-440-845D-3	Sequence 3, Appli	931	27	54.0	504	2	US-09-976-594-642	Sequence 642, App
859	27	54.0	411	2	US-08-868-458-3	Sequence 3, Appli	932	27	54.0	506	2	US-08-997-685A-6	Sequence 6, Appli
860	27	54.0	411	2	US-08-887-534A-80	Sequence 80, Appl	933	27	54.0	506	2	US-09-086-436-35	Sequence 35, Appl
861	27	54.0	411	2	US-09-527-431-80	Sequence 80, Appl	934	27	54.0	506	2	US-09-303-518D-692	Sequence 692, App
862	27	54.0	411	2	US-09-446-861-80	Sequence 80, Appl	935	27	54.0	506	2	US-09-303-518D-694	Sequence 694, App
863	27	54.0	413	2	US-09-252-991A-24646	Sequence 24646, A	936	27	54.0	506	2	US-09-303-518D-696	Sequence 696, App
864	27	54.0	414	2	US-09-134-001C-3357	Sequence 3357, Ap	937	27	54.0	515	2	US-09-949-016-5988	Sequence 5988, Ap
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866	27	54.0	414	2	US-09-583-110-4310	Sequence 4310, Ap	939	27	54.0	528	2	US-09-270-767-42895	Sequence 42895, A
867	27	54.0	414	2	US-09-769-787-76	Sequence 76, Appl	940	27	54.0	536	2	US-09-270-767-34532	Sequence 34532, A
868	27	54.0	415	2	US-09-107-433-3943	Sequence 3943, Ap	941	27	54.0	536	2	US-09-270-767-49749	Sequence 49749, A
869	27	54.0	420	2	US-08-685-871-58	Sequence 58, Appl	942	27	54.0	542	2	US-09-370-767-60932	Sequence 60932, A
870	27	54.0	423	2	US-09-710-279-3160	Sequence 3160, Ap	943	27	54.0	543	2	US-09-252-991A-18697	Sequence 18697, A
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872	27	54.0	427	2	US-09-540-236-3727	Sequence 3727, Ap	945	27	54.0	544	2	US-09-489-039A-13133	Sequence 13133, A
873	27	54.0	427	2	US-09-270-767-42751	Sequence 42751, A	946	27	54.0	546	2	US-09-489-039A-14231	Sequence 14231, A
874	27	54.0	428	2	US-09-173-300-36	Sequence 36, Appl	947	27	54.0	546	2	US-09-248-796A-17791	Sequence 17791, A
875	27	54.0	428	2	US-10-027-450-36	Sequence 36, Appl	948	27	54.0	549	2	US-09-107-532A-7304	Sequence 7304, Ap
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877	27	54.0	430	2	US-09-134-000C-4819	Sequence 4819, Ap	950	27	54.0	550	1	US-08-509-187D-4	Sequence 4, Appli
878	27	54.0	432	2	US-09-489-039A-8666	Sequence 8666, Ap	951	27	54.0	550	1	US-09-121-396-4	Sequence 4, Appli
879	27	54.0	433	2	US-10-152-886-11	Sequence 11, Appl	952	27	54.0	550	4	PCT-US93-09704A-4	Sequence 4, Appli
880	27	54.0	434	2	US-09-771-161A-92	Sequence 92, Appli	953	27	54.0	556	2	US-09-370-767-49749	Sequence 8, Appli
881	27	54.0	440	2	US-09-630-983A-9	Sequence 9, Appli	954	27	54.0	564	2	US-09-302-540-16486	Sequence 16486, A
882	27	54.0	440	2	US-09-603-208A-268	Sequence 268, App	955	27	54.0	566	2	US-09-514-245-18	Sequence 18, Appl
883	27	54.0	443	2	US-09-857-612A-14	Sequence 14, Appl	956	27	54.0	567	2	US-09-514-245-20	Sequence 20, Appl
884	27	54.0	455	1	US-08-278-729A-25	Sequence 25, Appl	957	27	54.0	569	2	US-09-949-016-6851	Sequence 6851, Ap
885	27	54.0	455	1	US-08-155-343A-25	Sequence 25, Appl	958	27	54.0	573	6	5215909-12	Patent No. 5215909
886	27	54.0	455	1	US-08-406-672-25	Sequence 25, Appl	959	27	54.0	574	2	US-09-248-796A-20132	Sequence 20132, A
887	27	54.0	455	1	US-08-643-563A-25	Sequence 25, Appl	960	27	54.0	576	2	US-09-540-236-2286	Sequence 2286, Ap
888	27	54.0	455	1	US-08-643-763A-25	Sequence 25, Appl	961	27	54.0	581	2	US-09-949-016-10225	Sequence 10225, A
889	27	54.0	455	1	US-08-462-623-25	Sequence 25, Appl	962	27	54.0	590	2	US-09-538-092-967	Sequence 967, App
890	27	54.0	455	1	US-08-451-953A-25	Sequence 25, Appl	963	27	54.0	590	2	US-09-826-509-517	Sequence 517, App
891	27	54.0	455	1	US-08-459-346-16	Sequence 16, Appl	964	27	54.0	610	2	US-09-270-767-46431	Sequence 46431, A
892	27	54.0	455	1	US-08-445-468A-25	Sequence 25, Appl	965	27	54.0	614	2	US-09-173-151A-16	Sequence 16, Appl
893	27	54.0	455	1	US-08-461-397A-25	Sequence 25, Appl	966	27	54.0	614	2	US-09-621-502-6	Sequence 6, Appli
894	27	54.0	455	1	US-08-912-088-25	Sequence 25, Appl	967	27	54.0	614	2	US-09-616-530A-2	Sequence 2, Appli
895	27	54.0	455	2	US-08-278-730A-25	Sequence 25, Appl	968	27	54.0	614	2	US-10-212-356A-2	Sequence 2, Appli
896	27	54.0	455	2	US-08-889-419-16	Sequence 16, Appl	969	27	54.0	614	2	US-10-212-287-2	Sequence 2, Appli
897	27	54.0	455	2	US-08-445-467-25	Sequence 25, Appl	970	27	54.0	615	1	US-08-272-255-7	Sequence 7, Appli
898	27	54.0	455	2	US-08-480-515A-25	Sequence 25, Appl	971	27	54.0	615	4	PCT-US95-08565-7	Sequence 7, Appli
899	27	54.0	455	2	US-08-271-556A-2	Sequence 2, Appli	972	27	54.0	617	2	US-09-565-264-2	Sequence 2, Appli
900	27	54.0	455	2	US-09-170-936-25	Sequence 25, Appl	973	27	54.0	617	2	US-09-565-264-4	Sequence 4, Appli
901	27	54.0	455	2	US-08-402-542-16	Sequence 16, Appl	974	27	54.0	618	2	US-09-134-000C-4522	Sequence 4522, Ap
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903	27	54.0	455	2	US-08-456-033-25	Sequence 25, Appl	976	27	54.0	633	2	US-09-583-110-4021	Sequence 4021, Ap

977 27 54.0 634 2 US-09-107-433-3905 Sequence 3905, Ap  
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979 27 54.0 649 2 US-09-605-703B-70 Sequence 70, Appl  
980 27 54.0 659 2 US-09-252-991A-19154 Sequence 19154, A  
981 27 54.0 659 2 US-09-489-039A-11739 Sequence 11739, A  
982 27 54.0 661 2 US-09-134-001C-4303 Sequence 4303, Ap  
983 27 54.0 663 2 US-09-270-767-45897 Sequence 45897, A  
984 27 54.0 667 2 US-09-902-540-15678 Sequence 15678, A  
985 27 54.0 671 2 US-09-248-796A-17595 Sequence 17595, A  
986 27 54.0 680 2 US-09-248-796A-15320 Sequence 15320, A  
987 27 54.0 680 2 US-09-902-540-16598 Sequence 16598, A  
988 27 54.0 686 2 US-09-134-000C-5166 Sequence 5166, Ap  
989 27 54.0 719 2 US-08-851-843A-7 Sequence 7, Appli  
990 27 54.0 719 2 US-08-974-549A-219 Sequence 219, App  
991 27 54.0 719 2 US-08-854-050-7 Sequence 7, Appli  
992 27 54.0 719 2 US-09-430-323-7 Sequence 7, Appli  
993 27 54.0 719 2 US-09-402-181B-219 Sequence 219, App  
994 27 54.0 719 2 US-09-721-456-219 Sequence 219, App  
995 27 54.0 719 2 US-09-766-253-7 Sequence 7, Appli  
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997 27 54.0 719 2 US-09-438-486A-7 Sequence 7, Appli  
998 27 54.0 722 2 US-09-198-452A-513 Sequence 513, App  
999 27 54.0 722 2 US-09-438-185A-477 Sequence 477, App  
1000 27 54.0 736 2 US-09-270-767-45427 Sequence 45427, A

ALIGNMENTS

RESULT 1  
US-09-489-039A-13868  
; Sequence 13868, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 13868  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13868

Query Match 78.0%; Score 39; DB 2; Length 585;  
Best Local Similarity 85.7%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
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Db 273 WFEIDVV 279

RESULT 2  
US-09-252-991A-24034  
; Sequence 24034, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 24034  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-24034

Query Match 72.0%; Score 36; DB 2; Length 373;  
Best Local Similarity 55.6%; Pred. No. 1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
: | | | | :  
Db 307 YLWVELDIV 315

RESULT 3  
US-09-266-225D-6  
; Sequence 6, Application US/09266225D  
; Patent No. 6573364  
; GENERAL INFORMATION:  
; APPLICANT: Nandabalan, Krishan  
; APPLICANT: Kingsmore, Stephen  
; APPLICANT: Tchernev, Velizar  
; TITLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak  
; TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein-  
; TITLE OF INVENTION: Interacting Proteins  
; FILE REFERENCE: 15966-523  
; CURRENT APPLICATION NUMBER: US/09/266,225D  
; CURRENT FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 700  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-266-225D-6

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Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
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Db 612 FLWFENDM 619

RESULT 4  
US-09-540-236-2405  
; Sequence 2405, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 2405  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: M.catarrhalis  
US-09-540-236-2405

Query Match 70.0%; Score 35; DB 2; Length 543;  
Best Local Similarity 55.6%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
| | | | |  
Db 308 FFWTEIDL 316



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RESULT 5
US-09-228-986-117
; Sequence 117, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-228-986-117

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Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEID 7
Db      33 LWFEVD 38

RESULT 6
US-10-101-464A-117
; Sequence 117, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-117

Query Match          70.0%; Score 35; DB 2; Length 599;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEID 7
Db      33 LWFEVD 38

RESULT 7
US-10-101-464A-827
; Sequence 827, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
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; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-827

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Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEID 7
Db      250 LWFEVD 255

RESULT 8
US-09-328-352-4456
; Sequence 4456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4456

Query Match          70.0%; Score 35; DB 2; Length 951;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEIDIV 9
Db      801 VWFKVDVV 808

RESULT 9
US-10-101-464A-976
; Sequence 976, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
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; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 976
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-976

Query Match      70.0%; Score 35; DB 2; Length 1240;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFELD 7
DB      674 LWFELD 679

RESULT 10
US-09-252-991A-29018
; Sequence 29018, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29018
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29018

Query Match      68.0%; Score 34; DB 2; Length 262;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFELD 7
DB      110 LWFELD 115

RESULT 11
US-09-270-767-60013
; Sequence 60013, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60013
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
```

```
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60013

Query Match      66.0%; Score 33; DB 2; Length 86;
Best Local Similarity 57.1%; Pred. No. 74;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEID 7
DB      78 FLWFEID 84

RESULT 12
US-08-952-736A-10
; Sequence 10, Application US/08952736A
; Patent No. 6320026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell Growth Inhibitory Factor
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,736A
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-952-736A-10

Query Match      66.0%; Score 33; DB 2; Length 309;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEID 7
DB      29 FKWFQID 35

RESULT 13
US-09-198-452A-1050
; Sequence 1050, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1050
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1050

Query Match      66.0%; Score 33; DB 2; Length 338;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEID 7
DB      115 FLWFEID 121
```

## RESULT 14

US-09-438-185A-979  
; Sequence 979, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kaiman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 979  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: Cpn0978  
US-09-438-185A-979

Query Match 66.0%; Score 33; DB 2; Length 347;  
Best Local Similarity 71.4%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:|:|:|  
Db 124 FIWFEKD 130

## RESULT 15

US-09-328-352-5961  
; Sequence 5961, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5961  
; LENGTH: 363  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5961

Query Match 66.0%; Score 33; DB 2; Length 363;  
Best Local Similarity 71.4%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:|:|:|  
Db 133 FIWFGID 139

## RESULT 16

US-08-676-166A-2  
; Sequence 2, Application US/08676166A  
; Patent No. 5955270  
; GENERAL INFORMATION:  
; APPLICANT: Radford, Alan  
; APPLICANT: Parish, John H.  
; TITLE OF INVENTION: EXPLOITATION OF THE CELLULASE COMPLEX OF  
; TITLE OF INVENTION: NEUROSPORA

Query Match 64.0%; Score 32; DB 2; Length 68;  
Best Local Similarity 62.5%; Pred. No. 88;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
STREET: Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/676,166A  
FILING DATE: 15-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1321-1-002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 516 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-676-166A-2

Query Match 66.0%; Score 33; DB 1; Length 516;  
Best Local Similarity 57.1%; Pred. No. 4.9e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEDI 8  
|:|:|:|  
Db 139 LWFVDVM 145

## RESULT 17

US-09-513-999C-4712  
; Sequence 4712, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4712  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -22...-1  
; OTHER INFORMATION: score 5.9  
; OTHER INFORMATION: seq LILWPFHLCVSS/IL  
US-09-513-999C-4712

Query Match 64.0%; Score 32; DB 2; Length 68;  
Best Local Similarity 62.5%; Pred. No. 88;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
QY      2 LWFEDIV 9
Db      13 LWFHDCV 20

RESULT 18
; Sequence 8587, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8587
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8587

Query Match      64.0%; Score 32; DB 2; Length 120;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      2 LWFEDIV 9
Db      34 MWIHDVI 41

RESULT 19
; Sequence 4094, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4094
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4094

Query Match      64.0%; Score 32; DB 2; Length 231;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 WFEIDIV 9
Db      108 WFDVDV 114

RESULT 20
; Sequence 5581, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
```

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; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5581
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5581

Query Match      64.0%; Score 32; DB 2; Length 279;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
Db      34 FIWFAGDLV 42

RESULT 21
; Sequence 7093, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7093
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7093

Query Match      64.0%; Score 32; DB 2; Length 308;
Best Local Similarity 62.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDI 8
Db      67 YLWFKPDI 74

RESULT 22
; Sequence 31938, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31938
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-31938

Query Match      64.0%; Score 32; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLWFE 5
          |||||
```

Db 223 FLWFE 227

RESULT 23

US-09-583-110-4999

; Sequence 4999, Application US/09583110

; Patent No. 6699703

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.

; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

; FILE REFERENCE: PAT00-07A

; CURRENT APPLICATION NUMBER: US/09/583,110

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/107,433

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/085,131

; PRIOR FILING DATE: 1998-05-12

; PRIOR APPLICATION NUMBER: US 60/051,553

; PRIOR FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 5322

; SEQ ID NO 4999

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

US-09-583-110-4999

Query Match 64.0%; Score 32; DB 2; Length 328;

Best Local Similarity 83.3%; Pred. No. 4.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEID 7

Db 73 LWFKID 78

RESULT 24

US-09-107-433-3112

; Sequence 3112, Application US/09107433

; Patent No. 6800744

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

; TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN

; THERAPEUTICS

; NUMBER OF SEQUENCES: 5206

; CORRESPONDENCE ADDRESS:

ADDRESSSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: CTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

US-09-107-433-3112

; INFORMATION FOR SEQ ID NO: 3112:

SEQUENCE CHARACTERISTICS:

LENGTH: 343 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (B) LOCATION 1...343

SEQUENCE DESCRIPTION: SEQ ID NO: 3112:

US-09-107-433-3112

Query Match 64.0%; Score 32; DB 2; Length 343;

Best Local Similarity 83.3%; Pred. No. 4.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEID 7

Db 88 LWFKID 93

RESULT 25

US-08-415-751-43

; Sequence 43, Application US/08415751

; Patent No. 5643772

; GENERAL INFORMATION:

; APPLICANT: PETERSEN, CAROLYN

; APPLICANT: LEECH, JAMES

; APPLICANT: NELSON, RICHARD, C.

; APPLICANT: GUT, JIRI

; TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-

; TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, DNA

; TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID

; TITLE OF INVENTION: VECTOR AND TRANSFORMED HOST AND

; TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

ADDRESSEE: PHILLIPS, MOORE, LEMPPIO & FINLEY

STREET: 385 Sherman Avenue, Suite 6

CITY: Palo Alto

STATE: California

COUNTRY: United States of America

ZIP: 94306-1840

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage

COMPUTER: PC

OPERATING SYSTEM: DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/415,751

FILING DATE: 03-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/071,880

FILING DATE: June 1, 1993

APPLICATION NUMBER: 07/891,301

FILING DATE: May 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Hana Dolezalova

REGISTRATION NUMBER: 30,518

REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-1677

TELEFAX: (415) 324-1678

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acid

STRANDEDNESS: single

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; NAME/KEY: Positions coded by nonsense codons are
; NAME/KEY: identified as Xaa.
US-08-415-751-43

Query Match          64.0%; Score 32; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
DB      236 FWFEPIDAV 244

RESULT 26
US-09-489-039A-12789
; Sequence 12789, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12789
; TYPE: PRT
; LENGTH: 419
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12789

Query Match          64.0%; Score 32; DB 2; Length 419;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDI 8
DB      45 FWFEEDEV 52

RESULT 27
US-09-107-532A-6160
; Sequence 6160, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
```

```
;
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...480
; SEQUENCE DESCRIPTION: SEQ ID NO: 6160:
US-09-107-532A-6160

Query Match          64.0%; Score 32; DB 2; Length 480;
Best Local Similarity 62.5%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDI 8
DB      99 FQWFEITV 106

RESULT 28
US-08-617-785-8
; Sequence 8, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopf, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-8

Query Match          64.0%; Score 32; DB 2; Length 481;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEID 7
DB      293 FIWFGVD 299

RESULT 29
```

US-09-817-464-8  
; Sequence 8, Application US/09817464  
; Patent No. 6515107  
; GENERAL INFORMATION:  
; APPLICANT: Flor, Peter J.  
; APPLICANT: Kuha, Ranier  
; APPLICANT: Lindaur, Kristen  
; APPLICANT: Putner, Irene  
; APPLICANT: Knopfel, Thomas  
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,  
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds  
; FILE REFERENCE: 4-19679/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/817,464  
; CURRENT FILING DATE: 2001-03-26  
; EARLIER APPLICATION NUMBER: US/08/617,785  
; EARLIER FILING DATE: 1996-03-19  
; EARLIER APPLICATION NUMBER: EPO 9416553.7  
; EARLIER FILING DATE: 1994-08-19  
; EARLIER APPLICATION NUMBER: EPO 93810663.0  
; EARLIER FILING DATE: 1993-09-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 481  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-817-464-8

Query Match 64.0%; Score 32; DB 2; Length 481;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:|:|:|  
Db 293 FWFQVD 299

RESULT 30  
US-08-657-749D-2  
; Sequence 2, Application US/08657749D  
; Patent No. 6828475  
; GENERAL INFORMATION:  
; APPLICANT: METZ, JAMES G.  
; APPLICANT: LARDIZABAL, KATHRYN D.  
; APPLICANT: LASSNER, MICHAEL  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING A PLANT CYTOPLASMIC  
; TITLE OF INVENTION: PROTEIN INVOLVED IN FATTY ACYL-COA METABOLISM  
; FILE REFERENCE: 16518.025  
; CURRENT APPLICATION NUMBER: US/08/657,749D  
; CURRENT FILING DATE: 1996-05-30  
; PRIOR APPLICATION NUMBER: PCT/US94/13686  
; PRIOR FILING DATE: 1994-11-30  
; PRIOR APPLICATION NUMBER: 08/265,047  
; PRIOR FILING DATE: 1994-06-23  
; PRIOR APPLICATION NUMBER: 08/160,602  
; PRIOR FILING DATE: 1993-11-30  
; PRIOR APPLICATION NUMBER: 08/066,299  
; PRIOR FILING DATE: 1993-05-20  
; PRIOR APPLICATION NUMBER: PCT/US92/09863  
; PRIOR FILING DATE: 1992-11-13  
; PRIOR APPLICATION NUMBER: 07/933,411  
; PRIOR FILING DATE: 1992-08-21  
; PRIOR APPLICATION NUMBER: 07/796,256  
; PRIOR FILING DATE: 1991-11-20  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 493  
; TYPE: PRT  
; ORGANISM: Simmondsia chinensis  
US-08-657-749D-2

Query Match 64.0%; Score 32; DB 2; Length 493;

Best Local Similarity 62.5%; Pred. No. 7.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9  
|:|:|:|  
Db 111 MWREIDVV 118

RESULT 31  
US-08-220-151-17  
; Sequence 17, Application US/08220151  
; Patent No. 5523780  
; GENERAL INFORMATION:  
; APPLICANT: Paoletti, Enzo  
; APPLICANT: Limbach, Keith J.  
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF  
; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC AND gD AND USES THEREFOR  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris & Safford  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/220,151  
; FILING DATE: 30-MAR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frommer, William S.  
; REGISTRATION NUMBER: 25,506  
; REFERENCE/DOCKET NUMBER: 454310-2540  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; TELEX: 425086 CURTWS  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 511 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal  
US-08-220-151-17

Query Match 64.0%; Score 32; DB 1; Length 511;  
Best Local Similarity 71.4%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:|:|:|  
Db 299 FWFQVD 305

RESULT 32  
US-08-413-118-17  
; Sequence 17, Application US/08413118  
; Patent No. 5688920  
; GENERAL INFORMATION:  
; APPLICANT: PAOLETTI, ENZO  
; APPLICANT: LIMBACH, KEITH J.  
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF  
; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.  
US-08-413-118-17

STREET: 530 FIFTH AVENUE, 25TH FLOOR  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/413,118  
FILING DATE: 29-MAR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/220,151  
FILING DATE: 30-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROMMER, WILLIAM S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2670  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 511 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-413-118-17

Query Match 64.0%; Score 32; DB 1; Length 511;  
Best Local Similarity 71.4%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:| | | |  
Db 299 FVWFEDD 305

RESULT 33  
US-08-473-446-17  
; Sequence 17, Application US/08473446  
; Patent No. 6017542  
; GENERAL INFORMATION:  
; APPLICANT: PAOLETTI, ENZO  
; APPLICANT: LIMBACH, KEITH J.  
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF  
; TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: CURTIS MORRIS & SAFFORD, P.C.  
; STREET: 530 FIFTH AVENUE, 25TH FLOOR  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/473,446  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/413,118  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

NAME: FROMMER, WILLIAM S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2670  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 511 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-473-446-17

Query Match 64.0%; Score 32; DB 2; Length 511;  
Best Local Similarity 71.4%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
|:| | | |  
Db 299 FVWFEDD 305

RESULT 34  
US-10-104-047-3625  
; Sequence 3625, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241el full length cdna  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 3625  
; LENGTH: 563  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3625

Query Match 64.0%; Score 32; DB 2; Length 563;  
Best Local Similarity 75.0%; Pred. No. 8.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9  
| | | | |  
Db 247 LWFGYDIV 254

RESULT 35  
US-09-248-796A-17643  
; Sequence 17643, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 17643  
; LENGTH: 575  
; TYPE: PRT



```
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (53),(57),(59)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-17643

Query Match      64.0%; Score 32; DB 2; Length 575;
Best Local Similarity 42.9%; Pred. No. 8.4e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLWFEID 7
Db      416 YLWYQVD 422

RESULT 36
US-09-252-991A-33133
; Sequence 33133, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33133
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33133

Query Match      64.0%; Score 32; DB 2; Length 754;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 WFEID 7
Db      235 WFEID 239

RESULT 37
US-10-101-464A-934
; Sequence 934, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 934
; LENGTH: 828
; TYPE: PRT
```

```
; ORGANISM: Pinus radiata
US-10-101-464A-934

Query Match      64.0%; Score 32; DB 2; Length 828;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLWFE 5
Db      292 FLWFE 296

RESULT 38
US-08-617-785-4
; Sequence 4, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-4

Query Match      64.0%; Score 32; DB 2; Length 867;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FLWFEID 7
Db      663 FIWFGVD 669

RESULT 39
US-09-817-464-4
; Sequence 4, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
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```
; SEQ ID NO 4
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-464-4

Query Match          64.0%; Score 32; DB 2; Length 867;
Best Local Similarity 57.1%; Pred. NO. 1.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEID 7
      |:|:|:|
Db       663 FIFWFGVD 669

RESULT 40
US-08-453-862-2
; Sequence 2, Application US/08453862
; Patent No. 5738999
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/452,734A
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-452-734A-2

Query Match          64.0%; Score 32; DB 1; Length 915;
Best Local Similarity 57.1%; Pred. NO. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEID 7
      |:|:|:|
Db       718 FIFWFGVD 724

RESULT 42
US-08-617-785-12
; Sequence 12, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttnher, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20

QY      1 FLWFEID 7
      |:|:|:|
Db       718 FIFWFGVD 724

RESULT 41
US-08-452-734A-2
; Sequence 2, Application US/08452734A
```

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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-12

Query Match          64.0%; Score 32; DB 2; Length 915;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLWFEID 7
Db 718 FIWFGVD 724

RESULT 43
US-08-176-401B-2
; Sequence 2, Application US/08176401B
; Patent No. 6274330
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,401B
; FILING DATE: 30-DECEMBER-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-401B-2

Query Match          64.0%; Score 32; DB 2; Length 915;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLWFEID 7
Db 718 FIWFGVD 724

RESULT 44
US-09-817-464-12
; Sequence 12, Application US/09817464
; Patent No. 6515107
```

```
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-464-12

Query Match          64.0%; Score 32; DB 2; Length 915;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLWFEID 7
Db 718 FIWFGVD 724

RESULT 45
PCT-US94-14989-2
; Sequence 2, Application PC/TUS9414989
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14989
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14989-2

Query Match          64.0%; Score 32; DB 4; Length 915;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLWFEID 7
```

```
Db          718 F1WFGVD 724
|:|:|:|
Matches      4;  Conservative      2;  Mismatches      1;  Indels      0;  Gaps      0;

RESULT 46
US-08-617-785-14
; Sequence 14, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopf, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-14

Query Match      64.0%;  Score 32;  DB 2;  Length 922;
Best Local Similarity 57.1%;  Pred. No. 1.4e+03;
Matches      4;  Conservative      2;  Mismatches      1;  Indels      0;  Gaps      0;

QY          1 F1WFEID 7
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Db          718 F1WFGVD 724

RESULT 47
US-09-817-464-14
; Sequence 14, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopf, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-464-14

Query Match      64.0%;  Score 32;  DB 2;  Length 922;
Best Local Similarity 57.1%;  Pred. No. 1.4e+03;
Matches      4;  Conservative      2;  Mismatches      1;  Indels      0;  Gaps      0;

QY          1 F1WFEID 7
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Db          718 F1WFGVD 724

RESULT 48
US-09-248-796A-21418
; Sequence 21418, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21418
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21418

Query Match      62.0%;  Score 31;  DB 2;  Length 63;
Best Local Similarity 66.7%;  Pred. No. 1.2e+02;
Matches      4;  Conservative      2;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 F1WFEI 6
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Db          57 F1WFEEL 62

RESULT 49
US-09-513-999C-5288
; Sequence 5288, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5288
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5288

Query Match      62.0%;  Score 31;  DB 2;  Length 65;
Best Local Similarity 57.1%;  Pred. No. 1.3e+02;
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|:|:|:|
Db          29 WFEEDVI 35

RESULT 50
US-09-248-796A-22411
; Sequence 22411, Application US/09248796A
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; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 22411  
; LENGTH: 66  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-22411

Query Match 62.0%; Score 31; DB 2; Length 66;  
Best Local Similarity 55.6%; Pred. No. 1.3e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

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Title: US-09-870-216C-7  
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Total number of hits satisfying chosen parameters: 1867569

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Post-processing: Minimum Match 0%  
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21	35	70.0	217	4	US-10-041-615-63
22	35	70.0	217	4	US-10-072-012-557
23	35	70.0	232	4	US-10-017-161-1002
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25	35	70.0	309	5	US-10-774-355A-1766
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37	35	70.0	326	4	US-10-292-798-446	Sequence 446, App
38	35	70.0	326	4	US-10-343-650A-640	Sequence 640, App
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40	35	70.0	599	5	US-10-864-252-117	Sequence 117, App
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108	32	64.0	54	4	US-10-437-963-157805	Sequence 157805,	181	32	64.0	464	3	US-09-815-242-13823	Sequence 13823, A
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114	32	64.0	63	3	US-09-864-761-38336	Sequence 38336, A	187	32	64.0	493	4	US-10-100-121-40	Sequence 40, Appl
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118	32	64.0	81	4	US-10-425-115-305248	Sequence 305248,	191	32	64.0	537	4	US-10-437-963-115732	Sequence 115732,
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142	32	64.0	229	3	US-09-815-242-5017	Sequence 5017, Ap	215	32	64.0	915	4	US-10-722-339-26	Sequence 26, Appl
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146	32	64.0	229	4	US-10-282-122A-51964	Sequence 51964, A	219	32	64.0	926	4	US-10-369-493-6955	Sequence 6955, Ap
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148	32	64.0	230	3	US-09-815-242-13052	Sequence 13052, A	221	32	64.0	1072	4	US-10-210-152-24	Sequence 24, Appl
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152	32	64.0	231	4	US-10-282-122A-71707	Sequence 71707, A	225	32	64.0	1264	4	US-10-375-693-30	Sequence 30, Appl
153	32	64.0	234	4	US-10-724-972A-5308	Sequence 5308, Ap	226	32	64.0	1827	4	US-10-425-115-272622	Sequence 272622,
154	32	64.0	254	4	US-10-424-599-143930	Sequence 143930,	227	31.5	63.0	1225	4	US-10-424-599-173554	Sequence 173554,
155	32	64.0	255	4	US-10-425-115-312766	Sequence 312766,	228	31	62.0	24	5	US-10-808-187-1911	Sequence 1911, Ap
156	32	64.0	258	4	US-10-437-963-181629	Sequence 181629,	229	31	62.0	24	5	US-10-807-807-1911	Sequence 1911, Ap
157	32	64.0	265	4	US-10-437-963-187113	Sequence 187113,	230	31	62.0	38	5	US-10-450-763-30873	Sequence 30873, A
158	32	64.0	278	4	US-10-425-115-205979	Sequence 205979,	231	31	62.0	46	4	US-10-425-115-274400	Sequence 274400,
159	32	64.0	285	5	US-10-851-921-12	Sequence 12, Appl	232	31	62.0	48	4	US-10-424-599-211940	Sequence 211940,
160	32	64.0	305	4	US-10-425-115-205981	Sequence 205981,	233	31	62.0	48	4	US-10-437-963-180494	Sequence 180494,
161	32	64.0	306	4	US-10-425-114-64430	Sequence 64430, A	234	31	62.0	52	3	US-09-864-761-44492	Sequence 44492, A
162	32	64.0	314	4	US-10-425-114-55956	Sequence 55956, A	235	31	62.0	56	4	US-10-424-599-150983	Sequence 150983,
163	32	64.0	328	3	US-09-815-242-13242	Sequence 13242, A	236	31	62.0	59	4	US-10-424-599-185465	Sequence 185465,
164	32	64.0	328	4	US-10-282-122A-73699	Sequence 73699, A	237	31	62.0	60	4	US-10-424-599-184567	Sequence 184567,
165	32	64.0	328	4	US-10-282-122A-74524	Sequence 74524, A	238	31	62.0	63	4	US-10-425-115-285330	Sequence 285330,
166	32	64.0	328	4	US-10-474-776-752	Sequence 752, App	239	31	62.0	71	4	US-10-424-599-283142	Sequence 283142,
167	32	64.0	328	5	US-10-472-928-4908	Sequence 4908, Ap	240	31	62.0	73	3	US-09-973-278-183	Sequence 183, App
168	32	64.0	342	4	US-10-369-493-8532	Sequence 8532, Ap	241	31	62.0	74	3	US-09-983-802-210	Sequence 210, App
169	32	64.0	343	5	US-10-617-320-3112	Sequence 3112, Ap	242	31	62.0	83	4	US-09-984-490-210	Sequence 210, App
170	32	64.0	357	5	US-10-732-923-11210	Sequence 11210, A	243	31	62.0	84	4	US-10-437-963-190127	Sequence 190127,
171	32	64.0	364	4	US-10-108-260A-4612	Sequence 4612, Ap	244	31	62.0	85	4	US-10-424-599-252408	Sequence 252408,
172	32	64.0	399	4	US-10-425-115-358093	Sequence 358093,	245	31	62.0	92	4	US-10-425-115-211858	Sequence 211858,
173	32	64.0	400	4	US-10-425-114-64282	Sequence 64282, A	246	31	62.0	94	4	US-10-424-599-191533	Sequence 191533,



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248	31	62.0	101	4	US-10-437-963-158983	Sequence 158983,	321	31	62.0	557	4	US-10-094-749-2409	Sequence 2409, Ap
249	31	62.0	104	4	US-10-424-599-254751	Sequence 254751,	322	31	62.0	569	4	US-10-014-137-3	Sequence 3, Appli
250	31	62.0	108	4	US-10-425-115-231740	Sequence 231740,	323	31	62.0	569	6	US-11-097-143-5388	Sequence 5388, Ap
251	31	62.0	112	4	US-10-424-599-239480	Sequence 239480,	324	31	62.0	569	4	US-10-437-963-195197	Sequence 195197,
252	31	62.0	113	4	US-10-108-2608-3204	Sequence 3204, Ap	325	31	62.0	585	4	US-10-437-963-158013	Sequence 158013,
253	31	62.0	113	5	US-10-482-029-206	Sequence 206, App	326	31	62.0	591	4	US-10-479-435-18	Sequence 18, Appl
254	31	62.0	119	4	US-10-424-599-268611	Sequence 268611,	327	31	62.0	622	3	US-09-966-803-2	Sequence 2, Appli
255	31	62.0	121	4	US-10-424-599-282373	Sequence 282373,	328	31	62.0	623	3	US-09-159-469-68	Sequence 68, Appl
256	31	62.0	140	4	US-10-156-761-9614	Sequence 9614, Ap	329	31	62.0	623	3	US-09-798-042-68	Sequence 68, Appl
257	31	62.0	144	4	US-10-767-701-61195	Sequence 61195, A	330	31	62.0	623	3	US-09-953-108-68	Sequence 146017,
258	31	62.0	147	4	US-10-767-701-36763	Sequence 36763, A	331	31	62.0	634	4	US-10-424-599-146017	Sequence 17823, A
259	31	62.0	150	4	US-10-767-701-60282	Sequence 60282, A	332	31	62.0	649	4	US-10-369-493-17823	Sequence 3971, Ap
260	31	62.0	152	5	US-10-732-923-6640	Sequence 6640, Ap	333	31	62.0	663	4	US-10-369-493-3971	Sequence 4877, Ap
261	31	62.0	154	4	US-10-424-599-145641	Sequence 145641,	334	31	62.0	680	3	US-09-738-626-4877	Sequence 11838,
262	31	62.0	167	4	US-10-424-599-184809	Sequence 184809,	335	31	62.0	693	4	US-10-437-963-111838	Sequence 11838,
263	31	62.0	175	3	US-09-159-469-29	Sequence 29, Appl	336	31	62.0	754	4	US-10-425-563-18	Sequence 18, Appl
264	31	62.0	175	3	US-09-798-042-29	Sequence 29, Appl	337	31	62.0	754	5	US-10-972-789A-18	Sequence 18, Appl
265	31	62.0	175	3	US-09-953-108-29	Sequence 29, Appl	338	31	62.0	811	3	US-09-975-719-93	Sequence 93, Appl
266	31	62.0	191	4	US-10-080-170-199	Sequence 199, App	339	31	62.0	841	5	US-10-499-580-11	Sequence 11, Appl
267	31	62.0	191	4	US-10-080-170-199	Sequence 199, App	340	31	62.0	859	4	US-10-437-963-110627	Sequence 110627,
268	31	62.0	191	4	US-10-468-356-199	Sequence 199, App	341	31	62.0	861	4	US-10-437-963-102699	Sequence 102699,
269	31	62.0	198	4	US-10-425-115-287806	Sequence 287806,	342	31	62.0	878	4	US-10-369-493-3401	Sequence 3401, Ap
270	31	62.0	199	4	US-10-767-701-56889	Sequence 56889, A	343	31	62.0	889	5	US-10-732-923-16965	Sequence 16965, A
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272	31	62.0	220	6	US-10-424-599-179129	Sequence 179129,	345	31	62.0	890	4	US-10-060-425-8	Sequence 8, Appli
273	31	62.0	221	4	US-10-424-599-179130	Sequence 179130,	346	31	62.0	890	4	US-10-060-425-10	Sequence 10, Appl
274	31	62.0	223	3	US-09-864-408A-8706	Sequence 8706, Ap	347	31	62.0	893	5	US-10-450-763-57336	Sequence 57336, A
275	31	62.0	223	5	US-10-474-792-466	Sequence 466, App	348	31	62.0	904	3	US-09-801-368-272	Sequence 272, App
276	31	62.0	229	4	US-10-282-122A-60423	Sequence 60423, A	349	31	62.0	904	4	US-10-149-310-186	Sequence 186, App
277	31	62.0	247	4	US-10-425-115-206664	Sequence 206664,	350	31	62.0	908	4	US-10-225-567A-184	Sequence 184, App
278	31	62.0	247	4	US-10-424-599-179129	Sequence 179129,	351	31	62.0	908	4	US-10-353-690-86	Sequence 86, Appl
279	31	62.0	255	4	US-10-282-122A-46977	Sequence 46977, A	352	31	62.0	908	4	US-10-722-357-28	Sequence 28, Appl
280	31	62.0	256	4	US-10-424-599-152516	Sequence 152516,	353	31	62.0	908	4	US-10-757-262-80	Sequence 80, Appl
281	31	62.0	259	4	US-10-282-122A-46698	Sequence 46698, A	354	31	62.0	908	5	US-10-482-029-279	Sequence 279, App
282	31	62.0	262	4	US-10-469-552-2	Sequence 2, Appli	355	31	62.0	908	5	US-10-967-091-4	Sequence 4, Appli
283	31	62.0	264	4	US-10-425-115-362770	Sequence 362770,	356	31	62.0	908	5	US-10-499-580-3	Sequence 3, Appli
284	31	62.0	275	3	US-09-966-521-114	Sequence 114, App	357	31	62.0	908	5	US-10-499-580-5	Sequence 5, Appli
285	31	62.0	275	4	US-10-429-094-114	Sequence 114, App	358	31	62.0	908	5	US-10-499-580-7	Sequence 7, Appli
286	31	62.0	278	4	US-10-424-599-173186	Sequence 173186,	359	31	62.0	908	5	US-10-499-580-9	Sequence 9, Appli
287	31	62.0	282	4	US-10-051-874-97	Sequence 97, Appl	360	31	62.0	913	5	US-10-450-763-59811	Sequence 59811, A
288	31	62.0	284	4	US-10-724-972A-4940	Sequence 4940, Ap	361	31	62.0	973	4	US-10-437-963-110483	Sequence 110483,
289	31	62.0	285	4	US-10-437-963-200631	Sequence 200631,	362	31	62.0	1003	4	US-10-437-963-174214	Sequence 174214,
290	31	62.0	286	4	US-10-437-963-149193	Sequence 149193,	363	31	62.0	1019	4	US-10-183-992-8	Sequence 8, Appli
291	31	62.0	289	4	US-10-437-963-158981	Sequence 158981,	364	31	62.0	1019	4	US-10-638-125-4	Sequence 4, Appli
292	31	62.0	290	4	US-10-282-122A-44286	Sequence 44286, A	365	31	62.0	1019	5	US-10-480-254-8	Sequence 8, Appli
293	31	62.0	290	5	US-10-857-625-726	Sequence 726, App	366	31	62.0	1078	4	US-10-437-963-110520	Sequence 110520,
294	31	62.0	290	5	US-10-470-048B-219	Sequence 219, App	367	31	62.0	1083	4	US-10-183-992-6	Sequence 6, Appli
295	31	62.0	298	4	US-10-424-599-249024	Sequence 249024,	368	31	62.0	1083	4	US-10-638-125-2	Sequence 2, Appli
296	31	62.0	299	4	US-10-032-585-7087	Sequence 7087, Ap	369	31	62.0	1083	5	US-10-480-254-6	Sequence 106873,
297	31	62.0	303	4	US-10-437-963-196593	Sequence 196593,	370	31	62.0	1141	4	US-10-437-963-106873	Sequence 8430, Ap
298	31	62.0	316	4	US-10-425-115-270124	Sequence 270124,	371	31	62.0	1141	5	US-10-732-923-8430	Sequence 59810, A
299	31	62.0	322	4	US-10-051-874-96	Sequence 96, Appl	372	31	62.0	1142	5	US-10-450-763-59810	Sequence 7858, Ap
300	31	62.0	360	4	US-10-156-761-8903	Sequence 8903, Ap	373	31	62.0	1262	4	US-10-032-585-7858	Sequence 7, Appli
301	31	62.0	362	4	US-10-424-599-268108	Sequence 268108,	374	31	62.0	2005	5	US-10-768-791-7	Sequence 7, Appli
302	31	62.0	363	4	US-10-099-322-120	Sequence 120, App	375	31	62.0	2005	5	US-10-469-865-5	Sequence 5, Appli
303	31	62.0	363	4	US-10-044-564-120	Sequence 120, App	376	31	62.0	2329	5	US-10-469-865-2	Sequence 2, Appli
304	31	62.0	374	5	US-10-732-923-6483	Sequence 6483, Ap	377	31	62.0	2335	5	US-10-469-865-4	Sequence 4, Appli
305	31	62.0	380	4	US-10-369-493-22339	Sequence 22339, A	378	31	62.0	2396	5	US-10-469-865-4	Sequence 4, Appli
306	31	62.0	391	4	US-10-437-963-161769	Sequence 161769,	379	31	62.0	2396	6	US-11-097-143-18933	Sequence 18933, A
307	31	62.0	396	4	US-10-156-761-12672	Sequence 12672, A	380	31	62.0	2416	4	US-10-032-585-7352	Sequence 7352, Ap
308	31	62.0	407	4	US-10-437-963-135581	Sequence 135581,	381	31	62.0	2749	4	US-10-360-101-265	Sequence 265, App
309	31	62.0	423	4	US-10-437-963-128665	Sequence 128665,	382	31	62.0	4472	6	US-11-097-143-7095	Sequence 7095, Ap
310	31	62.0	439	4	US-10-437-963-146385	Sequence 146385,	383	31	62.0	4544	4	US-10-085-198-22	Sequence 22, Appl
311	31	62.0	460	4	US-10-369-493-5528	Sequence 5528, Ap	384	31	62.0	4585	5	US-10-917-242-6	Sequence 6, Appli
312	31	62.0	462	4	US-10-437-963-123441	Sequence 123441,	385	31	62.0	4588	5	US-10-917-242-8	Sequence 8, Appli
313	31	62.0	464	3	US-09-815-242-10202	Sequence 10202, A	386	31	62.0	4588	5	US-10-917-242-2	Sequence 2, Appli
314	31	62.0	475	4	US-10-369-493-18894	Sequence 18894, A	387	30.5	61.0	50	4	US-10-437-963-109071	Sequence 109071,
315	31	62.0	479	6	US-11-097-143-12792	Sequence 12792, A	388	30	60.0	12	4	US-10-353-929-189	Sequence 189, App
316	31	62.0	486	4	US-10-369-493-21930	Sequence 21930, A	389	30	60.0	12	4	US-10-225-567A-2041	Sequence 2041, App
317	31	62.0	496	4	US-10-425-563-16	Sequence 16, Appl	390	30	60.0	15	5	US-10-946-647-772	Sequence 772, App
318	31	62.0	497	5	US-10-972-789A-16	Sequence 16, Appl	391	30	60.0	35	3	US-09-885-441-3	Sequence 3, Appli
319	31	62.0	533	4	US-10-282-122A-77235	Sequence 77235, A	392	30	60.0	35	4	US-10-424-836-3	Sequence 3, Appli

393	30	60.0	41	4	US-10-425-115-271912	Sequence 271912,	466	30	60.0	243	4	US-10-424-599-261103	Sequence 261103,
394	30	60.0	42	3	US-09-885-441-7	Sequence 7, Appli	467	30	60.0	247	4	US-10-425-114-62079	Sequence 62079, A
395	30	60.0	42	4	US-10-424-836-7	Sequence 7, Appli	468	30	60.0	255	5	US-10-739-930-8954	Sequence 8954, Ap
396	30	60.0	43	4	US-10-425-115-301637	Sequence 301637,	469	30	60.0	259	4	US-10-369-493-20007	Sequence 20007, A
397	30	60.0	46	4	US-10-425-115-230274	Sequence 290274,	470	30	60.0	260	3	US-09-885-441-58	Sequence 58, Appl
398	30	60.0	51	4	US-10-424-599-139716	Sequence 199716,	471	30	60.0	260	4	US-10-424-836-58	Sequence 58, Appl
399	30	60.0	54	4	US-10-425-115-367857	Sequence 367857,	472	30	60.0	261	4	US-10-369-493-21010	Sequence 21010, A
400	30	60.0	57	4	US-10-424-599-166309	Sequence 166309,	473	30	60.0	262	4	US-10-262-511-74	Sequence 74, Appl
401	30	60.0	62	4	US-10-425-115-368168	Sequence 368168,	474	30	60.0	262	4	US-10-767-701-34983	Sequence 34983, A
402	30	60.0	64	4	US-10-424-599-134352	Sequence 134352,	475	30	60.0	265	4	US-10-425-115-312829	Sequence 312829,
403	30	60.0	69	4	US-10-425-115-195415	Sequence 195415,	476	30	60.0	269	4	US-10-467-042-1	Sequence 1, Appli
404	30	60.0	70	4	US-10-437-963-112853	Sequence 112853,	477	30	60.0	269	6	US-11-046-868-1	Sequence 1, Appli
405	30	60.0	71	4	US-10-424-599-184926	Sequence 184926,	478	30	60.0	270	4	US-10-282-122A-57762	Sequence 57762, A
406	30	60.0	75	4	US-10-424-599-275692	Sequence 275692,	479	30	60.0	272	4	US-10-424-599-155379	Sequence 155379,
407	30	60.0	74	4	US-10-425-115-359523	Sequence 359523,	480	30	60.0	275	3	US-09-885-441-2	Sequence 2, Appli
408	30	60.0	76	4	US-10-424-599-196619	Sequence 196619,	481	30	60.0	279	4	US-10-424-836-2	Sequence 2, Appli
409	30	60.0	77	4	US-10-437-963-119210	Sequence 119210,	482	30	60.0	280	4	US-10-424-599-190352	Sequence 190352,
410	30	60.0	77	4	US-10-767-701-41937	Sequence 41937, A	483	30	60.0	281	4	US-10-424-599-239902	Sequence 239902,
411	30	60.0	83	4	US-10-425-115-358586	Sequence 358586,	484	30	60.0	284	4	US-10-425-115-312761	Sequence 312761,
412	30	60.0	85	4	US-10-437-963-169921	Sequence 169921,	485	30	60.0	287	4	US-10-424-599-185725	Sequence 185725,
413	30	60.0	86	4	US-10-424-599-199921	Sequence 199921,	486	30	60.0	289	4	US-10-407-960-2	Sequence 2, Appli
414	30	60.0	86	4	US-10-425-115-191833	Sequence 191833,	487	30	60.0	290	3	US-09-999-121-3	Sequence 3, Appli
415	30	60.0	87	5	US-10-450-763-48796	Sequence 48796, A	488	30	60.0	292	3	US-09-051-755-10	Sequence 10, Appl
416	30	60.0	92	4	US-10-437-963-121092	Sequence 121092,	489	30	60.0	292	4	US-10-231-055-10	Sequence 10, Appl
417	30	60.0	94	4	US-10-437-963-151265	Sequence 151265,	490	30	60.0	296	3	US-09-888-615-85	Sequence 85, Appl
418	30	60.0	102	4	US-10-425-115-235769	Sequence 235769,	491	30	60.0	297	6	US-11-044-853-22	Sequence 22, Appl
419	30	60.0	107	3	US-09-864-408A-494	Sequence 494, App	492	30	60.0	305	3	US-09-885-441-57	Sequence 57, Appl
420	30	60.0	108	4	US-10-767-701-50047	Sequence 50047, A	493	30	60.0	305	4	US-10-239-663-56	Sequence 56, Appl
421	30	60.0	116	4	US-10-424-599-233059	Sequence 233059,	494	30	60.0	306	5	US-10-424-836-57	Sequence 57, Appl
422	30	60.0	118	4	US-10-424-599-245418	Sequence 245418,	495	30	60.0	306	5	US-10-015-989A-53	Sequence 53, Appl
423	30	60.0	130	4	US-10-425-115-314009	Sequence 314009,	496	30	60.0	308	5	US-10-739-930-8860	Sequence 8860, Ap
424	30	60.0	133	4	US-10-437-963-170597	Sequence 170597,	497	30	60.0	311	4	US-10-117-323-41	Sequence 41, Appl
425	30	60.0	135	4	US-10-424-599-233949	Sequence 233949,	498	30	60.0	312	4	US-10-040-647-4	Sequence 4, Appli
426	30	60.0	135	4	US-10-424-599-246693	Sequence 246693,	499	30	60.0	312	4	US-10-051-874-100	Sequence 100, App
427	30	60.0	136	4	US-10-767-701-60129	Sequence 60129, A	500	30	60.0	312	4	US-10-173-999-138	Sequence 138, App
428	30	60.0	138	4	US-10-425-115-208990	Sequence 208990,	501	30	60.0	314	3	US-09-968-415-3	Sequence 3, Appli
429	30	60.0	146	4	US-10-424-599-193495	Sequence 193495,	502	30	60.0	314	3	US-09-909-320-257	Sequence 257, App
430	30	60.0	156	4	US-10-424-599-178418	Sequence 178418,	503	30	60.0	314	3	US-09-885-441-14	Sequence 14, Appl
431	30	60.0	162	4	US-10-437-963-130749	Sequence 130749,	504	30	60.0	314	3	US-09-909-088B-257	Sequence 257, App
432	30	60.0	164	4	US-10-424-599-226733	Sequence 226733,	505	30	60.0	314	3	US-09-905-291A-257	Sequence 257, App
433	30	60.0	169	4	US-10-425-115-191361	Sequence 191361,	506	30	60.0	314	3	US-09-902-853-257	Sequence 257, App
434	30	60.0	170	4	US-10-437-963-192346	Sequence 192346,	507	30	60.0	314	3	US-09-907-824-257	Sequence 257, App
435	30	60.0	174	4	US-10-424-599-234872	Sequence 234872,	508	30	60.0	314	3	US-09-907-841-257	Sequence 257, App
436	30	60.0	174	4	US-10-276-774-1849	Sequence 1849, Ap	509	30	60.0	314	3	US-09-904-011-257	Sequence 257, App
437	30	60.0	178	4	US-10-425-115-214175	Sequence 214175,	510	30	60.0	314	3	US-09-903-640-257	Sequence 257, App
438	30	60.0	178	4	US-10-425-115-293216	Sequence 293216,	511	30	60.0	314	3	US-09-908-093-257	Sequence 257, App
439	30	60.0	179	4	US-10-424-599-265698	Sequence 265698,	512	30	60.0	314	3	US-09-906-742-257	Sequence 257, App
440	30	60.0	181	4	US-10-437-963-170717	Sequence 170717,	513	30	60.0	314	3	US-09-906-838-257	Sequence 257, App
441	30	60.0	188	4	US-10-425-114-58068	Sequence 58068, A	514	30	60.0	314	3	US-09-907-613-257	Sequence 257, App
442	30	60.0	191	4	US-10-437-963-192345	Sequence 192345,	515	30	60.0	314	3	US-09-907-942-257	Sequence 257, App
443	30	60.0	192	5	US-10-472-928-1138	Sequence 1138, Ap	516	30	60.0	314	3	US-09-904-859-257	Sequence 257, App
444	30	60.0	192	5	US-10-617-320-4762	Sequence 4762, Ap	517	30	60.0	314	3	US-09-908-204-257	Sequence 257, App
445	30	60.0	193	4	US-10-424-599-277691	Sequence 277691,	518	30	60.0	314	3	US-09-904-820-257	Sequence 257, App
446	30	60.0	194	3	US-09-252-088-24	Sequence 24, Appl	519	30	60.0	314	3	US-09-904-786-257	Sequence 257, App
447	30	60.0	194	4	US-10-340-792-24	Sequence 24, Appl	520	30	60.0	314	3	US-09-906-646-257	Sequence 257, App
448	30	60.0	195	4	US-10-282-122A-72459	Sequence 72459, A	521	30	60.0	314	3	US-09-906-700-257	Sequence 257, App
449	30	60.0	197	5	US-10-501-282-1854	Sequence 1854, Ap	522	30	60.0	314	3	US-09-903-786-257	Sequence 257, App
450	30	60.0	199	4	US-10-282-122A-61680	Sequence 61680, A	523	30	60.0	314	3	US-09-902-933-257	Sequence 257, App
451	30	60.0	200	4	US-10-424-599-226505	Sequence 226505,	524	30	60.0	314	3	US-09-903-749A-257	Sequence 257, App
452	30	60.0	201	4	US-10-282-122A-62557	Sequence 62557, A	525	30	60.0	314	3	US-09-904-119-257	Sequence 257, App
453	30	60.0	201	4	US-10-282-122A-62550	Sequence 62550, A	526	30	60.0	314	3	US-09-904-956-257	Sequence 257, App
454	30	60.0	202	4	US-10-282-122A-53741	Sequence 53741, A	527	30	60.0	314	3	US-09-902-736-257	Sequence 257, App
455	30	60.0	211	3	US-09-738-626-5266	Sequence 5266, Ap	528	30	60.0	314	3	US-09-907-794-257	Sequence 257, App
456	30	60.0	211	3	US-09-791-932-97	Sequence 97, Appl	529	30	60.0	314	3	US-09-903-943-257	Sequence 257, App
457	30	60.0	213	4	US-10-424-599-268438	Sequence 268438,	530	30	60.0	314	3	US-09-904-462-257	Sequence 257, App
458	30	60.0	215	4	US-10-767-701-38925	Sequence 38925, A	531	30	60.0	314	3	US-09-907-925-257	Sequence 257, App
459	30	60.0	216	5	US-10-501-282-1856	Sequence 1856, Ap	532	30	60.0	314	3	US-09-902-692-257	Sequence 257, App
460	30	60.0	218	4	US-10-424-599-231242	Sequence 231242,	533	30	60.0	314	3	US-09-903-520-257	Sequence 257, App
461	30	60.0	226	4	US-10-437-963-182765	Sequence 182765,	534	30	60.0	314	3	US-09-905-056-257	Sequence 257, App
462	30	60.0	233	5	US-10-450-763-53130	Sequence 53130, A	535	30	60.0	314	3	US-09-908-084-257	Sequence 257, App
463	30	60.0	239	4	US-10-424-599-233058	Sequence 233058,	536	30	60.0	314	3	US-09-904-553-257	Sequence 257, App
464	30	60.0	240	3	US-09-978-248-4	Sequence 4, Appli	537	30	60.0	314	3	US-09-905-381-257	Sequence 257, App
465	30	60.0	241	4	US-10-425-114-68628	Sequence 68628, A	538	30	60.0	314	3	US-09-904-485-257	Sequence 257, App

539	30	60.0	314	3	US-09-905-348-257	Sequence 257, App	612	30	60.0	322	4	US-10-321-807-20	Sequence 20, Appl
540	30	60.0	314	3	US-09-905-088-257	Sequence 257, App	613	30	60.0	322	4	US-10-314-048A-20	Sequence 20, Appl
541	30	60.0	314	3	US-09-907-575-257	Sequence 257, App	614	30	60.0	322	5	US-10-481-161-2	Sequence 2, Appl
542	30	60.0	314	3	US-09-905-075-257	Sequence 257, App	615	30	60.0	322	5	US-10-897-815-20	Sequence 20, Appl
543	30	60.0	314	3	US-09-902-759-257	Sequence 257, App	616	30	60.0	322	5	US-10-957-135-16	Sequence 16, Appl
544	30	60.0	314	3	US-09-902-634-257	Sequence 257, App	617	30	60.0	322	5	US-10-930-662-20	Sequence 20, Appl
545	30	60.0	314	3	US-09-902-713-257	Sequence 257, App	618	30	60.0	322	6	US-11-083-611-16	Sequence 16, Appl
546	30	60.0	314	3	US-09-907-979-257	Sequence 257, App	619	30	60.0	322	6	US-11-117-746-4	Sequence 4, Appl
547	30	60.0	314	3	US-09-902-615-257	Sequence 257, App	620	30	60.0	323	3	US-09-791-932-119	Sequence 119, App
548	30	60.0	314	3	US-09-903-925-257	Sequence 257, App	621	30	60.0	323	3	US-10-333-156-1	Sequence 1, Appl
549	30	60.0	314	3	US-09-906-760A-257	Sequence 257, App	622	30	60.0	334	3	US-09-885-441-56	Sequence 56, Appl
550	30	60.0	314	3	US-09-903-823-257	Sequence 257, App	623	30	60.0	334	4	US-10-424-836-56	Sequence 56, Appl
551	30	60.0	314	3	US-09-907-652-257	Sequence 257, App	624	30	60.0	334	4	US-10-425-115-337582	Sequence 337582, Appl
552	30	60.0	314	3	US-09-902-572A-257	Sequence 257, App	625	30	60.0	336	4	US-10-425-114-64770	Sequence 64770, A
553	30	60.0	314	3	US-09-902-979-257	Sequence 257, App	626	30	60.0	336	4	US-10-425-115-362664	Sequence 362664, A
554	30	60.0	314	3	US-09-905-125-257	Sequence 257, App	627	30	60.0	339	4	US-10-283-122A-78104	Sequence 78104, A
555	30	60.0	314	3	US-09-906-815A-257	Sequence 257, App	628	30	60.0	340	3	US-09-815-242-5044	Sequence 5044, Ap
556	30	60.0	314	3	US-09-905-449-257	Sequence 257, App	629	30	60.0	341	3	US-09-815-242-10462	Sequence 10462, A
557	30	60.0	314	3	US-09-903-806-257	Sequence 257, App	630	30	60.0	341	3	US-09-815-242-11726	Sequence 11726, A
558	30	60.0	314	3	US-09-904-992-257	Sequence 257, App	631	30	60.0	341	4	US-10-282-122A-43415	Sequence 43415, A
559	30	60.0	314	3	US-09-904-838-257	Sequence 257, App	632	30	60.0	341	4	US-10-282-122A-56319	Sequence 56319, A
560	30	60.0	314	3	US-09-906-777-257	Sequence 257, App	633	30	60.0	341	4	US-10-282-122A-56801	Sequence 56801, A
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562	30	60.0	314	3	US-09-904-532-257	Sequence 257, App	635	30	60.0	341	4	US-10-437-963-176081	Sequence 176081, A
563	30	60.0	314	3	US-09-904-766-257	Sequence 257, App	636	30	60.0	343	4	US-10-424-599-251373	Sequence 251373, A
564	30	60.0	314	3	US-09-904-920A-257	Sequence 257, App	637	30	60.0	344	4	US-10-437-963-135989	Sequence 135989, A
565	30	60.0	314	3	US-09-904-877A-257	Sequence 257, App	638	30	60.0	344	4	US-10-724-972A-7313	Sequence 7313, Ap
566	30	60.0	314	3	US-09-903-562-257	Sequence 257, App	639	30	60.0	349	4	US-10-369-493-14180	Sequence 14180, A
567	30	60.0	314	3	US-09-906-618-257	Sequence 257, App	640	30	60.0	349	4	US-10-369-493-14836	Sequence 14836, A
568	30	60.0	314	3	US-09-907-728-257	Sequence 257, App	641	30	60.0	349	5	US-10-450-763-49975	Sequence 49975, A
569	30	60.0	314	3	US-09-904-805-257	Sequence 257, App	642	30	60.0	362	4	US-10-369-493-11522	Sequence 11522, A
570	30	60.0	314	3	US-09-904-938A-257	Sequence 257, App	643	30	60.0	368	4	US-10-032-585-7910	Sequence 7910, Ap
571	30	60.0	314	3	US-09-906-722A-257	Sequence 257, App	644	30	60.0	368	4	US-10-264-237-1842	Sequence 1842, Ap
572	30	60.0	314	3	US-09-908-576-257	Sequence 257, App	645	30	60.0	369	5	US-10-739-930-7357	Sequence 7357, Ap
573	30	60.0	314	4	US-10-040-647-6	Sequence 6, Appl	646	30	60.0	379	4	US-10-156-761-9821	Sequence 9821, Ap
574	30	60.0	314	4	US-10-180-713-3	Sequence 3, Appl	647	30	60.0	381	4	US-10-437-963-111033	Sequence 111033, A
575	30	60.0	314	4	US-10-299-976-257	Sequence 257, App	648	30	60.0	385	4	US-10-425-114-63705	Sequence 63705, A
576	30	60.0	314	4	US-10-299-937-257	Sequence 257, App	649	30	60.0	390	4	US-10-369-493-2037	Sequence 2037, Ap
577	30	60.0	314	4	US-10-074-566-124	Sequence 124, App	650	30	60.0	392	4	US-10-425-115-262580	Sequence 262580, A
578	30	60.0	314	4	US-10-298-993-257	Sequence 257, App	651	30	60.0	396	4	US-10-424-599-224104	Sequence 224104, A
579	30	60.0	314	4	US-10-424-836-14	Sequence 14, Appl	652	30	60.0	399	4	US-10-425-114-6775	Sequence 67775, A
580	30	60.0	314	4	US-10-448-923-257	Sequence 257, App	653	30	60.0	399	4	US-10-425-115-17950	Sequence 197950, A
581	30	60.0	314	4	US-10-331-496A-64	Sequence 64, Appl	654	30	60.0	403	4	US-10-369-493-19185	Sequence 19185, A
582	30	60.0	314	4	US-10-295-027-540	Sequence 54, App	655	30	60.0	406	4	US-10-369-493-20485	Sequence 20485, A
583	30	60.0	314	4	US-10-173-999-136	Sequence 136, App	656	30	60.0	414	4	US-10-437-963-157829	Sequence 157829, A
584	30	60.0	314	4	US-10-449-656-257	Sequence 257, App	657	30	60.0	414	4	US-10-767-701-46410	Sequence 46410, A
585	30	60.0	314	4	US-10-448-713-257	Sequence 257, App	658	30	60.0	421	4	US-10-369-493-11027	Sequence 11027, A
586	30	60.0	314	4	US-10-425-447-257	Sequence 257, App	659	30	60.0	426	4	US-10-051-874-34	Sequence 34, Appl
587	30	60.0	314	4	US-10-262-511-76	Sequence 76, Appl	660	30	60.0	429	3	US-09-860-113-1	Sequence 1, Appl
588	30	60.0	314	4	US-10-215-371-257	Sequence 257, App	661	30	60.0	431	4	US-10-369-493-11545	Sequence 11545, A
589	30	60.0	314	4	US-10-797-366-257	Sequence 257, App	662	30	60.0	431	4	US-10-369-493-14714	Sequence 14714, A
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591	30	60.0	314	5	US-10-723-860-552	Sequence 552, App	664	30	60.0	436	4	US-10-369-493-15993	Sequence 16993, A
592	30	60.0	314	5	US-10-963-467-257	Sequence 257, App	665	30	60.0	441	6	US-11-097-143-8379	Sequence 8379, Ap
593	30	60.0	314	5	US-10-978-255-257	Sequence 257, App	666	30	60.0	441	6	US-11-097-143-27369	Sequence 27369, A
594	30	60.0	314	5	US-10-756-149-4867	Sequence 4867, Ap	667	30	60.0	442	4	US-10-425-114-40452	Sequence 40452, A
595	30	60.0	314	5	US-10-970-823-257	Sequence 257, App	668	30	60.0	442	5	US-10-732-923-11405	Sequence 11405, A
596	30	60.0	314	5	US-11-045-577-3	Sequence 3, Appl	669	30	60.0	444	4	US-10-425-114-59719	Sequence 59719, A
597	30	60.0	318	4	US-10-471-040-2	Sequence 2, Appl	670	30	60.0	446	4	US-10-136-517-19	Sequence 19, Appl
598	30	60.0	318	5	US-10-960-929-12	Sequence 12, Appl	671	30	60.0	446	6	US-11-009-008-19	Sequence 19, Appl
599	30	60.0	319	4	US-10-072-012-174	Sequence 174, App	672	30	60.0	446	6	US-11-033-663-19	Sequence 19, Appl
600	30	60.0	322	4	US-10-183-116-16	Sequence 16, Appl	673	30	60.0	447	4	US-10-288-798-15	Sequence 15, Appl
601	30	60.0	322	4	US-10-079-384-4	Sequence 4, Appl	674	30	60.0	447	4	US-10-108-260A-4600	Sequence 4600, Ap
602	30	60.0	322	4	US-10-017-161-1056	Sequence 1056, Ap	675	30	60.0	447	4	US-10-362-892-15	Sequence 15, Appl
603	30	60.0	322	4	US-10-240-998-4	Sequence 4, Appl	676	30	60.0	447	4	US-10-425-115-346290	Sequence 346290, A
604	30	60.0	322	4	US-10-321-807-20	Sequence 20, Appl	677	30	60.0	447	6	US-11-097-143-17619	Sequence 17619, A
605	30	60.0	322	4	US-10-237-467-12	Sequence 12, Appl	678	30	60.0	450	4	US-10-437-963-119875	Sequence 119875, A
606	30	60.0	322	4	US-10-292-798-898	Sequence 898, App	679	30	60.0	450	4	US-10-437-963-139500	Sequence 139500, A
607	30	60.0	322	4	US-10-016-248-81	Sequence 81, Appl	680	30	60.0	462	4	US-10-424-599-162819	Sequence 162819, A
608	30	60.0	322	4	US-10-072-012-172	Sequence 172, App	681	30	60.0	464	3	US-09-925-302-775	Sequence 775, App
609	30	60.0	322	4	US-10-072-012-527	Sequence 527, App	682	30	60.0	464	3	US-09-925-302-775	Sequence 775, App
610	30	60.0	322	4	US-10-072-012-533	Sequence 533, App	683	30	60.0	465	4	US-10-369-493-9941	Sequence 9941, Ap
611	30	60.0	322	4	US-10-343-650A-44	Sequence 44, Appl	684	30	60.0	473	4	US-10-282-132A-78320	Sequence 78320, A

685	30	60.0	476	4	US-10-282-122A-46116	Sequence 46116, A	758	30	60.0	1079	6	US-11-097-143-35724	Sequence 35724, A
686	30	60.0	479	4	US-10-369-493-19106	Sequence 19106, A	759	30	60.0	1119	4	US-10-282-122A-49472	Sequence 49472, A
687	30	60.0	491	4	US-10-282-122A-60713	Sequence 60713, A	760	30	60.0	1119	6	US-11-097-143-18789	Sequence 18789, A
688	30	60.0	493	4	US-10-016-248-101	Sequence 101, App	761	30	60.0	1196	4	US-10-369-493-18491	Sequence 18491, A
689	30	60.0	496	4	US-10-424-599-202664	Sequence 202664, A	762	30	60.0	1223	4	US-10-389-566-696	Sequence 696, App
690	30	60.0	500	4	US-10-437-963-151311	Sequence 151311, A	763	30	60.0	1233	5	US-10-732-923-17029	Sequence 17029, A
691	30	60.0	508	4	US-10-369-493-5279	Sequence 5279, App	764	30	60.0	1256	6	US-11-097-143-27939	Sequence 27939, A
692	30	60.0	510	4	US-10-389-566-621	Sequence 621, App	765	30	60.0	1357	5	US-10-732-923-8307	Sequence 8307, App
693	30	60.0	517	4	US-10-369-493-12083	Sequence 12083, A	766	30	60.0	1571	4	US-10-369-493-1776	Sequence 1776, App
694	30	60.0	527	6	US-11-097-143-14499	Sequence 14499, A	767	30	60.0	1589	4	US-10-072-012-528	Sequence 528, App
695	30	60.0	529	4	US-10-425-114-55592	Sequence 55592, A	768	30	60.0	1589	4	US-10-072-012-532	Sequence 532, App
696	30	60.0	544	4	US-10-369-493-5969	Sequence 5969, App	769	30	60.0	1612	4	US-10-369-493-1628	Sequence 1628, App
697	30	60.0	546	4	US-10-282-122A-78516	Sequence 78516, A	770	30	60.0	2217	6	US-11-097-143-41892	Sequence 41892, A
698	30	60.0	550	5	US-10-732-923-11288	Sequence 11288, A	771	29.5	59.0	15	3	US-09-865-644-110	Sequence 110, Appl
699	30	60.0	560	4	US-10-282-122A-67752	Sequence 67752, A	772	29.5	59.0	46	4	US-10-425-115-220766	Sequence 220766, A
700	30	60.0	561	5	US-10-505-486-107	Sequence 107, App	773	29.5	59.0	153	4	US-10-052-586-564	Sequence 564, App
701	30	60.0	562	4	US-10-282-122A-69650	Sequence 69650, A	774	29.5	59.0	153	4	US-10-174-590-564	Sequence 564, App
702	30	60.0	578	4	US-10-282-122A-66857	Sequence 66857, A	775	29.5	59.0	153	4	US-10-176-758-564	Sequence 564, App
703	30	60.0	590	4	US-10-437-963-143500	Sequence 143500, A	776	29.5	59.0	153	4	US-10-175-737-564	Sequence 564, App
704	30	60.0	592	4	US-10-282-122A-48301	Sequence 48301, A	777	29.5	59.0	153	4	US-10-174-581-564	Sequence 564, App
705	30	60.0	594	4	US-10-369-493-4986	Sequence 4986, App	778	29.5	59.0	153	4	US-10-176-483-564	Sequence 564, App
706	30	60.0	604	4	US-10-303-664A-57	Sequence 57, Appl	779	29.5	59.0	153	4	US-10-176-749-564	Sequence 564, App
707	30	60.0	611	4	US-10-424-599-204138	Sequence 204138, A	780	29.5	59.0	153	4	US-10-176-914-564	Sequence 564, App
708	30	60.0	614	4	US-10-335-977-8238	Sequence 8238, App	781	29.5	59.0	153	4	US-10-176-915-564	Sequence 564, App
709	30	60.0	615	4	US-10-335-977-8239	Sequence 8239, App	782	29.5	59.0	153	4	US-10-173-706-564	Sequence 564, App
710	30	60.0	625	4	US-10-282-122A-48261	Sequence 48261, A	783	29.5	59.0	153	4	US-10-175-738-564	Sequence 564, App
711	30	60.0	634	4	US-10-353-929-52	Sequence 52, Appl	784	29.5	59.0	153	4	US-10-175-752-564	Sequence 564, App
712	30	60.0	640	5	US-10-732-923-17030	Sequence 17030, A	785	29.5	59.0	153	4	US-10-176-482-564	Sequence 564, App
713	30	60.0	642	4	US-10-437-963-204918	Sequence 204918, A	786	29.5	59.0	153	4	US-10-176-757-564	Sequence 564, App
714	30	60.0	644	4	US-10-437-963-180909	Sequence 180909, A	787	29.5	59.0	153	4	US-10-176-913-564	Sequence 564, App
715	30	60.0	669	5	US-10-946-647-1407	Sequence 1407, App	788	29.5	59.0	153	4	US-10-180-552-564	Sequence 564, App
716	30	60.0	696	5	US-10-625-972-5	Sequence 5, Appl	789	29.5	59.0	153	4	US-10-180-557-564	Sequence 564, App
717	30	60.0	702	4	US-10-354-437-100	Sequence 100, App	790	29.5	59.0	153	4	US-10-173-700-564	Sequence 564, App
718	30	60.0	735	4	US-10-471-601-1	Sequence 1, Appl	791	29.5	59.0	153	4	US-10-174-572-564	Sequence 564, App
719	30	60.0	746	4	US-10-112-944-319	Sequence 319, App	792	29.5	59.0	153	4	US-10-174-579-564	Sequence 564, App
720	30	60.0	748	4	US-10-369-493-17299	Sequence 17299, A	793	29.5	59.0	153	4	US-10-174-582-564	Sequence 564, App
721	30	60.0	752	5	US-10-741-849-7021	Sequence 7021, App	794	29.5	59.0	153	4	US-10-174-588-564	Sequence 564, App
722	30	60.0	817	6	US-11-097-143-19062	Sequence 19062, A	795	29.5	59.0	153	4	US-10-175-739-564	Sequence 564, App
723	30	60.0	823	6	US-11-097-143-23151	Sequence 23151, A	796	29.5	59.0	153	4	US-10-175-740-564	Sequence 564, App
724	30	60.0	834	4	US-10-437-963-157801	Sequence 157801, A	797	29.5	59.0	153	4	US-10-175-743-564	Sequence 564, App
725	30	60.0	855	6	US-11-097-143-5877	Sequence 5877, App	798	29.5	59.0	153	4	US-10-176-488-564	Sequence 564, App
726	30	60.0	875	6	US-11-097-143-40008	Sequence 40008, A	799	29.5	59.0	153	4	US-10-176-492-564	Sequence 564, App
727	30	60.0	885	4	US-10-424-599-161220	Sequence 161220, A	800	29.5	59.0	153	4	US-10-176-747-564	Sequence 564, App
728	30	60.0	891	4	US-10-437-963-121169	Sequence 121169, A	801	29.5	59.0	153	4	US-10-176-750-564	Sequence 564, App
729	30	60.0	900	4	US-10-282-122A-76841	Sequence 76841, A	802	29.5	59.0	153	4	US-10-176-985-564	Sequence 564, App
730	30	60.0	915	4	US-10-156-761-10050	Sequence 10050, A	803	29.5	59.0	153	4	US-10-176-987-564	Sequence 564, App
731	30	60.0	930	4	US-10-408-765A-2639	Sequence 2639, App	804	29.5	59.0	153	4	US-10-176-992-564	Sequence 564, App
732	30	60.0	949	6	US-11-097-143-6360	Sequence 6360, App	805	29.5	59.0	153	4	US-10-176-993-564	Sequence 564, App
733	30	60.0	949	6	US-11-097-143-6360	Sequence 6360, App	806	29.5	59.0	153	4	US-10-184-658-564	Sequence 564, App
734	30	60.0	998	4	US-10-282-122A-66768	Sequence 66768, A	807	29.5	59.0	153	4	US-10-176-991-564	Sequence 564, App
735	30	60.0	1006	4	US-10-369-493-2877	Sequence 2877, App	808	29.5	59.0	153	4	US-10-173-695-564	Sequence 564, App
736	30	60.0	1006	5	US-10-732-923-16953	Sequence 16953, A	809	29.5	59.0	153	4	US-10-173-697-564	Sequence 564, App
737	30	60.0	1019	5	US-10-473-127-1642	Sequence 1642, App	810	29.5	59.0	153	4	US-10-173-705-564	Sequence 564, App
738	30	60.0	1019	5	US-10-473-127-1642	Sequence 1642, App	811	29.5	59.0	153	4	US-10-174-576-564	Sequence 564, App
739	30	60.0	1037	5	US-10-645-756-22	Sequence 22, Appl	812	29.5	59.0	153	4	US-10-174-585-564	Sequence 564, App
740	30	60.0	1037	5	US-10-645-756-22	Sequence 22, Appl	813	29.5	59.0	153	4	US-10-174-586-564	Sequence 564, App
741	30	60.0	1051	4	US-10-171-311-97	Sequence 97, Appl	814	29.5	59.0	153	4	US-10-175-747-564	Sequence 564, App
742	30	60.0	1051	4	US-10-116-275-203	Sequence 203, App	815	29.5	59.0	153	4	US-10-173-697-564	Sequence 564, App
743	30	60.0	1051	4	US-10-173-999-146	Sequence 146, App	816	29.5	59.0	153	4	US-10-176-481-564	Sequence 564, App
744	30	60.0	1051	4	US-10-741-601-482	Sequence 482, App	817	29.5	59.0	153	4	US-10-176-485-564	Sequence 564, App
745	30	60.0	1051	4	US-10-741-601-485	Sequence 485, App	818	29.5	59.0	153	4	US-10-176-487-564	Sequence 564, App
746	30	60.0	1051	5	US-10-473-127-1641	Sequence 1641, App	819	29.5	59.0	153	4	US-10-176-493-564	Sequence 564, App
747	30	60.0	1051	5	US-10-473-127-1644	Sequence 1644, App	820	29.5	59.0	153	4	US-10-176-756-564	Sequence 564, App
748	30	60.0	1051	5	US-10-473-127-1645	Sequence 1645, App	821	29.5	59.0	153	4	US-10-176-911-564	Sequence 564, App
749	30	60.0	1051	5	US-10-482-029-34	Sequence 34, Appl	822	29.5	59.0	153	4	US-10-176-919-564	Sequence 564, App
750	30	60.0	1051	5	US-10-756-149-5483	Sequence 5483, App	823	29.5	59.0	153	4	US-10-176-925-564	Sequence 564, App
751	30	60.0	1066	4	US-10-097-340-155	Sequence 155, App	824	29.5	59.0	153	4	US-10-176-978-564	Sequence 564, App
752	30	60.0	1066	4	US-10-171-311-99	Sequence 99, Appl	825	29.5	59.0	153	4	US-10-179-510-564	Sequence 564, App
753	30	60.0	1066	4	US-10-173-999-148	Sequence 148, App	826	29.5	59.0	153	4	US-10-180-543-564	Sequence 564, App
754	30	60.0	1066	4	US-10-741-601-483	Sequence 483, App	827	29.5	59.0	153	4	US-10-180-544-564	Sequence 564, App
755	30	60.0	1066	4	US-10-741-601-484	Sequence 484, App	828	29.5	59.0	153	4	US-10-180-546-564	Sequence 564, App
756	30	60.0	1066	5	US-10-473-127-1646	Sequence 1646, App	829	29.5	59.0	153	4	US-10-180-547-564	Sequence 564, App
757	30	60.0	1066	5	US-10-473-127-1647	Sequence 1647, App	830	29.5	59.0	153	4	US-10-180-549-564	Sequence 564, App
						Sequence 155, App		29.5	59.0			US-10-180-555-564	Sequence 564, App



977 29.5 59.0 153 4 US-10-201-856-564 Sequence 564, App  
978 29.5 59.0 153 4 US-10-202-468-564 Sequence 564, App  
979 29.5 59.0 153 4 US-10-202-470-564 Sequence 564, App  
980 29.5 59.0 153 4 US-10-202-476-564 Sequence 564, App  
981 29.5 59.0 153 4 US-10-202-934-564 Sequence 564, App  
982 29.5 59.0 153 4 US-10-202-935-564 Sequence 564, App  
983 29.5 59.0 153 4 US-10-202-936-564 Sequence 564, App  
984 29.5 59.0 153 4 US-10-202-938-564 Sequence 564, App  
985 29.5 59.0 153 4 US-10-205-504-564 Sequence 564, App  
986 29.5 59.0 153 4 US-10-205-509-564 Sequence 564, App  
987 29.5 59.0 153 4 US-10-205-895-564 Sequence 564, App  
988 29.5 59.0 153 4 US-10-205-899-564 Sequence 564, App  
989 29.5 59.0 153 4 US-10-205-900-564 Sequence 564, App  
990 29.5 59.0 153 4 US-10-205-908-564 Sequence 564, App  
991 29.5 59.0 153 4 US-10-195-890-564 Sequence 564, App  
992 29.5 59.0 153 4 US-10-183-002-564 Sequence 564, App  
993 29.5 59.0 153 4 US-10-184-621-564 Sequence 564, App  
994 29.5 59.0 153 4 US-10-184-638-564 Sequence 564, App  
995 29.5 59.0 153 4 US-10-187-752-564 Sequence 564, App  
996 29.5 59.0 153 4 US-10-187-887-564 Sequence 564, App  
997 29.5 59.0 153 4 US-10-194-461-564 Sequence 564, App  
998 29.5 59.0 153 4 US-10-195-892-564 Sequence 564, App  
999 29.5 59.0 153 4 US-10-196-751-564 Sequence 564, App  
1000 29.5 59.0 153 4 US-10-197-694-564 Sequence 564, App

## ALIGNMENTS

RESULT 1  
US-09-870-216C-7  
; Sequence 7, Application US/09870216C  
; Publication No. US20040138135A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Nicolette  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER  
; FILE REFERENCE: 68126891210100  
; CURRENT APPLICATION NUMBER: US/09/870,216C  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: 60/209,391  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 60/226,256  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/257,008  
; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-870-216C-7

Query Match 100.0%; Score 50; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
Db 1 FLWFEIDIV 9

RESULT 2  
US-10-017-327-7  
; Sequence 7, Application US/10017327  
; Publication No. US20020155471A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Nicolette  
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND  
; TITLE OF INVENTION: METHODS FOR USING SAME  
; FILE REFERENCE: GZ 2101.20  
; CURRENT APPLICATION NUMBER: US/10/017,327  
; CURRENT FILING DATE: 2001-12-06

; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-327-7

Query Match 100.0%; Score 50; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
Db 1 FLWFEIDIV 9

RESULT 3  
US-10-425-115-206553  
; Sequence 206553, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 206553  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(94)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_119961C.1.pep  
US-10-425-115-206553

Query Match 78.0%; Score 39; DB 4; Length 94;  
Best Local Similarity 55.6%; Pred. No. 31;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
Db 26 FLWYELDVI 34

RESULT 4  
US-10-496-207-45  
; Sequence 45, Application US/10496207  
; Publication No. US20050079168A1  
; GENERAL INFORMATION:  
; APPLICANT: Karlyshev, Andrey  
; APPLICANT: Wren, Brendan  
; TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use  
; FILE REFERENCE: GJE-6947  
; CURRENT APPLICATION NUMBER: US/10/496,207  
; CURRENT FILING DATE: 2004-05-19  
; PRIOR APPLICATION NUMBER: PCT/GB02/05212  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 587  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-496-207-45

Query Match 78.0%; Score 39; DB 5; Length 587;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
DB 272 WFEIDVV 278

RESULT 5  
US-10-126-339-2  
; Sequence 2, Application US/10126339  
; Publication No. US20030166891A1  
; GENERAL INFORMATION:  
; APPLICANT: Flannagan, Ronald D.  
; APPLICANT: Mathis, John P.  
; APPLICANT: Meyer, Terry E.  
; TITLE OF INVENTION: No. US20030166891A1el Bt Toxin Receptors From  
; TITLE OF INVENTION: Lepidopteran Insects and Methods of Use  
; FILE REFERENCE: 35718/204664  
; CURRENT APPLICATION NUMBER: US/10/126.339  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1717  
; TYPE: PRT  
; ORGANISM: Ostrinia nubilalis  
US-10-126-339-2

Query Match 78.0%; Score 39; DB 4; Length 1717;  
Best Local Similarity 85.7%; Pred. No. 4.7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
DB 650 YLWFEID 656

RESULT 6  
US-10-126-148-2  
; Sequence 2, Application US/10126148  
; Publication No. US20030170787A1  
; GENERAL INFORMATION:  
; APPLICANT: Flannagan, Ronald D.  
; APPLICANT: Mathis, John P.  
; APPLICANT: Meyer, Terry E.  
; TITLE OF INVENTION: No. US20030170787A1el Bt Toxin Receptors From  
; TITLE OF INVENTION: Lepidopteran Insects and Methods of Use  
; FILE REFERENCE: 35718/204664  
; CURRENT APPLICATION NUMBER: US/10/126.148  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR FILING DATE: 1999-11-18  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1717  
; TYPE: PRT  
; ORGANISM: Ostrinia nubilalis  
US-10-126-148-2

Query Match 78.0%; Score 39; DB 4; Length 1717;  
Best Local Similarity 85.7%; Pred. No. 4.7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
DB 650 YLWFEID 656

Db 650 YLWFEID 656

RESULT 7  
US-10-798-058-8  
; Sequence 8, Application US/10798058  
; Publication No. US20040209329A1  
; GENERAL INFORMATION:  
; APPLICANT: Mathis, John P.  
; TITLE OF INVENTION: Novel Bt Toxin Receptors and Methods of  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: 35718/274644  
; CURRENT APPLICATION NUMBER: US/10/798.058  
; CURRENT FILING DATE: 2004-03-11  
; PRIOR APPLICATION NUMBER: US 60/455,085  
; PRIOR FILING DATE: 2003-03-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 1717  
; TYPE: PRT  
; ORGANISM: Ostrinia nubilalis  
US-10-798-058-8

Query Match 78.0%; Score 39; DB 4; Length 1717;  
Best Local Similarity 85.7%; Pred. No. 4.7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
DB 650 YLWFEID 656

RESULT 8  
US-10-424-599-183462  
; Sequence 183462, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 183462  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(112)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_13667C.1.pep  
US-10-424-599-183462

Query Match 76.0%; Score 38; DB 4; Length 112;  
Best Local Similarity 77.8%; Pred. No. 54;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
DB 39 FLWFNIDKV 47

RESULT 9  
US-10-482-029-213  
; Sequence 213, Application US/10482029  
; Publication No. US20050037445A1

;  
; GENERAL INFORMATION:  
; APPLICANT: ODIN medical A/S  
; TITLE OF INVENTION: Oncology drug innovation  
; FILE REFERENCE: P 573 PC00  
; CURRENT APPLICATION NUMBER: US/10/482,029  
; CURRENT FILING DATE: 2003-12-29  
; NUMBER OF SEQ ID NOS: 437  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 213  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-482-029-213

Query Match 74.0%; Score 37; DB 5; Length 112;  
Best Local Similarity 55.6%; Pred. No. 81;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
Db 10 FLWLQDLV 18

RESULT 10  
US-10-369-493-18446  
; Sequence 18446, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 18446  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Lactococcus lactis  
US-10-369-493-18446

Query Match 74.0%; Score 37; DB 4; Length 529;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
Db 49 FLWLAIIDII 57

RESULT 11  
US-10-424-599-144215  
; Sequence 144215, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 144215  
; LENGTH: 58

;  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_101239C.1.pep  
US-10-424-599-144215

Query Match 72.0%; Score 36; DB 4; Length 58;  
Best Local Similarity 75.0%; Pred. No. 65;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWFIEDIV 9  
Db 45 LWFVIDII 52

RESULT 12  
US-10-450-763-31511  
; Sequence 31511, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 31511  
; LENGTH: 280  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (226)..(246)  
; OTHER INFORMATION: Phospholipase D Active site proteins motifs. domain  
; OTHER INFORMATION: identified by eMATRIX, accession number PF00614B, p-value=4.774e-  
; OTHER INFORMATION: 14, raw score of 14.45  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (108)..(248)  
; OTHER INFORMATION: Phospholipase D. Active site motif domain identified by PFam,  
; OTHER INFORMATION: accession name PLDC, E-value=7e-10, PFam score of 46.3  
US-10-450-763-31511

Query Match 72.0%; Score 36; DB 5; Length 280;  
Best Local Similarity 62.5%; Pred. No. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
Db 40 FIWFEDDV 47

RESULT 13  
US-10-369-493-20052  
; Sequence 20052, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493



; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 20052  
; LENGTH: 402  
; TYPE: PRT  
; ORGANISM: No. US20030233675Altoc punctiforme  
US-10-369-493-20052

Query Match 72.0%; Score 36; DB 4; Length 402;  
Best Local Similarity 71.4%; Pred. No. 4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
|:|:|:  
DB 245 WFEVDIL 251

RESULT 14  
US-10-450-763-31518  
; Sequence 31518, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 31518  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (267)..(294)  
; OTHER INFORMATION: Phospholipase D. Active site motif domain identified by Pfam.  
; OTHER INFORMATION: accession name PLDC, E-value=6.7e-07, Pfam score of 36.4  
US-10-450-763-31518

Query Match 72.0%; Score 36; DB 5; Length 410;  
Best Local Similarity 62.5%; Pred. No. 4.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
|:|:|:  
DB 200 FIWFEDDV 207

RESULT 15  
US-10-408-765A-2042  
; Sequence 2042, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Pabry, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A

; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2042  
; LENGTH: 700  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-2042

Query Match 72.0%; Score 36; DB 4; Length 700;  
Best Local Similarity 75.0%; Pred. No. 6.8e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
|:|:|:|:  
DB 612 FIWFEDDM 619

RESULT 16  
US-10-450-763-31510  
; Sequence 31510, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 31510  
; LENGTH: 1097  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (456)..(476)  
; OTHER INFORMATION: Phospholipase D Active site proteins motifs. domain  
; OTHER INFORMATION: identified by eMATRIX, accession number PF00614B, p-value=4.774e  
; OTHER INFORMATION: 14, raw score of 14.45  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (613)..(714)  
; OTHER INFORMATION: Sodium:sulfate symporter transmembran domain identified by  
; OTHER INFORMATION: Pfam, accession name Na\_sulph\_symp, E-value=6.1e-46, Pfam score  
; OTHER INFORMATION: 163.9  
US-10-450-763-31510

Query Match 72.0%; Score 36; DB 5; Length 1097;  
Best Local Similarity 62.5%; Pred. No. 1e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
|:|:|:|:  
DB 270 FIWFEDDV 277

RESULT 17  
US-10-798-058-2  
; Sequence 2, Application US/10798058  
; Publication No. US20040209329A1  
; GENERAL INFORMATION:  
; APPLICANT: Mathis, John P.  
; TITLE OF INVENTION: Novel Bt Toxin Receptors and Methods of  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: 35718/274644  
; CURRENT APPLICATION NUMBER: US/10/798,058

```
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US 60/455,085
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1759
; TYPE: PRT
; ORGANISM: Agrotis ipsilon
US-10-798-058-2

Query Match      72.0%; Score 36; DB 4; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFELD 7
DB      668 LWFELD 673

RESULT 18
US-10-424-599-273756
; Sequence 273756, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 273756
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89222C.1.pep
US-10-424-599-273756

Query Match      70.0%; Score 35; DB 4; Length 37;
Best Local Similarity 71.4%; Pred. No. 64;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLWFELD 7
DB      13 FLWFELD 19

RESULT 19
US-10-774-355A-2401
; Sequence 2401, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; APPLICANT: Zhang, Ximin
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
; FILE REFERENCE: A34570-PC7-USA-A 070050.2520
; CURRENT APPLICATION NUMBER: US/10/774,355A
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: PCT/US02/25556
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/311,159
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/339,694
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 2596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2401
; LENGTH: 194
```

```
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-774-355A-2401

Query Match      70.0%; Score 35; DB 5; Length 194;
Best Local Similarity 55.6%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFELDIV 9
DB      40 FLWFEPVII 48

RESULT 20
US-10-424-599-236699
; Sequence 236699, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 236699
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(210)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_55766C.1.pep
US-10-424-599-236699

Query Match      70.0%; Score 35; DB 4; Length 210;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFELD 7
DB      55 FLWFELD 61

RESULT 21
US-10-041-615-63
; Sequence 63, Application US/10041615
; Publication No. US20040014038A1
; GENERAL INFORMATION:
; APPLICANT: Casman, Stacie J
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Smithson, Glennda
; APPLICANT: Kekuda, Ramesh
; TITLE OF INVENTION: No. US20040014038A1el GPCR-Like Proteins and Nucleic Acids Encod
; FILE REFERENCE: 21402-233-061
; CURRENT APPLICATION NUMBER: US/10/041,615
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/259,552
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/260,544
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/277,405
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 63
```

```
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-615-63

Query Match          70.0%; Score 35; DB 4; Length 217;
Best Local Similarity 77.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
Db      86 FLWFLPIV 94

RESULT 22
US-10-072-012-557
; Sequence 557, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Bastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grossee, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 557
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match          70.0%; Score 35; DB 4; Length 217;
Best Local Similarity 77.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
Db      86 FLWFLPIV 94

RESULT 23
US-10-017-161-1002
; Sequence 1002, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1002
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1002

Query Match          70.0%; Score 35; DB 4; Length 232;
Best Local Similarity 77.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
Db      168 FLWFLPIV 176

RESULT 24
US-10-292-798-852
; Sequence 852, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 852
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-852

Query Match          70.0%; Score 35; DB 4; Length 232;
Best Local Similarity 77.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
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Db      168 FLWFLPIV 176
|||||
US-10-774-355A-1766
; Sequence 1766, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
; FILE REFERENCE: A34570-PCT-USA-A 070050.2520
; CURRENT APPLICATION NUMBER: US/10/774,355A
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: PCT/US02/25556
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/311,159
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/339,694
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 2596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1766
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-774-355A-1766

Query Match      70.0%; Score 35; DB 5; Length 309;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
|||||
Db      155 FLWFPVPII 163

RESULT 26
US-10-774-355A-1767
; Sequence 1767, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
; FILE REFERENCE: A34570-PCT-USA-A 070050.2520
; CURRENT APPLICATION NUMBER: US/10/774,355A
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: PCT/US02/25556
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/311,159
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/339,694
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 2596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1767
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-774-355A-1767

Query Match      70.0%; Score 35; DB 5; Length 311;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
|||||
Db      157 FLWFPVPII 165

RESULT 27
US-10-774-355A-1768
; Sequence 1768, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
; FILE REFERENCE: A34570-PCT-USA-A 070050.2520
; CURRENT APPLICATION NUMBER: US/10/774,355A
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: PCT/US02/25556
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/311,159
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/339,694
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 2596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1768
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-774-355A-1768

Query Match      70.0%; Score 35; DB 5; Length 311;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
|||||
Db      157 FLWFPVPII 165

RESULT 28
US-10-774-355A-2007
; Sequence 2007, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
; FILE REFERENCE: A34570-PCT-USA-A 070050.2520
; CURRENT APPLICATION NUMBER: US/10/774,355A
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: PCT/US02/25556
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/311,159
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/339,694
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 2596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2007
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-774-355A-2007

Query Match      70.0%; Score 35; DB 5; Length 311;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
|||||
Db      157 FLWFPVPII 165

RESULT 29
US-10-041-615-16
; Sequence 16, Application US/10041615
; Publication No. US20040014038A1
; GENERAL INFORMATION:
; APPLICANT: Casman, Stacie J
```

```
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Smithson, Glennda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014038A1el GPCR-Like Proteins and Nucleic Acids Encodi
; FILE REFERENCE: 21402-233-061
; CURRENT APPLICATION NUMBER: US/10/041.615
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/259,552
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/260,544
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/277,405
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-615-16

Query Match          70.0%; Score 35; DB 4; Length 315;
Best Local Similarity 77.8%; Pred. No. 4.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLWFEIDIV 9
Db 157 FLWFLPIV 165

RESULT 30
US-10-072-012-192
; Sequence 192, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Bsha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395

; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Smithson, Glennda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014038A1el GPCR-Like Proteins and Nucleic Acids Encodi
; FILE REFERENCE: 21402-233-061
; CURRENT APPLICATION NUMBER: US/10/041.615
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/259,552
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/260,544
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/277,405
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-615-16

Query Match          70.0%; Score 35; DB 4; Length 315;
Best Local Similarity 77.8%; Pred. No. 4.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLWFEIDIV 9
Db 157 FLWFLPIV 165

RESULT 31
US-10-774-355A-2203
; Sequence 2203, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; APPLICANT: Zhang, Ximin
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
; FILE REFERENCE: A34570-PCT-USA-A 070050.2520
; CURRENT APPLICATION NUMBER: US/10/774,355A
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: PCT/US02/25556
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/311,159
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/339,694
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 2596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2203
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (177)...(183)
; OTHER INFORMATION: Any amino acid
US-10-774-355A-2203

Query Match          70.0%; Score 35; DB 5; Length 318;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLWFEIDIV 9
Db 157 FLWFPVPII 165

RESULT 32
US-10-774-355A-2569
; Sequence 2569, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
```

; APPLICANT: Zhang, Ximin  
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY  
; FILE REFERENCE: A34570-PCT-USA-A 070050.2520  
; CURRENT APPLICATION NUMBER: US/10/774,355A  
; CURRENT FILING DATE: 2004-02-06  
; PRIOR APPLICATION NUMBER: PCT/US02/25556  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 60/311,159  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/339,694  
; PRIOR FILING DATE: 2001-12-12  
; NUMBER OF SEQ ID NOS: 2596  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2569  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-774-355A-2569

Query Match 70.0%; Score 35; DB 5; Length 322;  
Best Local Similarity 55.6%; Pred. No. 4.9e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 2

QY 1 FLWFEIDIV 9  
||| :|  
Db 156 FLWFPVPII 164

RESULT 33  
US-10-017-161-460  
; Sequence 460, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 460  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-460

Query Match 70.0%; Score 35; DB 4; Length 326;  
Best Local Similarity 77.8%; Pred. No. 5e+02; Indels 2; Gaps 0;  
Matches 7; Conservative 0; Mismatches 2

QY 1 FLWFEIDIV 9  
||| :|  
Db 168 FLWFLPIIV 176

RESULT 34  
US-10-017-161-506  
; Sequence 506, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 506  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-506

Query Match 70.0%; Score 35; DB 4; Length 326;  
Best Local Similarity 77.8%; Pred. No. 5e+02; Indels 2; Gaps 0;  
Matches 7; Conservative 0; Mismatches 2

QY 1 FLWFEIDIV 9  
||| :|  
Db 168 FLWFLPIIV 176

RESULT 35  
US-10-387-629-6  
; Sequence 6, Application US/10387629  
; Publication No. US20030221205A1  
; GENERAL INFORMATION:  
; APPLICANT: ChemCom S.A.  
; APPLICANT: Veithen, Alex  
; TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors  
; FILE REFERENCE: 9409/2192  
; CURRENT APPLICATION NUMBER: US/10/387,629  
; CURRENT FILING DATE: 2003-03-13  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-387-629-6

Query Match 70.0%; Score 35; DB 4; Length 326;  
Best Local Similarity 77.8%; Pred. No. 5e+02; Indels 2; Gaps 0;  
Matches 7; Conservative 0; Mismatches 2

QY 1 FLWFEIDIV 9  
||| :|  
Db 168 FLWFLPIIV 176

RESULT 36  
US-10-292-798-412  
; Sequence 412, Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 412  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-412

Query Match 70.0%; Score 35; DB 4; Length 326;

```
Best Local Similarity 77.8%; Pred. No. 5e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0;

QY 1 FLWFEIDIV 9
    |||||
Db 168 FLWFLPIV 176

RESULT 37
US-10-292-798-446
; Sequence 446, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 446
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-446

Query Match 70.0%; Score 35; DB 4; Length 326;
Best Local Similarity 77.8%; Pred. No. 5e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0;

QY 1 FLWFEIDIV 9
    |||||
Db 168 FLWFLPIV 176

RESULT 38
US-10-343-650A-640
; Sequence 640, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 640
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-640

Query Match 70.0%; Score 35; DB 4; Length 326;
Best Local Similarity 77.8%; Pred. No. 5e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0;

QY 1 FLWFEIDIV 9
    |||||
Db 168 FLWFLPIV 176
```

```
RESULT 39
US-10-101-464A-117
; Sequence 117, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-117

Query Match 70.0%; Score 35; DB 4; Length 599;
Best Local Similarity 83.3%; Pred. No. 8.8e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEID 7
    |||||
Db 33 LWFEVD 38

RESULT 40
US-10-864-252-117
; Sequence 117, Application US/10864252
; Publication No. US20050050583A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c3
; CURRENT APPLICATION NUMBER: US/10/864,252
; CURRENT FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: 10/101,464
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-864-252-117

Query Match 70.0%; Score 35; DB 5; Length 599;
Best Local Similarity 83.3%; Pred. No. 8.8e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LWFEID 7
Db      33 LWFEVD 38

RESULT 41
US-10-425-114-72890
; Sequence 72890, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72890
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana columbia
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-ATXLIB327417PID12_FLI pep
US-10-425-114-72890

Query Match          70.0%; Score 35; DB 4; Length 720;
Best Local Similarity 57.1%; Pred. No. 1e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLWFEID 7
Db      528 YWFEVD 534

RESULT 42
US-10-101-464A-827
; Sequence 827, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-827

Query Match          70.0%; Score 35; DB 5; Length 816;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEID 7
Db      250 LWFEVD 255

RESULT 43
US-10-864-252-827
; Sequence 827, Application US/10864252
; Publication No. US20050050583A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c3
; CURRENT APPLICATION NUMBER: US/10/864,252
; CURRENT FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: 10/101,464
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-864-252-827

Query Match          70.0%; Score 35; DB 5; Length 816;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEID 7
Db      250 LWFEVD 255

RESULT 44
US-10-101-464A-976
; Sequence 976, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 976
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-976
```



```
Query Match          70.0%; Score 35; DB 4; Length 1240;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LWFED 7
      |||||
Db      674 LWFED 679

RESULT 45
US-10-864-252-976
; Sequence 976, Application US/10864252
; Publication No. US20050050583A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c3
; CURRENT APPLICATION NUMBER: US/10/864,252
; CURRENT FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: 10/101,464
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 976
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-864-252-976

Query Match          70.0%; Score 35; DB 5; Length 1240;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LWFED 7
      |||||
Db      674 LWFED 679

RESULT 46
US-10-425-115-227895
; Sequence 227895, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 227895
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139435C.1.pep
US-10-425-115-227895

Query Match          68.0%; Score 34; DB 4; Length 44;
```

```
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLWFEI 6
      |||||
Db      30 FLWFEI 35

RESULT 47
US-09-798-029-21
; Sequence 21, Application US/09798029
; Patent No. US20020019030A1
; GENERAL INFORMATION:
; APPLICANT: Millenium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Rudolph-Owen, Laura
; TITLE OF INVENTION: 25324, 50287, 28899, 47007, and 42967
; TITLE OF INVENTION: TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
; FILE REFERENCE: 38155-20001.00
; CURRENT APPLICATION NUMBER: US/09/798,029
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/185,711
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-798-029-21

Query Match          68.0%; Score 34; DB 3; Length 51;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLWFEI 6
      |||||
Db      46 FLWFEI 51

RESULT 48
US-10-437-963-147599
; Sequence 147599, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147599
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48112C.1.pep
US-10-437-963-147599

Query Match          68.0%; Score 34; DB 4; Length 61;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 FLWFEIDI 8  
| | | | |  
Db 34 FRWFSIDV 41

QY 1 FLWFEIDIV 9  
| | | | |  
Db 2 FLWDDIDVL 10

Search completed: May 9, 2006, 02:35:58  
Job time : 92.8 secs

RESULT 49  
US-10-425-115-363307  
; Sequence 363307, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 363307  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(62)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_94508C.1.pap  
US-10-425-115-363307

Query Match 68.0%; Score 34; DB 4; Length 62;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
| | | | |  
Db 35 FVWXEIDSV 43

RESULT 50  
US-10-424-599-218678  
; Sequence 218678, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 218678  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(75)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_39495C.1.pap  
US-10-424-599-218678

Query Match 68.0%; Score 34; DB 4; Length 75;  
Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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## OM protein - protein search, using sw model

Run on: May 9, 2006, 02:28:58 ; Search time 12.8 Seconds  
(without alignments)  
32.544 Million cell updates/sec

Title: US-09-870-216C-7  
Perfect score: 50  
Sequence: 1 FLWFEIDIV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:  
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5: /SIDSS5/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep!.\*  
6: /SIDSS5/ptodata/2/pubpaa/US09\_NEW\_PUB.pep!.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	78.0	1717	11	US-11-192-967-2
2	39	78.0	1717	11	US-11-193-715-2
3	37	74.0	150	11	US-11-045-004-2043
4	36	72.0	700	9	US-10-501-035-314
5	35	70.0	541	11	US-11-098-686-11058
6	34	68.0	401	11	US-11-079-463-7895
7	34	68.0	534	11	US-11-188-298-17428
8	33	66.0	357	11	US-11-156-084-126
9	33	66.0	516	9	US-10-641-678-59
10	33	66.0	587	11	US-11-079-463-8026
11	32	64.0	145	11	US-11-188-298-14683
12	32	64.0	154	11	US-11-188-298-17540
13	32	64.0	178	11	US-11-188-298-1861
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15	32	64.0	185	11	US-11-188-298-19429
16	32	64.0	217	11	US-11-188-298-7973
17	32	64.0	249	11	US-11-188-298-7443
18	32	64.0	285	11	US-11-179-843-3
19	32	64.0	285	11	US-11-152-635-11
20	32	64.0	423	11	US-11-087-099-9700
21	32	64.0	438	11	US-11-079-463-9640

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23	64.0	443	11	US-11-188-298-4548	Sequence 4548, Ap
24	64.0	463	11	US-11-087-099-9184	Sequence 9184, Ap
25	64.0	467	11	US-11-045-004-358	Sequence 358, App
26	64.0	474	11	US-11-087-099-12372	Sequence 12372, A
27	64.0	537	11	US-11-188-298-16627	Sequence 16627, A
28	64.0	562	11	US-11-188-298-9104	Sequence 9104, Ap
29	64.0	563	11	US-11-072-512-3625	Sequence 3625, Ap
30	64.0	577	11	US-11-188-298-516	Sequence 516, App
31	64.0	1586	9	US-10-506-454-1041	Sequence 1041, App
32	63.0	527	11	US-11-188-298-17639	Sequence 17639, A
33	62.0	24	11	US-11-004-399-2604	Sequence 2604, Ap
34	62.0	66	11	US-11-079-463-7111	Sequence 7111, Ap
35	62.0	147	11	US-11-045-004-431	Sequence 431, App
36	62.0	219	11	US-11-188-298-13534	Sequence 13534, A
37	62.0	229	11	US-11-045-004-2278	Sequence 2278, Ap
38	62.0	284	11	US-11-096-568A-4083	Sequence 4083, Ap
39	62.0	301	11	US-11-096-568A-4082	Sequence 4082, Ap
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42	62.0	399	11	US-11-096-568A-20256	Sequence 20256, A
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44	62.0	509	11	US-11-096-568A-20254	Sequence 20254, A
45	62.0	533	11	US-11-188-298-18585	Sequence 18585, A
46	62.0	686	11	US-11-099-691-9	Sequence 9, Appl1
47	62.0	750	11	US-11-096-568A-30629	Sequence 30629, A
48	62.0	754	11	US-11-197-133A-18	Sequence 18, Appl
49	62.0	810	11	US-11-096-568A-30628	Sequence 30628, A
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52	62.0	2767	11	US-11-100-640-38	Sequence 38, Appl
53	60.0	13	11	US-11-152-974A-309	Sequence 309, App
54	60.0	13	11	US-11-153-143A-309	Sequence 309, App
55	60.0	23	9	US-10-895-064-876	Sequence 876, App
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57	60.0	23	11	US-11-129-741-3872	Sequence 3872, Ap
58	60.0	42	9	US-10-532-480-34	Sequence 34, Appl
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62	60.0	192	11	US-11-096-568A-19692	Sequence 19692, A
63	60.0	211	9	US-10-980-388-97	Sequence 97, Appl
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65	60.0	213	11	US-11-096-568A-5891	Sequence 5891, Ap
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72	60.0	305	11	US-11-137-465-56	Sequence 56, Appl
73	60.0	314	11	US-11-183-914-3	Sequence 3, Appl1
74	60.0	314	11	US-11-051-720-1318	Sequence 1318, Ap
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77	60.0	318	11	US-11-156-084-39	Sequence 39, Appl
78	60.0	318	11	US-11-228-659-30	Sequence 30, Appl
79	60.0	322	9	US-10-747-702-7	Sequence 7, Appl1
80	60.0	322	9	US-10-747-702-9	Sequence 9, Appl1
81	60.0	323	9	US-10-980-388-119	Sequence 119, App
82	60.0	326	11	US-11-051-720-1319	Sequence 1319, Ap
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89	60.0	435	11	US-11-188-298-3043	Sequence 3043, Ap
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91	60.0	460	11	US-11-096-568A-29062	Sequence 29062, A
92	60.0	491	11	US-11-045-004-1211	Sequence 1211, Ap
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97	30	60.0	585	11	US-11-188-298-6328	Sequence 6328, Ap	170	29	58.0	686	9	US-10-195-889-524	Sequence 524, App
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99	30	60.0	634	11	US-11-079-463-8156	Sequence 8156, Ap	172	29	58.0	905	11	US-11-072-512-2728	Sequence 2728, Ap
100	30	60.0	1066	11	US-11-169-041-148	Sequence 148, App	173	29	58.0	921	11	US-11-045-004-1387	Sequence 1387, Ap
101	30	60.0	1094	11	US-11-098-686-10160	Sequence 10160, A	174	29	58.0	1006	8	US-10-511-937-2425	Sequence 2425, Ap
102	29.5	59.0	153	9	US-10-194-487-564	Sequence 564, App	175	29	58.0	1006	11	US-11-203-251A-90	Sequence 90, Appl
103	29.5	59.0	153	9	US-10-195-883-564	Sequence 564, App	176	29	58.0	1029	9	US-10-821-234-908	Sequence 908, App
104	29.5	59.0	153	9	US-10-195-888-564	Sequence 564, App	177	29	58.0	1073	11	US-11-098-686-10413	Sequence 10413, A
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107	29	58.0	113	9	US-10-745-586-25	Sequence 25, Appl	180	29	58.0	1159	9	US-10-957-116-9	Sequence 9, Appl
108	29	58.0	138	11	US-11-264-096-568	Sequence 568, App	181	29	58.0	1159	11	US-11-242-822-9	Sequence 9, Appl
109	29	58.0	173	11	US-11-096-568A-9037	Sequence 9037, Ap	182	29	58.0	1942	9	US-10-506-454-1403	Sequence 1403, Ap
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111	29	58.0	175	11	US-11-096-568A-9036	Sequence 9036, Ap	184	29	58.0	2224	11	US-11-043-806-393	Sequence 393, App
112	29	58.0	198	11	US-11-156-084-76	Sequence 76, Appl	185	29	58.0	3482	11	US-11-087-099-2068	Sequence 2068, Ap
113	29	58.0	221	11	US-11-156-084-74	Sequence 74, Appl	186	29	58.0	3749	11	US-11-132-686-8	Sequence 8, Appl
114	29	58.0	237	11	US-11-156-084-73	Sequence 73, Appl	187	29	58.0	3749	11	US-11-132-686-6	Sequence 6, Appl
115	29	58.0	255	9	US-10-506-454-1677	Sequence 1677, Ap	188	29	58.0	3749	11	US-11-132-686-12	Sequence 12, Appl
116	29	58.0	262	11	US-11-156-084-112	Sequence 112, App	189	29	58.0	3912	11	US-11-132-686-7	Sequence 7, Appl
117	29	58.0	263	11	US-11-087-099-1373	Sequence 1373, Ap	190	29	58.0	3913	11	US-11-132-686-5	Sequence 5, Appl
118	29	58.0	264	11	US-11-096-568A-29097	Sequence 29097, A	191	29	58.0	3913	11	US-11-132-686-9	Sequence 9, Appl
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132	29	58.0	345	9	US-10-467-657-252	Sequence 252, App	205	28	56.0	243	11	US-11-096-568A-20843	Sequence 20843, A
133	29	58.0	345	9	US-10-467-657-3086	Sequence 3086, Ap	206	28	56.0	243	11	US-11-045-004-2758	Sequence 2758, Ap
134	29	58.0	350	11	US-11-228-659-39	Sequence 39, Appl	207	28	56.0	253	11	US-11-096-568A-20842	Sequence 20842, A
135	29	58.0	352	11	US-11-228-659-27	Sequence 27, Appl	208	28	56.0	263	11	US-11-096-568A-20841	Sequence 20841, A
136	29	58.0	353	11	US-11-156-084-138	Sequence 138, App	209	28	56.0	277	11	US-11-045-004-730	Sequence 730, App
137	29	58.0	353	11	US-11-228-659-23	Sequence 23, Appl	210	28	56.0	287	7	US-09-978-360A-427	Sequence 427, App
138	29	58.0	354	9	US-10-506-454-1387	Sequence 1387, Ap	211	28	56.0	299	11	US-11-156-084-47	Sequence 47, Appl
139	29	58.0	364	11	US-11-096-568A-24125	Sequence 24125, A	212	28	56.0	302	11	US-11-079-463-8568	Sequence 8568, Ap
140	29	58.0	365	11	US-11-096-568A-9478	Sequence 9478, Ap	213	28	56.0	303	11	US-11-156-084-232	Sequence 232, App
141	29	58.0	366	11	US-11-156-084-137	Sequence 137, App	214	28	56.0	304	11	US-11-079-463-9817	Sequence 9817, Ap
142	29	58.0	382	11	US-11-096-568A-24124	Sequence 24124, A	215	28	56.0	305	9	US-10-131-826A-264	Sequence 264, App
143	29	58.0	388	11	US-11-129-143-47	Sequence 47, Appl	216	28	56.0	305	9	US-10-821-234-1518	Sequence 1518, Ap
144	29	58.0	405	11	US-11-096-568A-24123	Sequence 24123, A	217	28	56.0	305	9	US-10-973-115B-264	Sequence 264, App
145	29	58.0	417	11	US-11-188-298-15840	Sequence 15840, A	218	28	56.0	305	9	US-10-137-873A-264	Sequence 264, App
146	29	58.0	417	11	US-11-188-298-16148	Sequence 16148, A	219	28	56.0	305	9	US-10-152-370-264	Sequence 264, App
147	29	58.0	455	11	US-11-087-099-2593	Sequence 2593, Ap	220	28	56.0	305	11	US-11-290-153-264	Sequence 264, App
148	29	58.0	468	11	US-11-156-084-135	Sequence 135, App	221	28	56.0	306	11	US-11-156-084-348	Sequence 348, App
149	29	58.0	473	11	US-11-096-568A-9477	Sequence 9477, Ap	222	28	56.0	308	11	US-11-043-788-390	Sequence 390, App
150	29	58.0	483	11	US-11-045-004-532	Sequence 532, App	223	28	56.0	312	11	US-11-188-298-14937	Sequence 14937, A
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152	29	58.0	495	11	US-11-124-367A-349	Sequence 349, App	225	28	56.0	330	11	US-11-156-084-48	Sequence 48, Appl
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156	29	58.0	519	11	US-11-079-463-9938	Sequence 9938, Ap	229	28	56.0	348	11	US-11-241-677-8	Sequence 8, Appl
157	29	58.0	536	9	US-10-641-678-70	Sequence 70, Appl	230	28	56.0	352	11	US-11-228-659-15	Sequence 15, Appl
158	29	58.0	537	11	US-11-098-686-10441	Sequence 10441, A	231	28	56.0	357	11	US-11-188-298-9430	Sequence 9430, Ap
159	29	58.0	544	9	US-10-793-626-38	Sequence 38, Appl	232	28	56.0	385	11	US-11-172-740-1790	Sequence 1790, Ap
160	29	58.0	551	11	US-11-188-298-15779	Sequence 15779, A	233	28	56.0	385	11	US-11-172-740-1788	Sequence 1788, Ap
161	29	58.0	581	11	US-11-188-298-7173	Sequence 7173, Ap	234	28	56.0	387	11	US-11-188-298-15055	Sequence 15055, A
162	29	58.0	602	11	US-11-087-099-11542	Sequence 11542, A	235	28	56.0	388	11	US-11-172-740-1789	Sequence 1789, Ap
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244	28	56.0	415	11	US-11-205-109-20	Sequence 20, Appl	317	28	56.0	4060	9	US-10-922-232B-55	Sequence 55, Appl
245	28	56.0	426	11	US-11-096-568A-30855	Sequence 30855, A	318	28	56.0	4386	11	US-11-004-399-714	Sequence 714, Appl
246	28	56.0	429	11	US-11-043-788-389	Sequence 389, Appl	319	28	56.0	4913	9	US-10-453-372-1142	Sequence 1142, Appl
247	28	56.0	432	11	US-11-087-099-2632	Sequence 2632, Appl	320	28	56.0	4961	9	US-10-453-372-1132	Sequence 1132, Appl
248	28	56.0	432	11	US-11-087-099-10706	Sequence 10706, A	321	28	56.0	6738	9	US-10-922-232B-56	Sequence 56, Appl
249	28	56.0	443	11	US-11-045-004-2482	Sequence 2482, A	322	27.5	55.0	382	11	US-11-096-568A-19714	Sequence 19714, A
250	28	56.0	450	11	US-11-077-386-20	Sequence 20, Appl	323	27.5	55.0	401	11	US-11-096-568A-19713	Sequence 19713, A
251	28	56.0	451	9	US-10-063-703-82	Sequence 82, Appl	324	27.5	55.0	470	11	US-11-096-568A-12906	Sequence 12906, A
252	28	56.0	451	9	US-10-194-487-282	Sequence 282, Appl	325	27.5	55.0	470	11	US-11-096-568A-12905	Sequence 12905, A
253	28	56.0	451	9	US-10-195-883-282	Sequence 282, Appl	326	27.5	55.0	542	11	US-11-096-568A-12905	Sequence 12905, A
254	28	56.0	451	9	US-10-195-889-282	Sequence 282, Appl	327	27.5	55.0	561	11	US-11-096-568A-12904	Sequence 12904, A
255	28	56.0	451	9	US-11-102-240-82	Sequence 82, Appl	328	27	54.0	10	11	US-11-107-096-44	Sequence 44, Appl
256	28	56.0	451	11	US-11-043-788-394	Sequence 394, Appl	329	27	54.0	13	11	US-11-153-974A-391	Sequence 391, Appl
257	28	56.0	451	11	US-11-103-195-82	Sequence 82, Appl	330	27	54.0	13	11	US-11-153-143A-391	Sequence 391, Appl
258	28	56.0	451	11	US-11-096-568A-22692	Sequence 22692, A	331	27	54.0	15	9	US-10-895-064-1132	Sequence 1192, Appl
259	28	56.0	464	11	US-11-098-686-11345	Sequence 11345, A	332	27	54.0	15	11	US-11-129-741-1192	Sequence 1192, Appl
260	28	56.0	473	11	US-11-096-568A-28409	Sequence 28409, A	333	27	54.0	20	9	US-10-895-064-706	Sequence 706, Appl
261	28	56.0	480	11	US-11-096-568A-28408	Sequence 28408, A	334	27	54.0	20	11	US-11-129-741-706	Sequence 706, Appl
262	28	56.0	480	11	US-11-096-568A-28408	Sequence 28408, A	335	27	54.0	55	11	US-11-004-399-2213	Sequence 2213, Appl
263	28	56.0	484	11	US-11-096-568A-22691	Sequence 22691, A	336	27	54.0	85	11	US-11-264-096-1213	Sequence 1213, Appl
264	28	56.0	498	11	US-11-079-463-6018	Sequence 6018, Appl	337	27	54.0	87	8	US-10-501-834-14	Sequence 14, Appl
265	28	56.0	510	11	US-11-096-568A-28407	Sequence 28407, A	338	27	54.0	89	11	US-11-096-568A-2163	Sequence 2163, Appl
266	28	56.0	521	11	US-11-188-298-19470	Sequence 19470, A	339	27	54.0	92	9	US-10-467-657-8388	Sequence 8388, Appl
267	28	56.0	521	11	US-11-188-298-19766	Sequence 19766, A	340	27	54.0	94	9	US-10-467-657-8388	Sequence 8388, Appl
268	28	56.0	525	9	US-10-131-826A-56	Sequence 56, Appl	341	27	54.0	94	11	US-11-096-568A-2162	Sequence 2162, Appl
269	28	56.0	525	9	US-10-973-115B-56	Sequence 56, Appl	342	27	54.0	110	11	US-11-240-769-91	Sequence 91, Appl
270	28	56.0	525	9	US-10-137-873A-56	Sequence 56, Appl	343	27	54.0	121	11	US-11-188-298-11355	Sequence 11355, A
271	28	56.0	525	9	US-10-152-370-56	Sequence 56, Appl	344	27	54.0	121	11	US-11-188-298-12895	Sequence 12895, A
272	28	56.0	525	11	US-11-290-153-56	Sequence 56, Appl	345	27	54.0	125	11	US-11-155-775-22	Sequence 22, Appl
273	28	56.0	539	11	US-11-043-788-464	Sequence 464, Appl	346	27	54.0	125	11	US-11-155-775-30	Sequence 30, Appl
274	28	56.0	549	11	US-11-043-788-467	Sequence 467, Appl	347	27	54.0	125	11	US-11-155-775-42	Sequence 42, Appl
275	28	56.0	549	11	US-11-043-788-468	Sequence 468, Appl	348	27	54.0	125	11	US-11-155-775-46	Sequence 46, Appl
276	28	56.0	558	11	US-11-078-189-19	Sequence 19, Appl	349	27	54.0	125	11	US-11-155-775-50	Sequence 50, Appl
277	28	56.0	611	11	US-11-087-099-5877	Sequence 5877, Appl	350	27	54.0	125	11	US-11-155-775-58	Sequence 58, Appl
278	28	56.0	631	9	US-10-813-646-22	Sequence 22, Appl	351	27	54.0	125	11	US-11-155-775-62	Sequence 62, Appl
279	28	56.0	676	11	US-11-045-004-435	Sequence 435, Appl	352	27	54.0	126	11	US-11-155-775-18	Sequence 18, Appl
280	28	56.0	693	11	US-11-098-686-11111	Sequence 11111, A	353	27	54.0	126	11	US-11-155-775-34	Sequence 34, Appl
281	28	56.0	694	11	US-11-078-189-16	Sequence 16, Appl	354	27	54.0	126	11	US-11-064-174-14	Sequence 14, Appl
282	28	56.0	703	11	US-11-078-189-13	Sequence 13, Appl	355	27	54.0	126	11	US-11-064-174-15	Sequence 15, Appl
283	28	56.0	708	11	US-11-174-150-25	Sequence 25, Appl	356	27	54.0	126	11	US-11-064-174-16	Sequence 16, Appl
284	28	56.0	708	11	US-11-078-189-10	Sequence 10, Appl	357	27	54.0	126	11	US-11-064-174-17	Sequence 17, Appl
285	28	56.0	724	11	US-11-078-189-15	Sequence 15, Appl	358	27	54.0	126	11	US-11-064-174-148	Sequence 148, Appl
286	28	56.0	735	9	US-10-652-893-2	Sequence 2, Appl	359	27	54.0	126	11	US-11-064-174-152	Sequence 152, Appl
287	28	56.0	734	9	US-10-194-487-458	Sequence 458, Appl	360	27	54.0	127	11	US-11-064-174-139	Sequence 139, Appl
288	28	56.0	734	9	US-10-195-883-458	Sequence 458, Appl	361	27	54.0	129	11	US-11-052-554A-317	Sequence 317, Appl
289	28	56.0	734	9	US-10-195-888-458	Sequence 458, Appl	362	27	54.0	132	11	US-11-098-686-10468	Sequence 10468, A
290	28	56.0	734	9	US-10-195-889-458	Sequence 458, Appl	363	27	54.0	149	11	US-11-079-463-8429	Sequence 8429, Appl
291	28	56.0	734	11	US-11-137-465-65	Sequence 65, Appl	364	27	54.0	150	11	US-11-045-004-1109	Sequence 1109, Appl
292	28	56.0	734	11	US-11-288-493-14	Sequence 14, Appl	365	27	54.0	152	11	US-11-096-568A-11875	Sequence 11875, A
293	28	56.0	736	11	US-11-174-150-26	Sequence 26, Appl	366	27	54.0	156	9	US-10-703-799B-186	Sequence 186, Appl
294	28	56.0	736	11	US-11-078-189-9	Sequence 9, Appl	367	27	54.0	159	9	US-10-467-657-3736	Sequence 3736, Appl
295	28	56.0	739	11	US-11-078-189-12	Sequence 12, Appl	368	27	54.0	162	9	US-10-793-626-2266	Sequence 2266, Appl
296	28	56.0	746	11	US-11-188-298-1134	Sequence 1134, Appl	369	27	54.0	171	11	US-11-188-298-11580	Sequence 11580, A
297	28	56.0	746	11	US-11-188-298-17421	Sequence 17421, A	370	27	54.0	174	9	US-10-501-035-387	Sequence 387, Appl
298	28	56.0	746	11	US-11-188-298-7117	Sequence 7117, Appl	371	27	54.0	174	11	US-11-090-617-704	Sequence 704, Appl
299	28	56.0	777	11	US-11-188-298-4859	Sequence 4859, Appl	372	27	54.0	175	11	US-11-098-686-10396	Sequence 10396, A
300	28	56.0	777	11	US-11-188-298-9417	Sequence 9417, Appl	373	27	54.0	179	11	US-11-096-568A-25693	Sequence 25693, A
301	28	56.0	777	11	US-11-188-298-15702	Sequence 15702, A	374	27	54.0	180	11	US-11-079-463-8612	Sequence 8612, Appl
302	28	56.0	787	9	US-10-467-657-2832	Sequence 2832, Appl	375	27	54.0	181	11	US-11-096-568A-22099	Sequence 22099, A
303	28	56.0	793	9	US-10-510-903-4	Sequence 4, Appl	376	27	54.0	193	11	US-11-188-298-10664	Sequence 10664, A
304	28	56.0	794	11	US-11-024-959-478	Sequence 478, Appl	377	27	54.0	199	11	US-11-264-096-425	Sequence 425, Appl
305	28	56.0	857	9	US-10-613-744-11	Sequence 11, Appl	378	27	54.0	207	11	US-11-096-568A-25690	Sequence 25690, A
306	28	56.0	901	9	US-10-793-626-342	Sequence 342, Appl	379	27	54.0	211	9	US-10-858-730-237	Sequence 237, Appl
307	28	56.0	988	9	US-10-472-808A-2	Sequence 2, Appl	380	27	54.0	212	11	US-11-096-568A-6062	Sequence 6062, Appl
308	28	56.0	988	9	US-10-472-808A-4	Sequence 4, Appl	381	27	54.0	212	11	US-11-188-298-12238	Sequence 12238, A
309	28	56.0	988	9	US-10-472-808A-5	Sequence 5, Appl	382	27	54.0	212	11	US-11-188-298-19740	Sequence 19740, A
310	28	56.0	1081	11	US-11-121-438-4	Sequence 4, Appl	383	27	54.0	214	11	US-11-188-298-2324	Sequence 2324, Appl
311	28	56.0	1438	9	US-10-511-559-73	Sequence 73, Appl	384	27	54.0	215	11	US-11-188-298-4832	Sequence 4832, Appl
312	28	56.0	2250	9	US-10-922-232B-57	Sequence 57, Appl	385	27	54.0	216	11	US-11-096-568A-26010	Sequence 26010, A
313	28	56.0	2351	10	US-11-183-218-30	Sequence 30, Appl	386	27	54.0	223	11	US-11-188-298-8531	Sequence 8531, Appl

387	27	54.0	224	9	US-10-216-161A-162	Sequence 162, App	460	27	54.0	335	11	US-11-096-568A-5324	Sequence 5324, Ap
388	27	54.0	228	9	US-10-467-657-7524	Sequence 7524, Ap	461	27	54.0	335	11	US-11-103-195-46	Sequence 46, Appl
389	27	54.0	228	11	US-11-156-084-100	Sequence 100, App	462	27	54.0	342	11	US-11-188-298-517	Sequence 517, App
390	27	54.0	235	11	US-11-216-267-14	Sequence 14, Appl	463	27	54.0	345	11	US-11-079-463-7507	Sequence 7507, Ap
391	27	54.0	235	11	US-11-232-382-14	Sequence 14, Appl	464	27	54.0	345	11	US-11-188-298-18006	Sequence 18006, A
392	27	54.0	237	11	US-11-188-298-3589	Sequence 3589, Ap	465	27	54.0	347	9	US-10-793-626-324	Sequence 324, App
393	27	54.0	237	11	US-11-188-298-4760	Sequence 4760, Ap	466	27	54.0	347	11	US-11-156-084-129	Sequence 129, App
394	27	54.0	237	11	US-11-188-298-11731	Sequence 11731, A	467	27	54.0	347	11	US-11-096-568A-15231	Sequence 15231, A
395	27	54.0	237	11	US-11-188-298-12773	Sequence 12773, A	468	27	54.0	347	11	US-11-228-659-66	Sequence 66, Appl
396	27	54.0	238	11	US-11-188-298-4054	Sequence 4054, Ap	469	27	54.0	348	11	US-11-096-568A-15230	Sequence 15230, A
397	27	54.0	238	11	US-11-188-298-16537	Sequence 16537, A	470	27	54.0	348	11	US-11-096-568A-7422	Sequence 7422, Ap
398	27	54.0	239	11	US-11-188-298-6667	Sequence 6667, Ap	471	27	54.0	355	11	US-11-096-568A-29792	Sequence 29792, A
399	27	54.0	239	11	US-11-188-298-10151	Sequence 10151, A	472	27	54.0	357	11	US-11-188-298-16709	Sequence 16709, A
400	27	54.0	239	11	US-11-188-298-18904	Sequence 18904, A	473	27	54.0	358	11	US-11-098-686-11346	Sequence 11346, A
401	27	54.0	241	11	US-11-188-298-11223	Sequence 11223, Ap	474	27	54.0	360	9	US-10-467-657-7666	Sequence 7666, Ap
402	27	54.0	241	11	US-11-188-298-5326	Sequence 5326, Ap	475	27	54.0	360	11	US-11-194-246-321	Sequence 321, App
403	27	54.0	241	11	US-11-188-298-16786	Sequence 16786, A	476	27	54.0	363	11	US-11-096-568A-25913	Sequence 25913, A
404	27	54.0	242	11	US-11-264-728-24	Sequence 24, Appl	477	27	54.0	363	11	US-11-188-298-17569	Sequence 17569, A
405	27	54.0	242	11	US-11-188-298-7986	Sequence 7986, Ap	478	27	54.0	365	11	US-11-087-099-11255	Sequence 11255, A
406	27	54.0	242	11	US-11-188-298-8277	Sequence 8277, Ap	479	27	54.0	367	11	US-11-096-568A-16420	Sequence 16420, A
407	27	54.0	242	11	US-11-188-298-9450	Sequence 9450, Ap	480	27	54.0	370	11	US-11-055-822-796	Sequence 796, App
408	27	54.0	242	11	US-11-188-298-12513	Sequence 12513, A	481	27	54.0	377	11	US-11-079-463-7761	Sequence 7761, Ap
409	27	54.0	242	11	US-11-188-298-22349	Sequence 22349, A	482	27	54.0	381	11	US-11-096-568A-24306	Sequence 24306, A
410	27	54.0	243	11	US-11-188-298-4163	Sequence 4163, Ap	483	27	54.0	381	11	US-11-096-568A-29791	Sequence 29791, A
411	27	54.0	243	11	US-11-188-298-9682	Sequence 9682, Ap	484	27	54.0	383	11	US-11-096-568A-29790	Sequence 29790, A
412	27	54.0	243	11	US-11-188-298-17312	Sequence 17312, A	485	27	54.0	384	11	US-11-188-298-19094	Sequence 19094, A
413	27	54.0	243	11	US-11-188-298-20194	Sequence 20194, A	486	27	54.0	387	9	US-10-990-477-2	Sequence 2, Appli
414	27	54.0	244	9	US-10-986-403-348	Sequence 348, App	487	27	54.0	387	9	US-10-990-477-6	Sequence 6, Appli
415	27	54.0	245	11	US-11-188-298-16265	Sequence 16265, A	488	27	54.0	389	9	US-10-534-583-1	Sequence 1, Appli
416	27	54.0	246	9	US-10-467-657-7246	Sequence 7246, Ap	489	27	54.0	390	11	US-11-188-298-16844	Sequence 16844, A
417	27	54.0	248	9	US-10-793-626-632	Sequence 632, App	490	27	54.0	392	11	US-11-188-298-19221	Sequence 19221, A
418	27	54.0	252	11	US-11-055-822-22	Sequence 22, Appl	491	27	54.0	393	11	US-11-218-272-10	Sequence 10, Appl
419	27	54.0	252	11	US-11-188-298-4113	Sequence 4113, Ap	492	27	54.0	394	11	US-11-188-298-1321	Sequence 1321, Ap
420	27	54.0	259	11	US-11-098-686-11084	Sequence 11084, A	493	27	54.0	397	11	US-11-188-298-6278	Sequence 6278, Ap
421	27	54.0	259	11	US-11-188-298-4817	Sequence 4817, Ap	494	27	54.0	398	11	US-11-072-512-2010	Sequence 2010, Ap
422	27	54.0	268	11	US-11-079-463-6336	Sequence 6336, Ap	495	27	54.0	402	9	US-10-506-454-788	Sequence 788, App
423	27	54.0	269	11	US-11-096-568A-6061	Sequence 6061, Ap	496	27	54.0	402	11	US-11-146-428-69	Sequence 69, Appl
424	27	54.0	273	9	US-10-506-454-1504	Sequence 1504, Ap	497	27	54.0	405	11	US-11-087-099-1685	Sequence 1685, Ap
425	27	54.0	276	11	US-11-188-298-19852	Sequence 19852, A	498	27	54.0	412	11	US-11-096-568A-7421	Sequence 7421, Ap
426	27	54.0	281	9	US-10-915-002-174	Sequence 174, App	499	27	54.0	413	11	US-11-096-568A-7420	Sequence 7420, Ap
427	27	54.0	282	11	US-11-096-568A-5326	Sequence 5326, Ap	500	27	54.0	414	9	US-10-873-528-76	Sequence 76, Appl
428	27	54.0	282	11	US-11-045-004-1357	Sequence 1357, Ap	501	27	54.0	414	11	US-11-096-568A-16419	Sequence 16419, A
429	27	54.0	287	11	US-11-096-568A-6060	Sequence 6060, Ap	502	27	54.0	417	11	US-11-096-568A-25912	Sequence 25912, A
430	27	54.0	287	11	US-11-188-298-3945	Sequence 3945, Ap	503	27	54.0	423	9	US-10-793-626-3160	Sequence 3160, Ap
431	27	54.0	288	11	US-11-037-243-115	Sequence 115, App	504	27	54.0	428	11	US-11-188-298-20204	Sequence 20204, A
432	27	54.0	294	11	US-11-098-686-10634	Sequence 10634, A	505	27	54.0	430	11	US-11-126-313-35	Sequence 35, Appl
433	27	54.0	294	11	US-11-188-298-10602	Sequence 10602, A	506	27	54.0	430	11	US-11-126-313-36	Sequence 36, Appl
434	27	54.0	301	11	US-11-188-298-3724	Sequence 3724, Ap	507	27	54.0	432	9	US-10-467-657-1890	Sequence 1890, Ap
435	27	54.0	305	11	US-11-113-424-58	Sequence 58, Appl	508	27	54.0	432	9	US-10-467-657-6128	Sequence 6128, Ap
436	27	54.0	306	11	US-11-156-084-178	Sequence 178, App	509	27	54.0	435	11	US-11-045-004-1551	Sequence 1551, Ap
437	27	54.0	306	11	US-11-079-463-5564	Sequence 5564, Ap	510	27	54.0	435	11	US-11-045-004-2678	Sequence 2678, Ap
438	27	54.0	308	11	US-11-079-463-5725	Sequence 5725, Ap	511	27	54.0	439	11	US-11-087-099-10158	Sequence 10158, A
439	27	54.0	309	11	US-11-096-568A-5325	Sequence 5325, Ap	512	27	54.0	440	9	US-10-606-302-9	Sequence 9, Appli
440	27	54.0	310	11	US-11-087-099-6235	Sequence 6235, Ap	513	27	54.0	440	9	US-10-703-7998-268	Sequence 268, App
441	27	54.0	310	11	US-11-087-099-12084	Sequence 12084, A	514	27	54.0	447	11	US-11-096-568A-5917	Sequence 5917, Ap
442	27	54.0	310	11	US-11-188-298-7152	Sequence 7152, Ap	515	27	54.0	450	11	US-11-079-463-8683	Sequence 8683, Ap
443	27	54.0	311	9	US-10-467-657-1638	Sequence 1638, Ap	516	27	54.0	451	11	US-11-188-298-12102	Sequence 12102, A
444	27	54.0	320	11	US-11-079-463-6400	Sequence 6400, Ap	517	27	54.0	452	9	US-10-467-657-1850	Sequence 1850, Ap
445	27	54.0	320	11	US-11-188-298-18723	Sequence 18723, A	518	27	54.0	455	9	US-10-650-326B-14	Sequence 14, Appl
446	27	54.0	324	11	US-11-188-298-6002	Sequence 6002, Ap	519	27	54.0	455	11	US-11-226-555-25	Sequence 25, Appl
447	27	54.0	332	11	US-11-113-424-55	Sequence 55, Appl	520	27	54.0	458	9	US-10-454-437-124	Sequence 124, App
448	27	54.0	333	11	US-11-188-298-1477	Sequence 1477, Ap	521	27	54.0	458	11	US-11-087-099-604	Sequence 604, App
449	27	54.0	334	11	US-11-188-298-1228	Sequence 1228, Ap	522	27	54.0	458	11	US-11-188-298-11567	Sequence 11567, A
450	27	54.0	334	11	US-11-188-298-17443	Sequence 17443, A	523	27	54.0	462	9	US-10-467-657-7636	Sequence 7636, Ap
451	27	54.0	335	9	US-10-063-703-46	Sequence 46, Appl	524	27	54.0	462	11	US-11-087-099-9021	Sequence 9021, Ap
452	27	54.0	335	9	US-10-982-357-2	Sequence 2, Appli	525	27	54.0	462	11	US-11-188-298-19348	Sequence 19348, A
453	27	54.0	335	9	US-10-194-487-192	Sequence 192, App	526	27	54.0	468	11	US-11-086-289-22	Sequence 22, Appl
454	27	54.0	335	9	US-10-195-883-192	Sequence 192, App	527	27	54.0	475	11	US-11-087-099-4120	Sequence 4120, Ap
455	27	54.0	335	9	US-10-195-888-192	Sequence 192, App	528	27	54.0	477	11	US-11-096-568A-25911	Sequence 25911, A
456	27	54.0	335	9	US-10-195-889-192	Sequence 192, App	529	27	54.0	477	11	US-11-188-298-552	Sequence 552, App
457	27	54.0	335	9	US-10-501-841-2	Sequence 2, Appli	530	27	54.0	480	11	US-11-087-099-9924	Sequence 9924, Ap
458	27	54.0	335	11	US-11-102-240-46	Sequence 46, Appl	531	27	54.0	481	11	US-11-188-298-13506	Sequence 13506, A
459	27	54.0	335	11	US-11-240-769-59	Sequence 59, Appl	532	27	54.0	483	11	US-11-188-298-14907	Sequence 14907, A

533	27	54.0	485	9	US-10-506-454-1364	Sequence 1364, Ap	606	27	54.0	818	11	US-11-087-099-12309	Sequence 12309, A
534	27	54.0	487	11	US-11-113-424-56	Sequence 56, Appl	607	27	54.0	818	11	US-11-188-298-11313	Sequence 11313, A
535	27	54.0	487	11	US-11-113-424-57	Sequence 57, Appl	608	27	54.0	834	11	US-11-087-099-10005	Sequence 10005, A
536	27	54.0	488	11	US-11-188-298-12582	Sequence 12582, A	609	27	54.0	893	11	US-11-079-463-8847	Sequence 8847, Ap
537	27	54.0	489	11	US-11-045-004-949	Sequence 949, App	610	27	54.0	900	11	US-11-182-016-37	Sequence 37, Appl
538	27	54.0	491	11	US-11-188-298-13154	Sequence 13154, A	611	27	54.0	941	11	US-11-079-463-6927	Sequence 6927, Ap
539	27	54.0	493	11	US-11-188-298-6241	Sequence 6241, Ap	612	27	54.0	1001	11	US-11-188-298-19405	Sequence 19405, A
540	27	54.0	495	9	US-10-613-744-5	Sequence 5, Appl	613	27	54.0	1032	11	US-11-079-463-10074	Sequence 10074, A
541	27	54.0	497	11	US-11-188-298-15272	Sequence 15272, A	614	27	54.0	1052	11	US-11-124-367A-323	Sequence 323, App
542	27	54.0	499	11	US-11-188-298-519	Sequence 519, App	615	27	54.0	1061	11	US-11-000-463-347	Sequence 347, App
543	27	54.0	502	11	US-11-096-568A-31734	Sequence 31734, A	616	27	54.0	1061	11	US-11-124-367A-325	Sequence 325, App
544	27	54.0	506	9	US-10-467-657-2088	Sequence 2088, Ap	617	27	54.0	1091	11	US-11-000-463-348	Sequence 348, App
545	27	54.0	508	11	US-11-188-298-22134	Sequence 22134, A	618	27	54.0	1162	11	US-11-096-568A-30849	Sequence 30849, A
546	27	54.0	510	11	US-11-096-568A-5916	Sequence 5916, Ap	619	27	54.0	1184	9	US-10-131-826A-412	Sequence 412, App
547	27	54.0	526	11	US-11-096-568A-5915	Sequence 5915, Ap	620	27	54.0	1184	9	US-10-973-115B-412	Sequence 412, App
548	27	54.0	527	11	US-11-096-568A-31733	Sequence 31733, A	621	27	54.0	1184	9	US-10-137-873A-412	Sequence 412, App
549	27	54.0	528	9	US-10-194-487-490	Sequence 490, App	622	27	54.0	1184	9	US-10-152-370-412	Sequence 412, App
550	27	54.0	528	9	US-10-195-883-490	Sequence 490, App	623	27	54.0	1184	11	US-11-290-153-412	Sequence 412, App
551	27	54.0	528	9	US-10-195-888-490	Sequence 490, App	624	27	54.0	1193	11	US-11-096-568A-32522	Sequence 32522, A
552	27	54.0	528	9	US-10-195-889-490	Sequence 490, App	625	27	54.0	1206	11	US-11-096-568A-30848	Sequence 30848, A
553	27	54.0	536	9	US-10-517-939-322	Sequence 322, App	626	27	54.0	1214	11	US-11-096-568A-29242	Sequence 29242, A
554	27	54.0	538	11	US-11-188-298-8585	Sequence 8585, Ap	627	27	54.0	1221	11	US-11-096-568A-29337	Sequence 29337, A
555	27	54.0	538	11	US-11-188-298-15993	Sequence 15993, A	628	27	54.0	1222	11	US-11-096-568A-29241	Sequence 29241, A
556	27	54.0	539	11	US-11-188-298-19657	Sequence 19657, A	629	27	54.0	1228	11	US-11-234-786-537	Sequence 537, App
557	27	54.0	540	11	US-11-188-298-316	Sequence 316, App	630	27	54.0	1229	11	US-11-096-568A-29336	Sequence 29336, A
558	27	54.0	545	11	US-11-188-298-14369	Sequence 14369, A	631	27	54.0	1235	11	US-11-096-568A-30847	Sequence 30847, A
559	27	54.0	548	11	US-11-188-298-9428	Sequence 9428, Ap	632	27	54.0	1237	11	US-11-096-568A-32521	Sequence 32521, A
560	27	54.0	554	11	US-11-188-298-17174	Sequence 17174, A	633	27	54.0	1247	11	US-11-096-568A-29240	Sequence 29240, A
561	27	54.0	556	9	US-10-613-744-8	Sequence 8, Appl	634	27	54.0	1254	11	US-11-096-568A-29335	Sequence 29335, A
562	27	54.0	557	11	US-11-096-568A-31732	Sequence 31732, A	635	27	54.0	1261	11	US-11-234-786-538	Sequence 538, App
563	27	54.0	564	9	US-10-485-517-253	Sequence 253, App	636	27	54.0	1266	11	US-11-096-568A-32520	Sequence 32520, A
564	27	54.0	564	9	US-10-485-517-290	Sequence 290, App	637	27	54.0	1325	9	US-10-329-258-10	Sequence 10, Appl
565	27	54.0	566	9	US-10-718-264-18	Sequence 18, Appl	638	27	54.0	1325	11	US-11-124-367A-410	Sequence 410, App
566	27	54.0	566	9	US-10-718-264-18	Sequence 18, Appl	639	27	54.0	1325	11	US-11-203-526-2	Sequence 2, Appl
567	27	54.0	566	11	US-11-176-667-18	Sequence 18, Appl	640	27	54.0	1388	9	US-10-501-035-350	Sequence 350, App
568	27	54.0	567	9	US-10-718-264-20	Sequence 20, Appl	641	27	54.0	1419	11	US-11-124-367A-324	Sequence 324, App
569	27	54.0	567	9	US-10-718-264-20	Sequence 20, Appl	642	27	54.0	1425	11	US-11-024-959-367	Sequence 367, App
570	27	54.0	567	11	US-11-176-667-20	Sequence 20, Appl	643	27	54.0	1428	11	US-11-124-367A-320	Sequence 320, App
571	27	54.0	569	11	US-11-079-463-8795	Sequence 8795, Ap	644	27	54.0	1798	11	US-11-080-991-96	Sequence 96, Appl
572	27	54.0	569	11	US-11-045-004-2706	Sequence 2706, Ap	645	27	54.0	1928	9	US-10-480-330-30	Sequence 30, Appl
573	27	54.0	573	11	US-11-188-298-4740	Sequence 4740, Ap	646	27	54.0	1965	9	US-10-480-330-4	Sequence 4, Appl
574	27	54.0	582	11	US-11-074-178-110	Sequence 110, App	647	27	54.0	1966	9	US-10-480-330-2	Sequence 2, Appl
575	27	54.0	587	11	US-11-188-298-296	Sequence 296, App	648	27	54.0	1966	9	US-10-480-330-6	Sequence 6, Appl
576	27	54.0	589	11	US-11-188-298-21096	Sequence 21096, A	649	27	54.0	1966	9	US-10-480-330-8	Sequence 8, Appl
577	27	54.0	590	11	US-11-124-368A-183	Sequence 183, App	650	27	54.0	1966	9	US-10-480-330-10	Sequence 10, Appl
578	27	54.0	590	11	US-11-127-877-54	Sequence 54, Appl	651	27	54.0	1966	9	US-10-480-330-12	Sequence 12, Appl
579	27	54.0	596	11	US-11-087-099-9309	Sequence 9309, Ap	652	27	54.0	1966	9	US-10-480-330-14	Sequence 14, Appl
580	27	54.0	596	11	US-11-188-298-19669	Sequence 19669, A	653	27	54.0	1966	9	US-10-480-330-16	Sequence 16, Appl
581	27	54.0	623	11	US-11-079-463-9893	Sequence 9893, Ap	654	27	54.0	1966	9	US-10-480-330-18	Sequence 18, Appl
582	27	54.0	625	11	US-11-188-298-6306	Sequence 6306, Ap	655	27	54.0	1966	9	US-10-480-330-20	Sequence 20, Appl
583	27	54.0	627	11	US-11-188-298-17226	Sequence 17226, A	656	27	54.0	1966	9	US-10-480-330-22	Sequence 22, Appl
584	27	54.0	634	11	US-11-188-298-21043	Sequence 21043, A	657	27	54.0	1966	9	US-10-480-330-24	Sequence 24, Appl
585	27	54.0	634	11	US-11-188-298-21912	Sequence 21912, A	658	27	54.0	1966	9	US-10-480-330-26	Sequence 26, Appl
586	27	54.0	642	11	US-11-079-463-6385	Sequence 6385, Ap	659	27	54.0	1966	9	US-10-480-330-28	Sequence 28, Appl
587	27	54.0	648	11	US-11-096-568A-27576	Sequence 27576, A	660	27	54.0	2048	11	US-11-285-818-12	Sequence 12, Appl
588	27	54.0	667	11	US-11-188-298-3641	Sequence 3641, Ap	661	27	54.0	2057	11	US-11-285-818-10	Sequence 10, Appl
589	27	54.0	668	11	US-11-188-298-6671	Sequence 6671, Ap	662	27	54.0	2058	11	US-11-072-175-188	Sequence 188, App
590	27	54.0	675	11	US-11-079-463-7192	Sequence 7192, Ap	663	27	54.0	2058	11	US-11-285-818-17	Sequence 17, Appl
591	27	54.0	693	9	US-10-467-657-6176	Sequence 6176, Ap	664	27	54.0	2061	11	US-11-077-386-27	Sequence 27, Appl
592	27	54.0	719	11	US-11-207-078-219	Sequence 219, App	665	27	54.0	2061	11	US-11-169-041-179	Sequence 179, App
593	27	54.0	727	9	US-10-506-454-527	Sequence 527, App	666	27	54.0	2080	9	US-10-821-234-1640	Sequence 1640, Ap
594	27	54.0	736	11	US-11-079-463-10098	Sequence 10098, A	667	27	54.0	2209	10	US-11-301-554-1303	Sequence 1303, Ap
595	27	54.0	738	9	US-10-505-263-4	Sequence 4, Appl	668	27	54.0	3377	11	US-11-124-367A-271	Sequence 271, App
596	27	54.0	751	11	US-11-087-099-4864	Sequence 4864, Ap	669	27	54.0	3841	11	US-11-124-367A-272	Sequence 272, App
597	27	54.0	758	9	US-10-505-263-2	Sequence 2, Appl	670	27	54.0	4074	8	US-10-501-834-2	Sequence 2, Appl
598	27	54.0	771	11	US-11-087-099-2268	Sequence 2268, Ap	671	27	54.0	4590	8	US-10-505-928-569	Sequence 569, App
599	27	54.0	773	11	US-11-188-298-18509	Sequence 18509, A	672	26	52.0	36	9	US-10-506-796A-5	Sequence 5, Appl
600	27	54.0	773	11	US-11-188-298-20645	Sequence 20645, A	673	26	52.0	42	9	US-10-532-480-35	Sequence 35, Appl
601	27	54.0	778	11	US-11-188-298-8840	Sequence 8840, Ap	674	26	52.0	49	11	US-11-183-567A-20	Sequence 20, Appl
602	27	54.0	793	11	US-11-188-298-11205	Sequence 11205, A	675	26	52.0	49	11	US-11-183-567A-21	Sequence 21, Appl
603	27	54.0	802	11	US-11-010-239-40	Sequence 40, Appl	676	26	52.0	49	11	US-11-183-567A-22	Sequence 22, Appl
604	27	54.0	802	11	US-11-188-298-5674	Sequence 5674, Ap	677	26	52.0	54	9	US-10-467-657-7102	Sequence 7102, Ap
605	27	54.0	802	11	US-11-188-298-20820	Sequence 20820, A	678	26	52.0	67	11	US-11-004-399-847	Sequence 847, App

679	26	52.0	74	9	US-10-467-657-3364	Sequence 3364, Ap	752	26	52.0	228	11	US-11-188-298-6216	Sequence 6216, Ap
680	26	52.0	75	11	US-11-079-463-9936	Sequence 9936, Ap	753	26	52.0	228	11	US-11-188-298-6383	Sequence 6383, Ap
681	26	52.0	83	11	US-11-000-463-246	Sequence 246, App	754	26	52.0	234	11	US-11-079-463-8366	Sequence 8366, Ap
682	26	52.0	83	11	US-11-096-568A-27339	Sequence 27339, A	755	26	52.0	235	9	US-10-506-454-98	Sequence 98, Appl
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684	26	52.0	85	11	US-11-096-568A-27338	Sequence 27338, A	757	26	52.0	239	11	US-11-096-568A-6548	Sequence 6548, Ap
685	26	52.0	91	9	US-10-506-454-69	Sequence 69, Appl	758	26	52.0	241	9	US-10-873-528-116	Sequence 116, App
686	26	52.0	94	11	US-11-188-298-16410	Sequence 16410, A	759	26	52.0	245	11	US-11-188-298-8399	Sequence 8399, Ap
687	26	52.0	94	11	US-11-188-298-21883	Sequence 21883, A	760	26	52.0	247	9	US-10-467-657-918	Sequence 918, App
688	26	52.0	95	11	US-11-188-298-18878	Sequence 18878, A	761	26	52.0	248	11	US-11-045-004-249	Sequence 249, App
689	26	52.0	100	11	US-11-096-568A-6932	Sequence 6932, Ap	762	26	52.0	248	11	US-11-045-004-1033	Sequence 1033, Ap
690	26	52.0	104	11	US-11-096-568A-7689	Sequence 7689, Ap	763	26	52.0	249	11	US-11-096-568A-26331	Sequence 26331, A
691	26	52.0	109	9	US-10-475-075-812	Sequence 812, App	764	26	52.0	251	11	US-11-188-298-12320	Sequence 12320, A
692	26	52.0	111	11	US-11-087-099-9880	Sequence 9880, Ap	765	26	52.0	251	11	US-11-188-298-14313	Sequence 14313, A
693	26	52.0	114	11	US-11-087-099-2019	Sequence 2019, Ap	766	26	52.0	257	11	US-11-172-740-1715	Sequence 1715, Ap
694	26	52.0	115	11	US-11-072-512-2181	Sequence 2181, Ap	767	26	52.0	257	11	US-11-188-298-3150	Sequence 3150, Ap
695	26	52.0	116	11	US-11-188-298-19304	Sequence 19304, A	768	26	52.0	260	11	US-11-096-568A-23293	Sequence 23293, A
696	26	52.0	118	11	US-11-072-512-3567	Sequence 3567, Ap	769	26	52.0	262	11	US-11-087-099-4850	Sequence 4850, Ap
697	26	52.0	119	11	US-11-072-512-2897	Sequence 2897, Ap	770	26	52.0	264	9	US-10-194-487-12	Sequence 12, Appl
698	26	52.0	121	11	US-11-031-206-118	Sequence 118, App	771	26	52.0	264	9	US-10-195-888-12	Sequence 12, Appl
699	26	52.0	126	11	US-11-188-298-4096	Sequence 4096, Ap	772	26	52.0	264	9	US-10-195-888-12	Sequence 12, Appl
700	26	52.0	129	9	US-10-993-543-160	Sequence 160, App	773	26	52.0	264	9	US-10-195-888-12	Sequence 12, Appl
701	26	52.0	129	11	US-11-096-568A-3150	Sequence 3150, Ap	774	26	52.0	270	11	US-11-045-004-2700	Sequence 2700, Ap
702	26	52.0	133	11	US-11-096-568A-7688	Sequence 7688, Ap	775	26	52.0	273	9	US-10-793-626-608	Sequence 608, App
703	26	52.0	136	11	US-11-087-099-9187	Sequence 9187, Ap	776	26	52.0	274	11	US-11-188-298-13383	Sequence 13383, A
704	26	52.0	138	11	US-11-096-568A-27337	Sequence 27337, A	777	26	52.0	275	11	US-11-079-463-6307	Sequence 6307, A
705	26	52.0	139	11	US-11-136-619-15	Sequence 15, Appl	778	26	52.0	275	11	US-11-188-298-10654	Sequence 10654, A
706	26	52.0	145	11	US-11-096-568A-3149	Sequence 3149, Ap	779	26	52.0	276	11	US-11-086-568A-4852	Sequence 4852, Ap
707	26	52.0	148	11	US-11-096-568A-3151	Sequence 3151, Ap	780	26	52.0	277	11	US-11-188-298-7243	Sequence 7243, Ap
708	26	52.0	148	11	US-11-136-619-29	Sequence 29, Appl	781	26	52.0	279	11	US-11-188-298-22291	Sequence 22291, A
709	26	52.0	150	11	US-11-188-298-3922	Sequence 3922, Ap	782	26	52.0	280	11	US-11-096-568A-4864	Sequence 4864, Ap
710	26	52.0	150	11	US-11-188-298-18483	Sequence 18483, A	783	26	52.0	280	11	US-11-096-568A-23292	Sequence 23292, A
711	26	52.0	151	9	US-10-506-454-919	Sequence 919, App	784	26	52.0	280	11	US-11-188-298-19189	Sequence 19189, A
712	26	52.0	152	11	US-11-136-619-27	Sequence 27, Appl	785	26	52.0	281	11	US-11-087-099-6234	Sequence 6234, Ap
713	26	52.0	154	11	US-11-188-298-8967	Sequence 8967, Ap	786	26	52.0	281	11	US-11-096-568A-6547	Sequence 6547, Ap
714	26	52.0	158	11	US-11-087-099-1462	Sequence 1462, Ap	787	26	52.0	281	11	US-11-096-568A-22353	Sequence 22353, A
715	26	52.0	159	11	US-11-072-512-3218	Sequence 3218, Ap	788	26	52.0	281	11	US-11-096-568A-27803	Sequence 27803, A
716	26	52.0	159	11	US-11-188-298-16499	Sequence 16499, A	789	26	52.0	284	11	US-11-188-298-381	Sequence 381, App
717	26	52.0	165	11	US-11-087-099-925	Sequence 925, App	790	26	52.0	284	11	US-11-188-298-9856	Sequence 9856, Ap
718	26	52.0	169	11	US-11-096-568A-33981	Sequence 33981, A	791	26	52.0	286	11	US-11-086-568A-6546	Sequence 6546, Ap
719	26	52.0	171	9	US-10-506-454-1551	Sequence 1551, Ap	792	26	52.0	287	11	US-11-096-568A-3952	Sequence 3952, A
720	26	52.0	172	11	US-11-188-298-2468	Sequence 2468, Ap	793	26	52.0	287	11	US-11-096-568A-28758	Sequence 28758, A
721	26	52.0	173	11	US-11-096-568A-33980	Sequence 33980, A	794	26	52.0	289	11	US-11-010-239-59	Sequence 59, Appl
722	26	52.0	176	11	US-11-136-619-28	Sequence 28, Appl	795	26	52.0	289	11	US-11-096-568A-22352	Sequence 22352, A
723	26	52.0	176	11	US-11-045-004-271	Sequence 271, Appl	796	26	52.0	289	11	US-11-188-298-10749	Sequence 10749, A
724	26	52.0	178	9	US-10-467-657-2220	Sequence 2220, Ap	797	26	52.0	290	11	US-11-086-568A-22351	Sequence 22351, A
725	26	52.0	178	11	US-11-143-984A-36	Sequence 36, Appl	798	26	52.0	290	11	US-11-188-298-19477	Sequence 19477, A
726	26	52.0	180	11	US-11-136-619-16	Sequence 16, Appl	799	26	52.0	291	11	US-11-010-239-119	Sequence 119, App
727	26	52.0	180	11	US-11-136-619-26	Sequence 26, Appl	800	26	52.0	292	11	US-11-188-298-6754	Sequence 6754, Ap
728	26	52.0	189	11	US-11-096-568A-26332	Sequence 26332, A	801	26	52.0	293	11	US-11-079-463-7594	Sequence 7594, Ap
729	26	52.0	191	11	US-11-096-568A-3982	Sequence 3982, Ap	802	26	52.0	293	11	US-11-188-298-3203	Sequence 3203, Ap
730	26	52.0	192	11	US-11-188-298-5032	Sequence 5032, Ap	803	26	52.0	293	11	US-11-188-298-3817	Sequence 3817, Ap
731	26	52.0	193	11	US-11-096-568A-9914	Sequence 9914, Ap	804	26	52.0	294	11	US-11-188-298-21645	Sequence 21645, A
732	26	52.0	194	11	US-11-096-568A-3981	Sequence 3981, Ap	805	26	52.0	295	9	US-10-330-773-161	Sequence 161, App
733	26	52.0	195	11	US-11-087-099-9464	Sequence 9464, Ap	806	26	52.0	297	11	US-11-079-463-6771	Sequence 6771, Ap
734	26	52.0	195	11	US-11-188-298-6818	Sequence 6818, Ap	807	26	52.0	297	11	US-11-188-298-4285	Sequence 4285, Ap
735	26	52.0	196	9	US-10-793-626-2584	Sequence 2584, Ap	808	26	52.0	298	11	US-11-188-298-4934	Sequence 4934, Ap
736	26	52.0	202	9	US-10-793-626-892	Sequence 892, App	809	26	52.0	302	11	US-11-072-512-2430	Sequence 2430, Ap
737	26	52.0	202	9	US-10-510-903-26	Sequence 26, Appl	810	26	52.0	303	9	US-10-055-877-123	Sequence 123, App
738	26	52.0	203	11	US-11-096-568A-7687	Sequence 7687, Ap	811	26	52.0	305	11	US-11-080-991-92	Sequence 92, Appl
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ALIGNMENTS

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US-11-192-967-2
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; Publication No. US20050262587A1
; GENERAL INFORMATION:
; APPLICANT: Flannagan, Ronald D.
; APPLICANT: Meyer, Terry E.
; TITLE OF INVENTION: Novel Bt Toxin Receptors From
; TITLE OF INVENTION: Lepidopteran Insects and Methods of Use
; FILE REFERENCE: 35718/204664
; CURRENT APPLICATION NUMBER: US/11/192,967
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/09/715,909
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,285
; PRIOR FILING DATE: 1999-11-18
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US-11-192-967-2
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; Sequence 2, Application US/11193715
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; GENERAL INFORMATION:
; APPLICANT: Flannagan, Ronald D.
; APPLICANT: Mathis, John P.
; APPLICANT: Meyer, Terry E.
; TITLE OF INVENTION: Novel Bt Toxin Receptors From
; TITLE OF INVENTION: Lepidopteran Insects and Methods of Use
; FILE REFERENCE: 35718/204664
; CURRENT APPLICATION NUMBER: US/11/193,715
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/09/715,909
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,285
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1717
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-11-193-715-2
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Best Local Similarity 85.7%; Pred. No. 36;
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; Publication No. US20060078901A1
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; APPLICANT: BUCHRIESEN, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, FRANCK
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GORBEI, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
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; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
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; SEQ ID NO 2043
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; ORGANISM: Listeria monocytogenes
US-11-045-004-2043

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; Publication No. US20060046249A1
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; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
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US-10-501-035-314

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RESULT 5
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; Sequence 11058, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
```

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; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11058
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11058

Query Match          70.0%; Score 35; DB 11; Length 541;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LWFEID 7
Db      429 LWFEVD 434

RESULT 6
US-11-079-463-7895
; Sequence 7895, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR.
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7895
; LENGTH: 401
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-7895

Query Match          68.0%; Score 34; DB 11; Length 401;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
Db      22 WLWFELMIV 30

RESULT 7
US-11-188-298-17428
; Sequence 17428, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452) B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 17428
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-188-298-17428

Query Match          68.0%; Score 34; DB 11; Length 534;
Best Local Similarity 66.7%; Pred. No. 16+02;
```

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLWFEIDIV 9  
|||::|  
Db 291 FNMFLVDIV 299

RESULT 8  
US-11-156-084-126  
; Sequence 126, Application US/11156084  
; Publication No. US20060010515A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to  
; TITLE OF INVENTION: agronomically interesting phenotypes  
; FILE REFERENCE: (38-21)  
; CURRENT APPLICATION NUMBER: US/11/156,084  
; CURRENT FILING DATE: 2005-06-17  
; NUMBER OF SEQ ID NOS: 364  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 126  
; LENGTH: 357  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-11-156-084-126

Query Match 66.0%; Score 33; DB 11; Length 357;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLWFEIDI 8  
|||::|  
Db 173 FLWVDVDL 180

RESULT 9  
US-10-641-678-59  
; Sequence 59, Application US/10641678  
; Publication No. US20050277172A1  
; GENERAL INFORMATION:  
; APPLICANT: Day, Anthony, G.  
; APPLICANT: Goedegebuur, Frits  
; APPLICANT: Gualfetti, Peter  
; APPLICANT: Mitchinson, Colin  
; APPLICANT: Neefe, Paulien  
; APPLICANT: Sandgren, Mats  
; APPLICANT: Shaw, Andrew  
; APPLICANT: Stahlberg, Jerry  
; TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1  
; FILE REFERENCE: GC772-3  
; CURRENT APPLICATION NUMBER: US/10/641,678  
; CURRENT FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: US 60/458,853  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/458,696  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/456,368  
; PRIOR FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US 60/404,063  
; PRIOR FILING DATE: 2002-08-16  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 516  
; TYPE: PRT  
; ORGANISM: Neurospora crassa  
US-10-641-678-59

Query Match 66.0%; Score 33; DB 9; Length 516;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LWFEIDI 8  
|||::|  
Db 139 LWFDVDM 145

RESULT 10  
US-11-079-463-8026  
; Sequence 8026, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA  
; FILE REFERENCE: PATH00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 8026  
; LENGTH: 587  
; TYPE: PRT  
; ORGANISM: B. fragilis  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (498)  
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno  
US-11-079-463-8026

Query Match 66.0%; Score 33; DB 11; Length 587;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LWFEIDI 8  
|||::|  
Db 304 LWFGIDI 310

RESULT 11  
US-11-188-298-14683  
; Sequence 14683, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 14683  
; LENGTH: 145  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(145)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-11-188-298-14683

Query Match 64.0%; Score 32; DB 11; Length 145;  
Best Local Similarity 55.6%; Pred. No. 74;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLWFEIDIV 9  
|||::|  
Db 83 FLWNHVDIL 91

RESULT 12

```
US-11-188-298-17540
; Sequence 17540, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 17540
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(154)
; OTHER INFORMATION: unsure at all Xaa locations
; US-11-188-298-17540

Query Match          64.0%; Score 32; DB 11; Length 154;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
      ||| :||:
Db      90 FLNHHVDIL 98

RESULT 13
US-11-188-298-1861
; Sequence 1861, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 1861
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Glycine max
; US-11-188-298-1861

Query Match          64.0%; Score 32; DB 11; Length 178;
Best Local Similarity 55.6%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
      ||| :||:
Db      41 FLNHHVDIL 49

RESULT 14
US-11-188-298-9805
; Sequence 9805, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 9805

US-11-188-298-17540
; Sequence 17540, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 17540
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(154)
; OTHER INFORMATION: unsure at all Xaa locations
; US-11-188-298-17540

Query Match          64.0%; Score 32; DB 11; Length 154;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
      ||| :||:
Db      90 FLNHHVDIL 98

RESULT 15
US-11-188-298-19429
; Sequence 19429, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19429
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Glycine max
; US-11-188-298-19429

Query Match          64.0%; Score 32; DB 11; Length 185;
Best Local Similarity 55.6%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
      ||| :||:
Db      61 FLNHHVDIL 69

RESULT 16
US-11-188-298-7973
; Sequence 7973, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7973
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Cytophaga hutchinsonii
; US-11-188-298-7973

Query Match          64.0%; Score 32; DB 11; Length 217;
Best Local Similarity 71.4%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 WFEIDIV 9
      ||| :||:
Db      32 WFEIDIM 38

RESULT 17
US-11-188-298-7443
; Sequence 7443, Application US/11188298
```

```
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7443
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Glycine max
US-11-188-298-7443

Query Match      64.0%; Score 32; DB 11; Length 249;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
Db      151 FLWNHVDIL 159

RESULT 18
US-11-179-843-3
; Sequence 3, Application US/11/179843
; Publication No. US20050277153A1
; GENERAL INFORMATION:
; APPLICANT: Thomae, Bianca A.
; APPLICANT: Wieben, Eric D.
; TITLE OF INVENTION: Sulfotransferase SULT2A21 Sequence
; TITLE OF INVENTION: Variants
; FILE REFERENCE: 07039-276001
; CURRENT APPLICATION NUMBER: US/11/179,843
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: US/10/177,570
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/300,165
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-179-843-3

Query Match      64.0%; Score 32; DB 11; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLWFE 5
Db      5 FLWFE 9

RESULT 19
US-11-152-635-11
; Sequence 11, Application US/11/152635
; Publication No. US20060024708A1
; GENERAL INFORMATION:
; APPLICANT: Squires, James
; APPLICANT: Sinclair, Philip
; TITLE OF INVENTION: Porcine Sulfotransferase 2A1 Polynucleotide Sequence, Protein, an
; TITLE OF INVENTION: Methods of Use for Same
; FILE REFERENCE: P06815US01
; CURRENT APPLICATION NUMBER: US/11/152,635
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/580,540
; PRIOR FILING DATE: 2005-06-17
```

```
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-152-635-11

Query Match      64.0%; Score 32; DB 11; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLWFE 5
Db      5 FLWFE 9

RESULT 20
US-11-087-099-9700
; Sequence 9700, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9700
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis MA-4680
US-11-087-099-9700

Query Match      64.0%; Score 32; DB 11; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLWFE 5
Db      186 FLWFE 190

RESULT 21
US-11-079-463-9640
; Sequence 9640, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES PRF
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 9640
; LENGTH: 438
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-9640

Query Match      64.0%; Score 32; DB 11; Length 438;
Best Local Similarity 44.4%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
Db      351 FLWFSVFLI 359
```

## RESULT 22

US-11-087-099-3160  
; Sequence 3160, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 3160  
; LENGTH: 439  
; TYPE: PRT  
; ORGANISM: Shewanella oneidensis MR-1  
US-11-087-099-3160

Query Match 64.0%; Score 32; DB 11; Length 439;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
: |||: |||:  
Db 168 WFWFDIDL 175

## RESULT 23

US-11-188-298-4548  
; Sequence 4548, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 4548  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(448)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-11-188-298-4548

Query Match 64.0%; Score 32; DB 11; Length 448;  
Best Local Similarity 55.6%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDIV 9  
: |||: |||:  
Db 330 FLWNVHVDIL 338

## RESULT 24

US-11-087-099-9184  
; Sequence 9184, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 9184  
; LENGTH: 463  
; TYPE: PRT

; ORGANISM: Glycine max  
US-11-087-099-9184

Query Match 64.0%; Score 32; DB 11; Length 463;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWFEID 7  
: |||: |||:  
Db 341 FLWKEVD 347

## RESULT 25

US-11-045-004-358  
; Sequence 358, Application US/11045004  
; Publication No. US20060078901A1  
; GENERAL INFORMATION:  
; APPLICANT: BUCHRIESER, CARMEN  
; APPLICANT: FRANGEUL, LIONEL  
; APPLICANT: COUVE, ELISABETH  
; APPLICANT: RUSNIOK, CHRISTOPHE  
; APPLICANT: PSIHL, HAFIDA  
; APPLICANT: DEHOUX, PIERRE  
; APPLICANT: DUSSURGET, OLIVIER  
; APPLICANT: CHETOUANI, FARID  
; APPLICANT: NEDJARI, HAFED  
; APPLICANT: GLASER, PHILIPPE  
; APPLICANT: KUNT, FRANCK  
; APPLICANT: COSSART, PASCALE  
; APPLICANT: DANIELS, JUSTIN  
; APPLICANT: GOEBEL, WERNER  
; APPLICANT: KREFT, JURGEN  
; APPLICANT: KUHN, MICHAEL  
; APPLICANT: NG, EVA  
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO  
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO  
; APPLICANT: GARRIDO-GARCIA, PATRICIA  
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO  
; APPLICANT: AMEND, ALEXANDRA  
; APPLICANT: CHAKRABORTY, TRINAD  
; APPLICANT: DOMANN, EUGEN  
; APPLICANT: HAIN, THORSTEN  
; APPLICANT: BERCHE, PATRICK  
; APPLICANT: CHARBIT, ALAIN  
; APPLICANT: DURANT, LIONEL  
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO  
; APPLICANT: BAQUERO, FERNANDO  
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO  
; APPLICANT: GOMEZ-LOPEZ, NURIA  
; APPLICANT: MADUENIO, ENCARNACION  
; APPLICANT: PABLOS, BETRIZ DE  
; APPLICANT: WEHLAND, JURGEN  
; APPLICANT: KARST, UWE  
; APPLICANT: ENTIAN, KARL-DIETER  
; APPLICANT: HAUF, JORG  
; APPLICANT: ROSE, MATTHIAS  
; APPLICANT: VOSS, HAMUT  
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES  
; FILE REFERENCE: 05394.0018-02  
; CURRENT APPLICATION NUMBER: US/11/045,004  
; CURRENT FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: 10/637,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: 10/257,023  
; PRIOR FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: PCT/FR01/01118  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: FR 00/04,629  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 2854  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 358  
; LENGTH: 467

```
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-358

Query Match      64.0%; Score 32; DB 11; Length 467;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEID 7
DB      404 YLWIEVD 410

RESULT 26
US-11-087-099-12372
; Sequence 12372, Application US/11087099
; Publication NO. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12372
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(474)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-12372

Query Match      64.0%; Score 32; DB 11; Length 474;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEID 7
DB      174 FAFQOLD 180

RESULT 27
US-11-188-298-16627
; Sequence 16627, Application US/11188298
; Publication NO. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 16627
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-11-188-298-16627

Query Match      64.0%; Score 32; DB 11; Length 537;
Best Local Similarity 55.6%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
DB      434 FLWNHVDIL 442

RESULT 28
US-11-188-298-9104
; Sequence 9104, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 9104
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-188-298-9104

Query Match      64.0%; Score 32; DB 11; Length 562;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
DB      425 FLWNHVDIL 433

RESULT 29
US-11-072-512-3625
; Sequence 3625, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3625
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3625

Query Match      64.0%; Score 32; DB 11; Length 563;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 LWFEIDIV 9
DB      247 LWFGYDIV 254
```



```
RESULT 30
US-11-188-298-516
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 516
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-188-298-516

Query Match      64.0%; Score 32; DB 11; Length 577;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLWFEIDIV 9
Db      440 FLWNHVDIL 448

RESULT 31
US-10-506-454-1041
; Sequence 1041, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozyavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1041
; LENGTH: 1586
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1041

Query Match      64.0%; Score 32; DB 9; Length 1586;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 WFEIDIV 9
Db      497 WFEEDVV 503

RESULT 32
US-11-188-298-17639
; Sequence 17639, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 516
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-188-298-17639

Query Match      63.0%; Score 31.5; DB 11; Length 527;
Best Local Similarity 35.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 11; Gaps 1;

QY      1 FLWPF-----RIDIV 9
Db      449 FIWFFYPETANRSLREIDII 468

RESULT 33
US-11-004-399-2604
; Sequence 2604, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S.
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2604
; LENGTH: 24
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-2604

Query Match      62.0%; Score 31; DB 11; Length 24;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLWFEIDI 8
Db      6 FVWFKADM 13

RESULT 34
US-11-079-463-7111
; Sequence 7111, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES PR.
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
```

; SEQ ID NO 7111  
; LENGTH: 66  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-11-079-463-7111

Query Match 62.0%; Score 31; DB 11; Length 66;  
Best Local Similarity 62.5%; Pred. No. 56;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LWFEDIV 9  
Db 20 LWFESINIL 27

RESULT 35  
US-11-045-004-431  
; Sequence 431, Application US/11045004  
; Publication No. US20060078901A1  
; GENERAL INFORMATION:  
; APPLICANT: BUCHRIEGER, CARMEN  
; APPLICANT: FRANGEUL, LIONEL  
; APPLICANT: COUVE, ELISABETH  
; APPLICANT: RUSNIOK, CHRISTOPHE  
; APPLICANT: FSIHI, HAFIDA  
; APPLICANT: DEHOUX, PIERRE  
; APPLICANT: DUSSURGET, OLIVIER  
; APPLICANT: CHETOUANI, FARID  
; APPLICANT: NEDJARI, HAFED  
; APPLICANT: GLASER, PHILIPPE  
; APPLICANT: KUNST, FRANCK  
; APPLICANT: COSSART, PASCALE  
; APPLICANT: DANIELS, JUSTIN  
; APPLICANT: GOEBEL, WERNER  
; APPLICANT: KREFT, JURGEN  
; APPLICANT: KUHN, MICHAEL  
; APPLICANT: NG, EVA  
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO  
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO  
; APPLICANT: GARRIDO-GARCIA, PATRICIA  
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO  
; APPLICANT: AMEND, ALEXANDRA  
; APPLICANT: CHAKRABORTY, TRINAD  
; APPLICANT: DOMANN, EUGEN  
; APPLICANT: HAIN, THORSTEN  
; APPLICANT: BERCHE, PATRICK  
; APPLICANT: CHARBIT, ALAIN  
; APPLICANT: DURANT, LIONEL  
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO  
; APPLICANT: BAQUERO, FERNANDO  
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO  
; APPLICANT: GOMEZ-LOPEZ, NURIA  
; APPLICANT: MADUENIO, ENCARNA  
; APPLICANT: PABLOS, BETRIZ DE  
; APPLICANT: WEHLAND, JURGEN  
; APPLICANT: KARST, UWE  
; APPLICANT: ENTIAN, KARL-DIETER  
; APPLICANT: HAUF, JORG  
; APPLICANT: ROSE, MATTHIAS  
; APPLICANT: VOSS, HAMUT  
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES  
; FILE REFERENCE: 05394-0018-02  
; CURRENT APPLICATION NUMBER: US/11/045,004  
; PRIOR FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: 10/637,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: 10/257,023  
; PRIOR FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: PCT/FR01/01118  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: FR 00/04,629  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 2854

; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 431  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-11-045-004-431

Query Match 62.0%; Score 31; DB 11; Length 147;  
Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLWFEID 7  
Db 66 YLWPHVD 72

RESULT 36  
US-11-188-298-13534  
; Sequence 13534, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 13534  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-188-298-13534

Query Match 62.0%; Score 31; DB 11; Length 219;  
Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WFEIDIV 9  
Db 2 WFLVDIV 8

RESULT 37  
US-11-045-004-2278  
; Sequence 2278, Application US/11045004  
; Publication No. US20060078901A1  
; GENERAL INFORMATION:  
; APPLICANT: BUCHRIEGER, CARMEN  
; APPLICANT: FRANGEUL, LIONEL  
; APPLICANT: COUVE, ELISABETH  
; APPLICANT: RUSNIOK, CHRISTOPHE  
; APPLICANT: FSIHI, HAFIDA  
; APPLICANT: DEHOUX, PIERRE  
; APPLICANT: DUSSURGET, OLIVIER  
; APPLICANT: CHETOUANI, FARID  
; APPLICANT: NEDJARI, HAFED  
; APPLICANT: GLASER, PHILIPPE  
; APPLICANT: KUNST, FRANCK  
; APPLICANT: COSSART, PASCALE  
; APPLICANT: DANIELS, JUSTIN  
; APPLICANT: GOEBEL, WERNER  
; APPLICANT: KREFT, JURGEN  
; APPLICANT: KUHN, MICHAEL  
; APPLICANT: NG, EVA  
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO  
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO  
; APPLICANT: GARRIDO-GARCIA, PATRICIA  
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO  
; APPLICANT: AMEND, ALEXANDRA  
; APPLICANT: CHAKRABORTY, TRINAD  
; APPLICANT: DOMANN, EUGEN

```
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL FORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNIA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2278
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-2278

Query Match 62.0%; Score 31; DB 11; Length 229;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WFEIDIV 9
|||:|:|
Db 108 WFDPDVI 114

RESULT 38
US-11-096-568A-4083
; Sequence 4083, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4083
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: misc feature
; LOCATION: (1)..(284)
; OTHER INFORMATION: Ceres Seq. ID no. 13594607
US-11-096-568A-4083

Query Match 62.0%; Score 31; DB 11; Length 284;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEID 7
|||:|
Db 108 WFDPDVI 114
```

```
Db 140 WFEVD 144

RESULT 39
US-11-096-568A-4082
; Sequence 4082, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4082
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: misc feature
; LOCATION: (1)..(301)
; OTHER INFORMATION: Ceres Seq. ID no. 13594606
US-11-096-568A-4082

Query Match 62.0%; Score 31; DB 11; Length 301;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEID 7
|||:|
Db 157 WFEVD 161

RESULT 40
US-11-096-568A-4081
; Sequence 4081, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4081
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: misc feature
; LOCATION: (1)..(307)
; OTHER INFORMATION: Ceres Seq. ID no. 13594605
US-11-096-568A-4081

Query Match 62.0%; Score 31; DB 11; Length 307;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEID 7
|||:|
Db 163 WFEVD 167

RESULT 41
US-11-054-281-120
; Sequence 120, Application US/11054281
; Publication No. US20060013813A1
; GENERAL INFORMATION:
; APPLICANT: Mezes et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
```

; CURRENT APPLICATION NUMBER: US/11/054,281  
; CURRENT FILING DATE: 2005-02-08  
; PRIOR APPLICATION NUMBER: 60/261,014  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/261,018  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/318,410  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/261,013  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/261,026  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/261,029  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/313,170  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 10/044,564  
; PRIOR FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 120  
; LENGTH: 363  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-054-281-120

Query Match 62.0%; Score 31; DB 11; Length 363;  
Best Local Similarity 71.4%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWPEID 7  
Db 140 FLWFGIE 146

RESULT 42  
US-11-096-568A-20256  
; Sequence 20256, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 20256  
; LENGTH: 399  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(399)  
; OTHER INFORMATION: Ceres Seq. ID no. 12381093  
US-11-096-568A-20256

Query Match 62.0%; Score 31; DB 11; Length 399;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9  
Db 27 IWFERDVL 34

RESULT 43  
US-11-197-133A-16  
; Sequence 16, Application US/11197133A  
; Publication No. US20060040361A1  
; GENERAL INFORMATION:  
; APPLICANT: De Le Fuente Jose de Jesus  
; APPLICANT: Kocan Katherine M.

; APPLICANT: Garcia-Almazan Consuelo  
; APPLICANT: Blouin Edwin F.  
; TITLE OF INVENTION: Protective antigens and vaccines for the control of multi species  
; TITLE OF INVENTION: infestations  
; FILE REFERENCE: 57338/05-261  
; CURRENT APPLICATION NUMBER: US/11/197,133A  
; CURRENT FILING DATE: 2005-08-04  
; PRIOR APPLICATION NUMBER: US 10/972789  
; PRIOR FILING DATE: 2004-10-25  
; PRIOR APPLICATION NUMBER: US 10/425563  
; PRIOR FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US 60/376251  
; PRIOR FILING DATE: 2002-04-29  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Ixodes scapularis  
US-11-197-133A-16

Query Match 62.0%; Score 31; DB 11; Length 497;  
Best Local Similarity 44.4%; Pred. No. 3.4e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLWPEIDIV 9  
Db 86 FFWMEVELV 94

RESULT 44  
US-11-096-568A-20254  
; Sequence 20254, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 20254  
; LENGTH: 509  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(509)  
; OTHER INFORMATION: Ceres Seq. ID no. 12381091  
US-11-096-568A-20254

Query Match 62.0%; Score 31; DB 11; Length 509;  
Best Local Similarity 50.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWFEIDIV 9  
Db 137 IWFERDVL 144

RESULT 45  
US-11-188-298-18585  
; Sequence 18585, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31

; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 18585  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Hordeum vulgare subsp. vulgare  
US-11-188-298-18585

Query Match 62.0%; Score 31; DB 11; Length 533;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WFEIDIV 9  
|||:|  
Db 303 WFLVDIV 309

## RESULT 46

US-11-099-691-9  
; Sequence 9, Application US/11099691  
; Publication No. US20050260644A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE PHARMACEUTICALS, INC.  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: LAL, Preeti  
; APPLICANT: YUE, Henry  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: YANG, Junming  
; TITLE OF INVENTION: CELL SIGNALING PROTEINS  
; FILE REFERENCE: PF-0521 PCT  
; CURRENT APPLICATION NUMBER: US/11/099,691  
; CURRENT FILING DATE: 2005-04-06  
; PRIOR APPLICATION NUMBER: US/09/700,444  
; PRIOR FILING DATE: 2002-08-26  
; PRIOR APPLICATION NUMBER: 60/085,343  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/098,010  
; PRIOR FILING DATE: 1998-08-26  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PERL Program  
; SEQ ID NO 9  
; LENGTH: 686  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc-feature  
; OTHER INFORMATION: Incyte Clone 1403604  
US-11-099-691-9

Query Match 62.0%; Score 31; DB 11; Length 686;  
Best Local Similarity 62.5%; Pred. No. 4.5e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLWFEIDI 8  
|||:|  
Db 572 FLWESVDI 579

## RESULT 47

US-11-096-568A-30629  
; Sequence 30629, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 30629

; LENGTH: 750  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: (1)..(750)  
; OTHER INFORMATION: Ceres Seq. ID no. 4965647  
US-11-096-568A-30629

Query Match 62.0%; Score 31; DB 11; Length 750;  
Best Local Similarity 66.7%; Pred. No. 4.9e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WFEIDI 8  
|||:|  
Db 381 WFEVEI 386

## RESULT 48

US-11-197-133A-18  
; Sequence 18, Application US/11197133A  
; Publication No. US20060040361A1  
; GENERAL INFORMATION:  
; APPLICANT: De Le Fuente Jose de Jesus  
; APPLICANT: Kocan Katherine M.  
; APPLICANT: Garcia-Almazan Consuelo  
; APPLICANT: Blouin Edwin F.  
; TITLE OF INVENTION: Protective antigens and vaccines for the control of multi specie  
; TITLE OF INVENTION: Infestations  
; FILE REFERENCE: 57338/05-261  
; CURRENT APPLICATION NUMBER: US/11/197,133A  
; CURRENT FILING DATE: 2005-08-04  
; PRIOR APPLICATION NUMBER: US 10/972789  
; PRIOR FILING DATE: 2004-10-25  
; PRIOR APPLICATION NUMBER: US 10/425563  
; PRIOR FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US 60/376251  
; PRIOR FILING DATE: 2002-04-29  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 18  
; LENGTH: 754  
; TYPE: PRT  
; ORGANISM: Ixodes scapularis  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: (438)..(438)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: (453)..(453)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-11-197-133A-18

Query Match 62.0%; Score 31; DB 11; Length 754;  
Best Local Similarity 42.9%; Pred. No. 4.9e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 LWFEIDI 8  
:|:|:|  
Db 653 MWFDLIDL 659

## RESULT 49

US-11-096-568A-30628  
; Sequence 30628, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 30629

; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 30628  
; LENGTH: 810  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(810)  
; OTHER INFORMATION: Ceres Seq. ID no. 4965646  
US-11-096-568A-30628

Query Match 62.0%; Score 31; DB 11; Length 810;  
Best Local Similarity 66.7%; Pred. No. 5.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WFEIDI 8  
|||::|  
Db 441 WFEVEI 446

RESULT 50  
US-11-096-568A-30627  
; Sequence 30627, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 30627  
; LENGTH: 842  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(842)  
; OTHER INFORMATION: Ceres Seq. ID no. 4965645  
US-11-096-568A-30627

Query Match 62.0%; Score 31; DB 11; Length 842;  
Best Local Similarity 66.7%; Pred. No. 5.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WFEIDI 8  
|||::|  
Db 473 WFEVEI 478

Search completed: May 9, 2006, 02:36:26  
Job time : 16.8 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:05:23 ; Search time 98.4 Seconds  
(without alignments)  
40.187 Million cell updates/sec

Title: US-09-870-216C-9

Perfect score: 45

Sequence: 1 FLSYDLFVV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 segs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- A\_Geneseq\_21.\*
- 1: Geneseq1980s.\*
  - 2: Geneseq1990s.\*
  - 3: Geneseq2000s.\*
  - 4: Geneseq2001s.\*
  - 5: Geneseq2002s.\*
  - 6: Geneseq2003as.\*
  - 7: Geneseq2003bs.\*
  - 8: Geneseq2004s.\*
  - 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	5	Abb08364 Synthetic
2	45	100.0	9	7	AbR82216 Human ant
3	45	100.0	352	5	Abb08369 Human can
4	36	80.0	51	4	Abb74753 Human sec
5	36	80.0	51	5	Abg65310 Human alb
6	36	80.0	51	8	Adl78577 Albumin f
7	35	77.8	65	2	Aay13169 Human sec
8	35	77.8	85	3	Aag01223 Human sec
9	35	77.8	130	2	Aay17226 Human sec
10	35	77.8	130	4	Aau38996 Human sec
11	35	77.8	130	5	Abb55705 Human pol
12	35	77.8	130	9	Adw09103 Human sec
13	35	77.8	160	2	Aay36168 Human sec
14	35	77.8	162	2	Aay36215 Human sec
15	35	77.8	162	3	Aay57894 Human tra
16	35	77.8	162	4	Aab88605 Human hyd
17	35	77.8	162	5	Abb89619 Human pol
18	35	77.8	162	5	Abp65087 Hypoxia-r
19	35	77.8	162	7	Add19028 Human dis
20	35	77.8	162	7	Adj45973 Novel hum
21	35	77.8	162	7	Adj46067 Novel hum
22	35	77.8	162	8	Adp19476 Human sec
23	35	77.8	162	8	Adp55495 Human PRO
24	35	77.8	163	2	Aaw74871 Human sec

25	77.8	163	5	ABG95322	Abg95322 Human nov
26	77.8	163	6	ABO34516	AbO34516 Region of
27	77.8	163	7	ADI23177	Adi23177 Novel hum
28	77.8	163	8	ADH74179	Adh74179 Human sec
29	77.8	177	5	ABB97496	Abb97496 Novel hum
30	77.8	203	5	AAE25673	Aae25673 Bacillus
31	77.8	203	7	ABR62959	AbR62959 Bctyl res
32	75.6	51	4	AAO08931	Aao08931 Human pol
33	75.6	55	5	ABP64088	Abp64088 Human ORF
34	75.6	98	4	AAG73909	Aag73909 Human col
35	75.6	160	7	ADC32867	Adc32867 Human nov
36	75.6	247	7	ADM04330	Adm04330 Human pro
37	75.6	363	6	ADA34406	Ada34406 Acinetoba
38	75.6	412	2	AAM98765	Aaw98765 H. pylori
39	75.6	516	5	ABB93691	Abb93691 Herbicida
40	75.6	576	7	ADM05144	Adm05144 Human pro
41	75.6	674	6	ADA55118	Ada55118 Human pro
42	75.6	1031	8	ADM72293	Adm72293 Equine TL
43	73.3	90	3	AAG38087	Aag38087 Arabidops
44	73.3	103	7	ADF04479	Adf04479 Bacterial
45	73.3	119	3	AAG14935	Aag14935 Arabidops
46	73.3	181	3	AAG38086	Aag38086 Arabidops
47	73.3	211	5	ADH32233	Adh32233 Novel yea
48	73.3	304	5	ABB55172	Abb55172 Lactococc
49	73.3	573	8	ADN19667	Adn19667 Bacterial
50	73.3	583	8	ADS44248	Ads44248 Bacterial
51	73.3	573	8	ADN19661	Adn19661 Bacterial
52	71.1	265	2	AAY09510	Aay09510 Human M6b
53	71.1	265	7	ADP49079	Adp49079 Human NOV
54	71.1	265	9	ADZ70472	Adz70472 Human pro
55	71.1	267	8	ADN04392	Adn04392 Antipeori
56	71.1	279	5	ABG70364	Abg70364 Novel hum
57	71.1	288	7	ADD49075	Add49075 Human NOV
58	71.1	305	7	ADD49073	Add49073 Human NOV
59	71.1	313	8	ADT56754	Adt56754 Plant pol
60	71.1	328	7	ADD49077	Add49077 Human NOV
61	71.1	328	7	ADD49071	Add49071 Human NOV
62	71.1	413	6	ABU35723	Abu35723 Protein e
63	71.1	555	6	ABM67718	Abm67718 Photorhab
64	71.1	555	6	ABM70540	Abm70540 Photorhab
65	71.1	555	6	ABM68760	Abm68760 Photorhab
66	71.1	865	5	ABF99375	Abf99375 Arabidops
67	71.1	1193	5	ABB90860	Abb90860 Herbicida
68	71.1	1503	8	ADN72701	Adn72701 Thale cre
69	68.9	9	6	ABJ20188	Abj20188 MHC bindi
70	68.9	36	3	AB45308	Ab45308 Human sec
71	68.9	36	3	AB63176	Ab63176 Human sec
72	68.9	46	4	AAM92211	Aam92211 Human dig
73	68.9	63	5	ABP33658	Abp33658 Human ORF
74	68.9	87	4	AAM85093	Aam85093 Human imm
75	68.9	104	6	ABM73433	Abm73433 Staphyloc
76	68.9	114	6	ABU01619	Abu01619 S. pneumo
77	68.9	158	8	ADK47356	Adk47356 Streptoco
78	68.9	170	8	ADR95130	Adr95130 Novel S.
79	68.9	226	6	ABU02635	Abu02635 S. pneumo
80	68.9	226	6	ABP81492	Abp81492 Streptoco
81	68.9	226	6	ABP81492	Abp81492 Streptoco
82	68.9	249	8	ADR96201	Adr96201 Novel S.
83	68.9	249	9	AEA60071	Aea60071 Streptoco
84	68.9	263	5	ABP65309	Abp65309 Bifidobac
85	68.9	273	6	ABM73517	Abm73517 Staphyloc
86	68.9	273	6	ABM71157	Abm71157 Staphyloc
87	68.9	275	6	ADA89686	Ada89686 Staphyloc
88	68.9	284	4	ABF78964	Abf78964 C. glutam
89	68.9	284	4	AAG89913	Aag89913 C. glutam
90	68.9	291	9	ABE39590	Aeb39590 L. pneumo
91	68.9	294	9	ABE36167	Aeb36167 L. pneumo
92	68.9	304	8	ADU29104	Abu29104 Protein e
93	68.9	330	6	ADSA2802	Adsa2802 Bacterial
94	68.9	333	6	ABM68053	Abm68053 Photorhab
95	68.9	344	6	ADC95919	Adc95919 E. faeciu
96	68.9	349	6	ADA35791	Ada35791 Acinetoba
97	68.9	349	6	ADA35791	Ada35791 Acinetoba

98	31	68.9	357	4	AAB84685	Aab464685 Amino aci	171	30	66.7	224	4	AAG72090	Aag72090 Human olf
99	31	68.9	357	4	AB559312	AB559312 Drosophil	172	30	66.7	230	8	ADT59969	Adt59969 Plant pol
100	31	68.9	357	5	AAB25826	Aab25826 Plant fly	173	30	66.7	231	8	ADX66400	Adx66400 Plant ful
101	31	68.9	360	8	ADX65964	Adx65964 Plant ful	174	30	66.7	242	4	AAU23778	Aau23778 Novel hum
102	31	68.9	394	8	ADN25094	Adn25094 Bacterial	175	30	66.7	250	8	ABO60049	AbO60049 Human gen
103	31	68.9	400	7	ADC96639	Adc96639 E. faeciu	176	30	66.7	250	8	ADQ36991	Adq36991 Cell prol
104	31	68.9	420	6	ABU39212	Abu39212 Protein e	177	30	66.7	250	8	ADQ15661	Adq15661 Rice stre
105	31	68.9	437	8	ADL04521	Adl04521 M. catarr	178	30	66.7	265	4	AAU23374	Aau23374 Novel hum
106	31	68.9	453	2	AAW48301	Aaw48301 Yeast CAA	179	30	66.7	265	4	AAE07096	Aae07096 Human gen
107	31	68.9	476	8	AD24414	Ad24414 Bacterial	180	30	66.7	265	5	ABG65093	Abg65093 Human alb
108	31	68.9	478	3	AA808406	Aa808406 Amino aci	181	30	66.7	265	8	ADL78360	Adl78360 Albumin f
109	31	68.9	478	8	ADJ92067	Adj92067 Cucumis s	182	30	66.7	266	2	AAy37483	Aay37483 Chlamydia
110	31	68.9	479	8	ADX76456	Adx76456 Plant ful	183	30	66.7	267	7	ABM74424	Abm74424 DNA clone
111	31	68.9	481	4	AAE09227	Aae09227 Musknelon	184	30	66.7	270	5	AAU91558	Aau91558 Amino aci
112	31	68.9	481	6	ABG72200	Abg72200 Musknelon	185	30	66.7	285	4	AAg71738	Aag71738 Human olf
113	31	68.9	481	8	ADJ92066	Adj92066 Cucumis m	186	30	66.7	286	4	AAW25910	Aaw25910 Human pro
114	31	68.9	487	4	AAE09237	Aae09237 Musknelon	187	30	66.7	290	6	ABU27130	Abu27130 Protein e
115	31	68.9	487	6	ABG72201	Abg72201 Musknelon	188	30	66.7	304	6	ABU60894	Abu60894 Human G p
116	31	68.9	529	4	AAU38342	Aau38342 Salmonell	189	30	66.7	305	3	AAy53022	Aay53022 Human sec
117	31	68.9	529	9	AE339754	Aeb339754 L. pneumo	190	30	66.7	309	4	AAU36124	Aau36124 Klebsiell
118	31	68.9	529	9	AE36337	Aeb36337 L. pneumo	191	30	66.7	310	4	AA868889	Aab68889 Human REC
119	31	68.9	610	4	AAg90741	Aag90741 C glutami	192	30	66.7	310	4	AAg71441	Aag71441 Human olf
120	31	68.9	610	6	ABU25778	Abu25778 Protein e	193	30	66.7	310	4	AAg72375	Aag72375 Human OR-
121	31	68.9	613	7	ADL13286	Adl13286 C. glutam	194	30	66.7	310	4	AAg71472	Aag71472 Human olf
122	31	68.9	621	5	ABP65366	Abp65366 Bifidobac	195	30	66.7	310	4	AAg72190	Aag72190 Human olf
123	31	68.9	695	4	AAg91773	Aag91773 C. glutami	196	30	66.7	310	4	AAU05132	Aau05132 Human odo
124	31	68.9	727	4	AAg84940	Aag84940 Shrimp wh	197	30	66.7	310	4	AAU05141	Aau05141 Human odo
125	31	68.9	735	5	AB891969	Ab891969 Herbicida	198	30	66.7	310	4	AAU05142	Aau05142 Human odo
126	31	68.9	909	3	AAg53638	Aag53638 Arabidops	199	30	66.7	310	5	AAU91543	Aau91543 Human PHO
127	31	68.9	951	4	AB867950	Ab867950 Drosophil	200	30	66.7	310	8	ADO30408	Ado30408 Human GPC
128	31	68.9	987	3	AAg53637	Aag53637 Arabidops	201	30	66.7	310	8	ADS10802	Ads10802 Human the
129	31	68.9	1020	3	AAg53636	Aag53636 Arabidops	202	30	66.7	312	4	AAg71635	Aag71635 Human olf
130	31	68.9	1032	8	ADN72301	Adm72301 Canine FL	203	30	66.7	312	4	AAU24584	Aau24584 Human olf
131	31	68.9	1444	4	AB859604	Ab859604 Drosophil	204	30	66.7	312	5	ABU04010	Abu04010 Human G-p
132	31	68.9	1837	4	AB862913	Ab862913 Drosophil	205	30	66.7	312	5	ABJ04011	Abj04011 Human G-p
133	31	68.9	2610	8	ADN23900	Adn23900 Bacterial	206	30	66.7	312	5	ABP95734	Abp95734 Human GPC
134	31	68.9	2610	9	AAU92400	Aau92400 PHOR1-P5D	207	30	66.7	312	5	AAU95543	Aau95543 Human olf
135	30	66.7	9	5	AAU92400	Aau92400 PHOR1-P5D	208	30	66.7	312	5	AAU85204	Aau85204 G-coupled
136	30	66.7	9	5	AAU92493	Aau92493 PHOR1-P5D	209	30	66.7	312	6	ABU11189	Abu11189 Human G-p
137	30	66.7	9	5	AAU92811	Aau92811 PHOR1-P5D	210	30	66.7	312	7	ADC85841	Adc85841 Human GPC
138	30	66.7	9	5	AAU92310	Aau92310 PHOR1-P5D	211	30	66.7	312	8	ADH30894	Adh30894 Human G-p
139	30	66.7	9	5	AAU92573	Aau92573 PHOR1-P5D	212	30	66.7	312	8	ADH30896	Adh30896 Human G-p
140	30	66.7	9	5	AAU92369	Aau92369 PHOR1-P5D	213	30	66.7	312	8	ADM11517	Adm11517 Human IVA
141	30	66.7	9	5	AAU92882	Aau92882 PHOR1-P5D	214	30	66.7	313	6	ABR01582	AbR01582 Human G p
142	30	66.7	9	7	ADW30747	Adw30747 HLA bindi	215	30	66.7	314	6	ABR01642	AbR01642 Human G p
143	30	66.7	10	5	AAU92436	Aau92436 PHOR1-P5D	216	30	66.7	316	9	ABE42496	Aeb42496 L. pneumo
144	30	66.7	10	5	AAU92423	Aau92423 PHOR1-P5D	217	30	66.7	318	4	AB811829	Ab811829 Human olf
145	30	66.7	10	5	AAU92632	Aau92632 PHOR1-P5D	218	30	66.7	318	8	ADS12055	Ads12055 Human the
146	30	66.7	10	5	AAU92630	Aau92630 PHOR1-P5D	219	30	66.7	320	5	ADI16548	Adi16548 Human NOV
147	30	66.7	10	5	AAU92550	Aau92550 PHOR1-P5D	220	30	66.7	320	6	ABU11219	Abu11219 Human G-p
148	30	66.7	42	5	ABJ04874	Abj04874 Human pro	221	30	66.7	320	7	ADC85979	Adc85979 Human GPC
149	30	66.7	50	8	ADY04748	Ady04748 Plant ful	222	30	66.7	320	8	ADN42202	Adn42202 Human nov
150	30	66.7	64	4	AAW91969	Aaw91969 Human dig	223	30	66.7	323	6	ABU19169	Abu19169 Protein e
151	30	66.7	64	4	AAU22497	Aau22497 Novel hum	224	30	66.7	323	6	ABU25642	Abu25642 Protein e
152	30	66.7	64	7	ADB32337	Adb32337 Human nov	225	30	66.7	323	8	ADJ67111	Adj67111 Borrelia
153	30	66.7	75	7	ADH87741	Adh87741 Enterococ	226	30	66.7	324	2	AAy35306	Aay35306 Chlamydia
154	30	66.7	86	6	ADB09887	Adb09887 Alloiococ	227	30	66.7	324	6	ABU26777	Abu26777 Protein e
155	30	66.7	126	3	AA808108	Aa808108 A polyphe	228	30	66.7	326	6	ABU39014	Abu39014 Protein e
156	30	66.7	129	6	ADA57620	Ada57620 Human sec	229	30	66.7	327	4	AAU35605	Aau35605 Haemophil
157	30	66.7	130	2	AAy35110	Aay35110 Chlamydia	230	30	66.7	327	6	ABU30512	Abu30512 Protein e
158	30	66.7	137	4	AAW25517	Aaw25517 Human pro	231	30	66.7	330	3	AAg11360	Aag11360 Arabidops
159	30	66.7	141	5	ABG61529	Abg61529 Iron upta	232	30	66.7	330	3	AAg53652	Aag53652 Arabidops
160	30	66.7	141	6	ABU00586	Abu00586 S. pneumo	233	30	66.7	330	3	ABU44882	Abu44882 Protein e
161	30	66.7	143	7	ADD27531	Add27531 Human adi	234	30	66.7	333	2	AAW40108	Aaw40108 Human her
162	30	66.7	163	8	AAW83814	Aaw83814 Human imm	235	30	66.7	333	6	ABU41230	Abu41230 Protein e
163	30	66.7	165	4	ADX68818	Adx68818 Plant ful	236	30	66.7	334	4	AAU34788	Aau34788 E. coli c
164	30	66.7	181	5	AAU91555	Aau91555 Amino aci	237	30	66.7	334	6	ABU27747	Abu27747 Protein e
165	30	66.7	185	8	ADN47493	Adn47493 Thermococ	238	30	66.7	334	6	ABU28814	Abu28814 Protein e
166	30	66.7	187	4	AAU18421	Aau18421 Human end	239	30	66.7	334	9	ADZ77678	Adz77678 Escherich
167	30	66.7	192	4	AAg72034	Aag72034 Human olf	240	30	66.7	335	5	ADI16546	Adi16546 Human NOV
168	30	66.7	200	7	ADO23574	Ado23574 Human pho	241	30	66.7	335	6	ABU50397	Abu50397 Protein e
169	30	66.7	207	6	ABU24967	Abu24967 Protein e	242	30	66.7	335	8	ADN42200	Adn42200 Human nov
170	30	66.7	211	8	ADX66323	Adx66323 Plant ful	243	30	66.7	337	3	AAy32196	Aay32196 Human rec



244	30	66.7	337	4	AAU38207	Aau38207 Salmonell	317	30	66.7	904	6	ABR53670	Abr53670 Protein e
245	30	66.7	337	6	ABU32105	Abu32105 Protein e	318	30	66.7	904	7	ADK64094	Adk64094 Disease t
246	30	66.7	337	6	ABU47548	Abu47548 Protein e	319	30	66.7	960	4	AAE60299	Aae60299 Human ami
247	30	66.7	339	4	AAG72953	Aag72953 Human olf	320	30	66.7	960	4	AAE04879	Aae04879 Human pro
248	30	66.7	339	4	AAG72954	Aag72954 Human olf	321	30	66.7	960	5	ABP69122	Abp69122 Human pol
249	30	66.7	340	6	ABW70371	Abw70371 Photorhab	322	30	66.7	990	7	ADB39017	Adb39017 Manduca s
250	30	66.7	342	4	ABG72273	Abg72273 Human olf	323	30	66.7	995	7	ADB39007	Adb39007 Manduca s
251	30	66.7	343	7	ABO64375	Abog64375 Klebsiell	324	30	66.7	1191	7	ADJ70371	Adj70371 Human hea
252	30	66.7	346	7	ADFO6431	Adf06431 Bacteri	325	30	66.7	1194	8	ADO34031	Ado34031 Human MBC
253	30	66.7	349	2	AAW06416	Aaw06416 Phosphotr	326	30	66.7	1305	8	ADI16235	Adi16235 Human nuc
254	30	66.7	349	4	AAW39747	Aaw39747 Human pol	327	30	66.7	1395	8	ADJ37231	Adj37231 Human nuc
255	30	66.7	349	5	ABBO7525	Abb07525 Human dru	328	30	66.7	1435	8	ABM81015	Abm81015 Tumour-as
256	30	66.7	349	8	ADP25013	Adp25013 PRO polyP	329	30	66.7	1450	8	ADO01059	Ado01059 Mouse hom
257	30	66.7	349	9	AEA24001	Aea24001 Human PRO	330	30	66.7	1493	7	ADC87423	Adc87423 Human GPC
258	30	66.7	363	3	AGAS3651	Agas3651 Arabidops	331	30	66.7	1737	8	ADO01057	Ado01057 Human hom
259	30	66.7	363	3	AGI11359	Agil1359 Arabidops	332	30	66.7	1774	5	ABG69800	Abg69800 Human REM
260	30	66.7	374	8	ADT60355	Adt60355 Plant pol	333	30	66.7	2778	7	ADC51660	Adc51660 Human MEG
261	30	66.7	377	8	ADT60354	Adt60354 Plant pol	334	30	66.7	2789	7	ADG75733	Adg75733 Human pro
262	30	66.7	380	4	AAW41533	Aaw41533 Human pol	335	30	66.7	2854	5	ADH48732	Adh48732 NOV7 prot
263	30	66.7	380	8	ADS12175	Ads12175 Human the	336	30	66.7	4064	8	ADL98334	Adl98334 TFR-1, SE
264	30	66.7	383	5	ADT57911	Adt57911 Plant pol	337	30	66.7	5002	4	ABB63723	Abb63723 Drosophil
265	30	66.7	387	5	ABBS3425	Abbs3425 Lactococc	338	29	64.4	10	2	AAW76016	Aaw76016 LM609 gra
266	30	66.7	388	3	AGS53650	Agss53650 Arabidops	339	29	64.4	10	4	ABE61374	Abeg61374 Mutant VH
267	30	66.7	388	3	AGI11358	Agil1358 Arabidops	340	29	64.4	10	6	ABO19812	Abol19812 Enhanced
268	30	66.7	394	4	ABW47287	Abw47287 Enterococ	341	29	64.4	10	7	ADG71826	Adg71826 Enhanced
269	30	66.7	400	3	AAW84642	Aay84642 Amino aci	342	29	64.4	10	8	ADJ58007	Adj58007 Murine LM
270	30	66.7	400	3	AAW84643	Aay84643 Amino aci	343	29	64.4	10	8	ABR01709	Abro1709 Human bre
271	30	66.7	402	4	AAW66117	Aag66117 Murine LI	344	29	64.4	39	4	ABB16296	Abb16296 Human ner
272	30	66.7	402	7	ADC95827	Adc95827 E. faeciu	345	29	64.4	42	8	ADS05561	Ads05561 Staphyloc
273	30	66.7	413	3	AAV51842	Aay51842 Murine em	346	29	64.4	48	2	AAW06711	Aaw06711 Helicobac
274	30	66.7	420	7	ABO81165	Abol1165 Pseudomon	347	29	64.4	74	7	ABO83219	Abol83219 Pseudomon
275	30	66.7	440	6	ADA36049	Ada36049 Acinetoba	348	29	64.4	103	4	AAW91945	Aam91945 Human dig
276	30	66.7	451	6	ADU20077	Abu20077 Protein e	349	29	64.4	103	4	AAU22477	Aau22477 Novel hum
277	30	66.7	451	8	ADS22008	Ads22008 Bacteri	350	29	64.4	103	7	ADB32317	Adb32317 Human nov
278	30	66.7	453	6	ABU22499	Abu22499 Protein e	351	29	64.4	122	6	ABU39187	Abu39187 Protein e
279	30	66.7	460	4	ABE60971	Abbe60971 Drosophil	352	29	64.4	123	3	AAW44772	Aay44772 Wheat ser
280	30	66.7	461	8	ADS24432	Ads24432 Bacteri	353	29	64.4	127	8	ADX79472	Adx79472 Plant ful
281	30	66.7	464	8	ADS22005	Ads22005 Bacteri	354	29	64.4	140	2	AAW76229	Aaw76229 Bacteri
282	30	66.7	476	8	ADS29237	Ads29237 Bacteri	355	29	64.4	146	9	ADZ65605	Adz65605 Tobacco p
283	30	66.7	476	8	ADS29056	Ads29056 Bacteri	356	29	64.4	149	8	ADN21069	Adn21069 Bacteri
284	30	66.7	496	8	ADT59923	Adt59923 Plant pol	357	29	64.4	152	8	ADP55455	Adp55455 Human PRO
285	30	66.7	502	6	ADA35681	Ada35681 Acinetoba	358	29	64.4	154	5	AAO21562	Aao21562 Murine To
286	30	66.7	518	5	ABP29415	Abp29415 Streptoco	359	29	64.4	156	2	AAI60068	Aay60068 Human end
287	30	66.7	525	6	ABU42055	Abu42055 Protein e	360	29	64.4	181	7	ADH85676	Adh85676 Enterococ
288	30	66.7	533	5	AD116859	Adil6859 Human NOV	361	29	64.4	187	8	ADS24192	Ads24192 Bacteri
289	30	66.7	533	8	ADS24756	Ads24756 Bacteri	362	29	64.4	188	7	ADC42712	Adc42712 Murine To
290	30	66.7	534	6	ABU39989	Abu39989 Protein e	363	29	64.4	197	5	ABE53888	Abbe53888 Lactococc
291	30	66.7	536	4	AAU36284	Aau36284 Pseudomon	364	29	64.4	203	6	ABF58459	Abf58459 Staphyloc
292	30	66.7	536	6	ABU38407	Abu38407 Protein e	365	29	64.4	208	3	AAW77968	Aay77968 A. thalia
293	30	66.7	547	4	AAW92422	Aag92422 C glutam	366	29	64.4	208	7	AAW37350	Aag37350 Arabidops
294	30	66.7	555	7	ABO81530	Abol1530 Pseudomon	367	29	64.4	208	3	AAW37350	Aag37350 Arabidops
295	30	66.7	555	8	ADS28628	Ads28628 Bacteri	368	29	64.4	208	7	ADG75259	Adg75259 Thale cre
296	30	66.7	556	8	ADN22226	Adn22226 Bacteri	369	29	64.4	208	8	ADN73911	Adn73911 Thale cre
297	30	66.7	565	7	ABO76294	Abog6294 Pseudomon	370	29	64.4	208	8	ADU92250	Adu92250 Thale cre
298	30	66.7	566	5	AAU76437	Aau76437 Novel des	371	29	64.4	214	6	ADH08066	Adh08066 Allotococ
299	30	66.7	569	8	ADS22497	Ads22497 Bacteri	372	29	64.4	219	3	AAW37350	Aag37350 Arabidops
300	30	66.7	580	6	ADA36369	Ada36369 Acinetoba	373	29	64.4	219	3	AAW37350	Aag37350 Arabidops
301	30	66.7	580	8	ADX90586	Adx90586 Plant ful	374	29	64.4	219	3	AAW37350	Aag37350 Arabidops
302	30	66.7	588	3	AAW32826	Aay32826 C. pneumo	375	29	64.4	222	5	ABP39903	Abp39903 Staphyloc
303	30	66.7	602	6	ABU16994	Abu16994 Protein e	376	29	64.4	222	8	ADG06970	Adg06970 Staphyloc
304	30	66.7	604	8	ADN17641	Adn17641 Bacteri	377	29	64.4	225	8	ADX71320	Adx71320 Plant ful
305	30	66.7	608	7	ADG94131	Adg94131 Alcohol/a	378	29	64.4	228	2	AAW37350	Aag37350 Arabidops
306	30	66.7	632	6	ABU48579	Abu48579 Protein e	379	29	64.4	228	2	AAW37350	Aag37350 Arabidops
307	30	66.7	645	3	AAW92825	Aay92825 C. pneumo	380	29	64.4	228	4	AAW37350	Aag37350 Arabidops
308	30	66.7	650	8	ADN20002	Adn20002 Bacteri	381	29	64.4	228	5	ABE76236	Abbe76236 Staphyloc
309	30	66.7	663	6	ABU18610	Abu18610 Protein e	382	29	64.4	237	3	AAW37350	Aag37350 Arabidops
310	30	66.7	748	9	AEF06391	Aef06391 Bacteri	383	29	64.4	237	3	AAW37350	Aag37350 Arabidops
311	30	66.7	752	9	AEF40354	Aef40354 L. pneumo	384	29	64.4	258	6	ABU79071	Abu79071 S. aureus
312	30	66.7	785	5	ABP36993	Abp36993 L. pneumo	385	29	64.4	258	8	ADP43294	Adp43294 Staphyloc
313	30	66.7	785	9	ABP63022	Abp63022 Human pol	386	29	64.4	258	8	ADP43294	Adp43294 Staphyloc
314	30	66.7	817	5	ABW92514	Abw92514 Herbicida	387	29	64.4	258	9	AEA02988	Aea02988 Staphyloc
315	30	66.7	846	5	ABW53611	Abw53611 Lactococc	388	29	64.4	268	2	AAW98833	Aaw98833 H. pylori
316	30	66.7	846	8	ADS29286	Ads29286 Bacteri	389	29	64.4	268	4	AAU35721	Aau35721 Helicobac

390	29	64.4	268	4	AAU35902	Aau35902 Helicobac	463	29	64.4	385	8	ADV81871	Adv81871 Streptoco
391	29	64.4	268	6	ABU30756	Abu30756 Protein e	464	29	64.4	385	8	ADV79713	Adv79713 Streptoco
392	29	64.4	268	8	ADf89835	Adf89835 Staphyloc	465	29	64.4	387	2	AAR58857	Aar58857 Fowlpox v
393	29	64.4	269	2	AAy08658	Aay08658 WO9927094	466	29	64.4	387	2	AAR49142	Aar49142 Fowlpox v
394	29	64.4	269	2	AAy08658	Aay08658 Human tra	467	29	64.4	387	2	AAW10726	Aaw10726 Homology
395	29	64.4	269	4	AAW08636	Aam78636 Human pro	468	29	64.4	387	2	AAy21981	Aay21981 Homology
396	29	64.4	269	8	ABM81093	Abm81093 Tumour-as	469	29	64.4	387	2	AAy58181	Aay58181 PPV prote
397	29	64.4	269	8	ADp55459	Adp55459 Human PRO	470	29	64.4	387	3	AAAB36037	Aab36037 Recombina
398	29	64.4	269	8	ADU06651	Adu06651 Novel bro	471	29	64.4	388	3	AAAB36037	Aab36037 Recombina
399	29	64.4	270	4	ABB62170	Abb62170 Drosophil	472	29	64.4	390	3	AAAG19346	Aag19346 Arabidops
400	29	64.4	271	4	AAU37334	Aau37334 Staphyloc	473	29	64.4	390	3	AAAG19346	Aag19346 Arabidops
401	29	64.4	271	4	AAU34355	Aau34355 Staphyloc	474	29	64.4	390	3	AAAG19346	Aag19346 Arabidops
402	29	64.4	271	4	ABG10266	Abg10266 Novel hum	475	29	64.4	395	8	ADJ48777	Adj48777 Oil-assoc
403	29	64.4	271	6	ABU16453	Abu16453 Protein e	476	29	64.4	402	5	AAU20527	Aau20527 Human sec
404	29	64.4	271	6	ABU42536	Abu42536 Protein e	477	29	64.4	402	5	ABP41935	Abp41935 Human ova
405	29	64.4	271	6	ABW72498	Abm72498 Staphyloc	478	29	64.4	402	5	ADP41430	Adp41430 Human CD-
406	29	64.4	273	5	ADP38629	Adp38629 Staphyloc	479	29	64.4	407	3	AAy75293	Aay75293 Neisseria
407	29	64.4	273	5	ADP38629	Adp38629 Staphyloc	480	29	64.4	408	9	ADZ10551	Adz10551 P. gingiv
408	29	64.4	276	3	AG434323	Aag434323 Arabidops	481	29	64.4	427	6	ADA33918	Ada33918 Acinetoba
409	29	64.4	276	3	AG434323	Aag434323 Arabidops	482	29	64.4	432	8	ADN18428	Adn18428 Bacterial
410	29	64.4	278	8	ADU23110	Adu23110 Bacterial	483	29	64.4	438	4	ADN18428	Adn18428 Bacterial
411	29	64.4	286	4	AG89167	Ag89167 Human sec	484	29	64.4	438	6	ABP81625	Abp81625 Streptoco
412	29	64.4	286	8	ADP25069	Adp25069 PRO polyp	485	29	64.4	438	6	ADK46773	Adk46773 Streptoco
413	29	64.4	294	4	ABB12313	Abb12313 Human SUR	486	29	64.4	451	5	ABP73363	Abp73363 Candida a
414	29	64.4	294	4	AAW79620	Aam79620 Human pro	487	29	64.4	465	5	ABP73363	Abp73363 Candida a
415	29	64.4	303	3	AAy44768	Aay44768 Rice seri	488	29	64.4	478	6	ABG74844	Abg74844 Potato 9-
416	29	64.4	306	6	ABU29759	Abu29759 Protein e	489	29	64.4	479	4	AAAG92294	Aag92294 C. glutami
417	29	64.4	306	6	ADC96647	Adc96647 E. faeciu	490	29	64.4	480	5	ABR38813	Abr38813 A. niger
418	29	64.4	308	3	ABW40734	Aab40734 Human ORF	491	29	64.4	480	5	ABR38850	Abr38850 A. niger
419	29	64.4	308	6	ABU29291	Abu29291 Protein e	492	29	64.4	483	8	ADN10571	Adn10571 Nicotiana
420	29	64.4	310	6	ABG41714	Abg41714 Arabidops	493	29	64.4	483	9	ADZ65259	Adz65259 Tobacco c
421	29	64.4	310	6	ABU09474	Abu09474 Corn seri	494	29	64.4	483	9	ADZ65259	Adz65259 Tobacco c
422	29	64.4	310	9	AEA16770	Aea16770 Corn seri	495	29	64.4	485	8	ADL05075	Adl05075 M. catarr
423	29	64.4	311	3	AG41713	Ag41713 Arabidops	496	29	64.4	496	7	ABM86707	Abm86707 Rice abio
424	29	64.4	314	7	ADC97660	Adc97660 E. faeciu	497	29	64.4	500	7	ADL65591	Adl65591 C. glutam
425	29	64.4	315	9	AEA49225	Aea49225 L. rhomoc	498	29	64.4	503	8	ADS24034	Ads24034 Bacterial
426	29	64.4	317	4	AAU35111	Aau35111 Enterococ	499	29	64.4	511	7	AAE38168	Aae38168 Fruit fly
427	29	64.4	319	5	ABW55189	Abw55189 Lactococc	500	29	64.4	522	8	ADN25829	Adn25829 Bacterial
428	29	64.4	321	7	ABH86554	Abh86554 Enterococ	501	29	64.4	527	2	AAW98268	Aaw98268 H. pylori
429	29	64.4	330	7	ABO60856	Abu60856 Klebsiell	502	29	64.4	529	6	ABU49867	Abu49867 Protein e
430	29	64.4	332	6	ADB10340	Adb10340 Alloiococ	503	29	64.4	530	6	ABU49867	Abu49867 Protein e
431	29	64.4	332	8	ADY06342	Ady06342 Plant ful	504	29	64.4	547	7	ABO61864	Abo61864 Klebsiell
432	29	64.4	332	8	ADY09994	Ady09994 Plant ful	505	29	64.4	548	6	ABU36994	Abu36994 Protein e
433	29	64.4	336	2	AAW86365	Aaw86365 Human DNA	506	29	64.4	548	6	ABU33969	Abu33969 Protein e
434	29	64.4	336	5	AAE16106	Aae16106 Human DNA	507	29	64.4	549	6	ABJ37090	Abj37090 High-affi
435	29	64.4	337	5	AAE16119	Aae16119 Human DNA	508	29	64.4	550	8	ADT05799	Adt05799 Human par
436	29	64.4	337	3	AAAG09611	Aag09611 Arabidops	509	29	64.4	551	6	ABU34792	Abu34792 Protein e
437	29	64.4	338	3	AAAG09611	Aag09611 Arabidops	510	29	64.4	555	8	ADS23174	Ads23174 Bacterial
438	29	64.4	342	4	ABB67133	Abb67133 Drosophil	511	29	64.4	568	3	AAy71120	Aay71120 Human mit
439	29	64.4	342	4	ABB62909	Abb62909 Drosophil	512	29	64.4	568	7	ABO61473	Abo61473 Klebsiell
440	29	64.4	342	4	ABB62909	Abb62909 Drosophil	513	29	64.4	568	8	ADG62950	Adg62950 Mox2. 3/2
441	29	64.4	352	7	ABR61774	AbR61774 B. burgdo	514	29	64.4	568	8	ADJ57245	Adj57245 Human NOX
442	29	64.4	352	7	ABR61774	AbR61775 B. burgdo	515	29	64.4	568	8	ADJ57247	Adj57247 Human NOX
443	29	64.4	352	7	ABR61772	AbR61772 B. burgdo	516	29	64.4	582	6	ABJ37089	Abj37089 High-affi
444	29	64.4	352	7	ABR61773	AbR61773 B. burgdo	517	29	64.4	590	8	ADS22613	Ads22613 Bacterial
445	29	64.4	354	5	ABW47974	Abw47974 BBK 32. 7	518	29	64.4	590	8	ADN20875	Adn20875 Bacterial
446	29	64.4	354	8	ADJ67105	Adj67105 Borrelia	519	29	64.4	602	8	ADN25941	Adn25941 Bacterial
447	29	64.4	360	7	ABR61776	AbR61776 B. burgdo	520	29	64.4	611	6	ABU33741	Abu33741 Protein e
448	29	64.4	360	7	ABR61777	AbR61777 B. burgdo	521	29	64.4	612	6	ABU34907	Abu34907 Protein e
449	29	64.4	360	7	ABR61778	AbR61778 B. burgdo	522	29	64.4	612	6	ABU36597	Abu36597 Protein e
450	29	64.4	360	7	ABR61779	AbR61779 B. burgdo	523	29	64.4	640	8	ADV16175	Adv16175 X. pelarg
451	29	64.4	363	3	AG434322	Aag434322 Arabidops	524	29	64.4	642	6	ABU29249	Abu29249 Protein e
452	29	64.4	363	3	AG06200	Ag06200 Arabidops	525	29	64.4	647	8	ADN21250	Adn21250 Bacterial
453	29	64.4	363	7	ADP75277	Adp75277 Thale cre	526	29	64.4	652	4	ABB60879	Abb60879 Drosophil
454	29	64.4	364	9	ABW36009	Aeb36009 L. pneumo	527	29	64.4	657	7	ABM87403	Abm87403 Rice abio
455	29	64.4	364	9	ABW36009	Aeb36009 L. pneumo	528	29	64.4	658	7	ABM87403	Abm87403 Rice abio
456	29	64.4	381	3	AAW59228	Aaw59228 Arabidops	529	29	64.4	660	8	AAU37655	Aau37655 Streptoco
457	29	64.4	381	3	AAW59228	Aaw59228 Arabidops	530	29	64.4	660	8	ADK47963	Adk47963 Streptoco
458	29	64.4	383	8	ADY24042	Ady24042 Plant ful	531	29	64.4	664	8	ADR94855	Adr94855 Novel S.
459	29	64.4	384	3	AAW59227	Aaw59227 Arabidops	532	29	64.4	664	9	AEA58725	Aea58725 Streptoco
460	29	64.4	385	3	AAW19347	Aag19347 Arabidops	533	29	64.4	693	5	AAE16111	Aae16111 Mouse DNA
461	29	64.4	385	5	ABP26360	Abp26360 Streptoco	534	29	64.4	726	4	ABG10264	Abg10264 Novel hum
462	29	64.4	385	8	ADV88460	Adv88460 Streptoco	535	29	64.4	774	2	AAW87502	Aaw87502 Human N-m

536	29	64.4	774	3	AAy56128	Human c1o	609	29	64.4	1032	6	ABU89627	Human PRO
537	29	64.4	774	3	AAB26230	Human N-m	610	29	64.4	1032	6	ABU86468	Human sec
538	29	64.4	774	5	AB56522	Human NMD	611	29	64.4	1032	6	ABU67681	Human sec
539	29	64.4	774	5	AAO18078	Human NMD	612	29	64.4	1032	6	ABU80709	Human PRO
540	29	64.4	774	6	ABU65893	Human N-m	613	29	64.4	1032	6	ABR99627	Human sec
541	29	64.4	774	6	ABU61438	Human N-m	614	29	64.4	1032	6	ABR99017	Human sec
542	29	64.4	774	6	ABU57675	Human N-m	615	29	64.4	1032	6	ABO16540	Human sec
543	29	64.4	774	6	ABO43085	Human NMD	616	29	64.4	1032	6	ABR92440	Human sec
544	29	64.4	774	7	AAE39249	Human NMD	617	29	64.4	1032	6	ABO19081	Human sec
545	29	64.4	775	7	AAR66057	Human NMD	618	29	64.4	1032	6	ABR78502	Human sec
546	29	64.4	801	5	ABB07524	Human dru	619	29	64.4	1032	6	ABU85238	Novel hum
547	29	64.4	821	5	ABB91742	Herbicida	620	29	64.4	1032	6	ABO00377	Novel hum
548	29	64.4	824	7	ABM86704	Rice abio	621	29	64.4	1032	6	ABO11709	Human sec
549	29	64.4	835	5	ABB07675	Human car	622	29	64.4	1032	6	ABO02354	Human sec
550	29	64.4	835	5	ABB97215	Novel hum	623	29	64.4	1032	6	ABU88928	Novel hum
551	29	64.4	835	5	AAE35020	Human dru	624	29	64.4	1032	6	ABU83623	Human sec
552	29	64.4	835	8	ADT05795	Human car	625	29	64.4	1032	6	ABO06424	Novel hum
553	29	64.4	836	8	ADT05798	Rat neuro	626	29	64.4	1032	6	ABR59460	Human sec
554	29	64.4	837	4	AAB62400	Human MBS	627	29	64.4	1032	6	ABO09522	Human sec
555	29	64.4	855	4	AAU02936	Angiotens	628	29	64.4	1032	6	ABO19386	Novel hum
556	29	64.4	884	4	ABB71494	Drosophil	629	29	64.4	1032	6	ABO11404	Human sec
557	29	64.4	945	2	AAR66060	Human NMD	630	29	64.4	1032	6	ABR67022	Human sec
558	29	64.4	962	2	AAR44194	Rat WMDA	631	29	64.4	1032	6	ABO16235	Human sec
559	29	64.4	977	4	ABG21179	Novel hum	632	29	64.4	1032	6	ABO13941	Human sec
560	29	64.4	990	8	ADN20877	Bacterial	633	29	64.4	1032	6	ABU65844	Human sec
561	29	64.4	995	8	ABM83900	Human dia	634	29	64.4	1032	6	ABO07692	Human PRO
562	29	64.4	1011	7	ADJ87683	G-coupled	635	29	64.4	1032	6	ABR43999	Human tol
563	29	64.4	1011	7	ADJ87724	G-coupled	636	29	64.4	1032	6	ABO03879	Human sec
564	29	64.4	1011	8	ADN38498	Human hum	637	29	64.4	1032	6	ABR67327	Human sec
565	29	64.4	1011	8	ADN38457	Novel hum	638	29	64.4	1032	6	ABO15930	Human sec
566	29	64.4	1014	5	AAAM47659	MOU1 prot	639	29	64.4	1032	6	ABU56211	Human sec
567	29	64.4	1014	7	ADJ87650	G-coupled	640	29	64.4	1032	6	ABU65539	Human PRO
568	29	64.4	1014	7	ADJ87728	G-coupled	641	29	64.4	1032	6	ABU95484	Novel hum
569	29	64.4	1014	8	ADN38383	Novel hum	642	29	64.4	1032	6	ABU71387	Human PRO
570	29	64.4	1014	8	ADN38502	Novel hum	643	29	64.4	1032	6	ABO07997	Human PRO
571	29	64.4	1019	7	ADJ87730	G-coupled	644	29	64.4	1032	6	ABR70238	Human sec
572	29	64.4	1019	7	ADJ87732	G-coupled	645	29	64.4	1032	6	ABR69571	Human sec
573	29	64.4	1019	8	ADN38504	Novel hum	646	29	64.4	1032	6	ABO01712	Human PRO
574	29	64.4	1019	8	ADN38506	Novel hum	647	29	64.4	1032	6	ABU81514	Human PRO
575	29	64.4	1023	5	ABBA48189	Listeria	648	29	64.4	1032	6	ABR60311	Human sec
576	29	64.4	1023	5	ABU32611	Protein e	649	29	64.4	1032	6	ABR68046	Human sec
577	29	64.4	1031	8	ADM72305	Feline TL	650	29	64.4	1032	6	ABR65434	Human sec
578	29	64.4	1031	9	ADM44372	Cat Toll-	651	29	64.4	1032	6	ABR68656	Human sec
579	29	64.4	1032	4	AAAG63016	Amino aci	652	29	64.4	1032	6	ABR72068	Human sec
580	29	64.4	1032	4	AAU29299	Human PRO	653	29	64.4	1032	6	ABU85548	Human PRO
581	29	64.4	1032	5	ABB08785	Human TLR	654	29	64.4	1032	6	ABU89238	Human sec
582	29	64.4	1032	5	ABB08786	Mouse TLR	655	29	64.4	1032	6	ABU83318	Human sec
583	29	64.4	1032	5	AAO21557	Murine To	656	29	64.4	1032	6	ABU95174	Novel hum
584	29	64.4	1032	5	AAO21556	Murine To	657	29	64.4	1032	6	ABU90722	Novel hum
585	29	64.4	1032	5	ABP43799	Toll-like	658	29	64.4	1032	6	ABU84233	Human sec
586	29	64.4	1032	6	ABU58675	Human PRO	659	29	64.4	1032	6	ABU93884	Novel hum
587	29	64.4	1032	6	ABU88223	Novel hum	660	29	64.4	1032	6	ABR65129	Human sec
588	29	64.4	1032	6	ABU84538	Human sec	661	29	64.4	1032	6	ABR68961	Human sec
589	29	64.4	1032	6	ABP97496	Murine To	662	29	64.4	1032	6	ABO06777	Human sec
590	29	64.4	1032	6	ABR84383	Human Tol	663	29	64.4	1032	6	ABR99322	Human sec
591	29	64.4	1032	6	ABR84384	Murine To	664	29	64.4	1032	6	ABU57206	Human PRO
592	29	64.4	1032	6	ABP97495	Human Tol	665	29	64.4	1032	6	ABU86158	Novel hum
593	29	64.4	1032	6	ABR66412	Human sec	666	29	64.4	1032	6	ABU82445	Novel hum
594	29	64.4	1032	6	ABR65802	Human sec	667	29	64.4	1032	6	ABU87456	Human PRO
595	29	64.4	1032	6	ABU99742	Human sec	668	29	64.4	1032	6	ABU83928	Human sec
596	29	64.4	1032	6	ABU82981	Human PRO	669	29	64.4	1032	6	ABO08302	Human PRO
597	29	64.4	1032	6	ABU90102	Novel hum	670	29	64.4	1032	6	ABU82013	Novel hum
598	29	64.4	1032	6	ABR68351	Human sec	671	29	64.4	1032	6	ABU66177	Novel hum
599	29	64.4	1032	6	ABU96404	Novel hum	672	29	64.4	1032	6	ABR60006	Human sec
600	29	64.4	1032	6	ABU92835	Human sec	673	29	64.4	1032	6	ABU94194	Novel hum
601	29	64.4	1032	6	ABO08912	Human sec	674	29	64.4	1032	6	ABO00067	Novel hum
602	29	64.4	1032	6	ABO02964	Human sec	675	29	64.4	1032	6	ABR66717	Human sec
603	29	64.4	1032	6	ABR75118	Human sec	676	29	64.4	1032	6	ABR91135	Human sec
604	29	64.4	1032	6	ABR94880	Human sec	677	29	64.4	1032	6	ABU94562	Human PRO
605	29	64.4	1032	6	ABU85853	Human PRO	678	29	64.4	1032	6	ABU79444	Human PRO
606	29	64.4	1032	6	ABU99013	Novel hum	679	29	64.4	1032	6	ABU86773	Human sec
607	29	64.4	1032	6	ABU98228	Novel hum	680	29	64.4	1032	6	ABU87078	Novel hum
608	29	64.4	1032	6	ABU91934	Novel hum	681	29	64.4	1032	6	ABU94867	Human PRO

682	29	64.4	1032	6	ABO04794	Human	PRO	Abo04794	Human	PRO	755	29	64.4	1032	6	ABM25916	Human	sec	Abm25916	Human	sec
683	29	64.4	1032	6	ABR70543	Human	sec	AbR70543	Human	sec	756	29	64.4	1032	6	ABM26221	Human	sec	Abm26221	Human	sec
684	29	64.4	1032	6	ABU98708	Human	PRO	Abu98708	Human	PRO	757	29	64.4	1032	6	ABO03574	Human	sec	Abo03574	Human	sec
685	29	64.4	1032	6	ABR66107	Human	sec	AbR66107	Human	sec	758	29	64.4	1032	6	ABO02859	Human	sec	AbO02859	Human	sec
686	29	64.4	1032	6	ABR64824	Human	sec	AbR64824	Human	sec	759	29	64.4	1032	6	ABR90830	Human	sec	AbR90830	Human	sec
687	29	64.4	1032	6	ABU79749	Human	PRO	Abu79749	Human	PRO	760	29	64.4	1032	6	ABR73898	Human	sec	AbR73898	Human	sec
688	29	64.4	1032	6	ABU93140	Human	sec	Abu93140	Human	sec	761	29	64.4	1032	6	ABO17150	Human	sec	Abo17150	Human	sec
689	29	64.4	1032	6	ABU96099	Human	PRO	Abu96099	Human	PRO	762	29	64.4	1032	6	ABR94575	Human	sec	AbR94575	Human	sec
690	29	64.4	1032	6	ABU91319	Novel	hum	Abu91319	Novel	hum	763	29	64.4	1032	6	ABR76082	Human	sec	AbR76082	Human	sec
691	29	64.4	1032	6	ABU90412	Novel	hum	Abu90412	Novel	hum	764	29	64.4	1032	6	ABR71458	Human	sec	AbR71458	Human	sec
692	29	64.4	1032	6	ABO09827	Human	sec	Abo09827	Human	sec	765	29	64.4	1032	6	ABR93355	Human	sec	AbR93355	Human	sec
693	29	64.4	1032	6	ABO11099	Human	sec	Abo11099	Human	sec	766	29	64.4	1032	6	ABR93660	Human	sec	AbR93660	Human	sec
694	29	64.4	1032	6	ABR71153	Human	sec	AbR71153	Human	sec	767	29	64.4	1032	6	ABR88085	Human	sec	AbR88085	Human	sec
695	29	64.4	1032	6	ABU87761	Human	PRO	Abu87761	Human	PRO	768	29	64.4	1032	6	ABO28085	Human	sec	Abo28085	Human	sec
696	29	64.4	1032	6	ABU91629	Human	PRO	Abu91629	Human	PRO	769	29	64.4	1032	6	ABO30220	Human	sec	Abo30220	Human	sec
697	29	64.4	1032	6	ABU84843	Human	sec	Abu84843	Human	sec	770	29	64.4	1032	6	ABO33429	Human	PRO	Abo33429	Human	PRO
698	29	64.4	1032	6	ABR69933	Human	sec	AbR69933	Human	sec	771	29	64.4	1032	6	ABM05117	Human	sec	Abm05117	Human	sec
699	29	64.4	1032	6	ABU80310	Human	PRO	Abu80310	Human	PRO	772	29	64.4	1032	6	ABM09077	Human	sec	Abm09077	Human	sec
700	29	64.4	1032	6	ABU93579	Human	PRO	Abu93579	Human	PRO	773	29	64.4	1032	6	ABO36677	Human	sec	Abo36677	Human	sec
701	29	64.4	1032	6	ABO10132	Human	sec	Abo10132	Human	sec	774	29	64.4	1032	6	ABO35762	Human	PRO	Abo35762	Human	PRO
702	29	64.4	1032	6	ABO09217	Human	sec	Abo09217	Human	sec	775	29	64.4	1032	6	ABO39727	Human	sec	Abo39727	Human	sec
703	29	64.4	1032	6	ABU10785	Human	sec	Abu10785	Human	sec	776	29	64.4	1032	6	ABM10602	Human	sec	Abm10602	Human	sec
704	29	64.4	1032	6	ABU95794	Human	PRO	Abu95794	Human	PRO	777	29	64.4	1032	6	ABM12127	Human	sec	Abm12127	Human	sec
705	29	64.4	1032	6	ABU97003	Novel	hum	Abu97003	Novel	hum	778	29	64.4	1032	6	ABO52273	Human	PRO	Abo52273	Human	PRO
706	29	64.4	1032	6	ABR70848	Human	sec	AbR70848	Human	sec	779	29	64.4	1032	6	ABO52578	Human	PRO	Abo52578	Human	PRO
707	29	64.4	1032	6	ABO05199	Novel	hum	Abo05199	Novel	hum	780	29	64.4	1032	6	ABO23896	Human	sec	Abo23896	Human	sec
708	29	64.4	1032	6	ABO08607	Human	sec	Abo08607	Human	sec	781	29	64.4	1032	6	ABR97382	Human	sec	AbR97382	Human	sec
709	29	64.4	1032	6	ABO05814	Human	sec	Abo05814	Human	sec	782	29	64.4	1032	6	ABR87170	Human	sec	AbR87170	Human	sec
710	29	64.4	1032	6	ABR74203	Human	sec	AbR74203	Human	sec	783	29	64.4	1032	6	ABM11212	Human	sec	Abm11212	Human	sec
711	29	64.4	1032	6	ABR95795	Human	sec	AbR95795	Human	sec	784	29	64.4	1032	6	ABM28356	Human	sec	Abm28356	Human	sec
712	29	64.4	1032	6	ABR81092	Human	sec	AbR81092	Human	sec	785	29	64.4	1032	6	ABO32355	Human	sec	Abo32355	Human	sec
713	29	64.4	1032	6	ABR81397	Human	sec	AbR81397	Human	sec	786	29	64.4	1032	6	ABM15482	Human	sec	Abm15482	Human	sec
714	29	64.4	1032	6	ABM01093	Human	sec	Abm01093	Human	sec	787	29	64.4	1032	6	ABM06637	Human	sec	Abm06637	Human	sec
715	29	64.4	1032	6	ABR88695	Human	sec	AbR88695	Human	sec	788	29	64.4	1032	6	ABM04448	Human	sec	Abm04448	Human	sec
716	29	64.4	1032	6	ABM77516	Human	sec	Abm77516	Human	sec	789	29	64.4	1032	6	ABM22561	Human	sec	Abm22561	Human	sec
717	29	64.4	1032	6	ABO29000	Human	sec	Abo29000	Human	sec	790	29	64.4	1032	6	ABM07857	Human	sec	Abm07857	Human	sec
718	29	64.4	1032	6	ABO31745	Human	sec	Abo31745	Human	sec	791	29	64.4	1032	6	ABO40947	Human	sec	Abo40947	Human	sec
719	29	64.4	1032	6	ABM08162	Human	sec	Abm08162	Human	sec	792	29	64.4	1032	6	ABM35594	Human	sec	Abm35594	Human	sec
720	29	64.4	1032	6	ABO40642	Human	sec	Abo40642	Human	sec	793	29	64.4	1032	6	ABM33357	Human	sec	Abm33357	Human	sec
721	29	64.4	1032	6	ABO36067	Human	PRO	Abo36067	Human	PRO	794	29	64.4	1032	6	ABO52883	Human	PRO	Abo52883	Human	PRO
722	29	64.4	1032	6	ABO44206	Human	PRO	Abo44206	Human	PRO	795	29	64.4	1032	6	ABO50443	Human	sec	Abo50443	Human	sec
723	29	64.4	1032	6	ADA78304	Human	sec	Ada78304	Human	sec	796	29	64.4	1032	6	ABU99437	Human	sec	Abu99437	Human	sec
724	29	64.4	1032	6	ABM25001	Human	sec	Abm25001	Human	sec	797	29	64.4	1032	6	ABO04489	Human	sec	Abo04489	Human	sec
725	29	64.4	1032	6	ABO03269	Human	sec	Abo03269	Human	sec	798	29	64.4	1032	6	ABM18659	Human	sec	Abm18659	Human	sec
726	29	64.4	1032	6	ABR90525	Human	sec	AbR90525	Human	sec	799	29	64.4	1032	6	ABR97687	Human	sec	AbR97687	Human	sec
727	29	64.4	1032	6	ABM17439	Human	sec	Abm17439	Human	sec	800	29	64.4	1032	6	ABR80787	Human	sec	AbR80787	Human	sec
728	29	64.4	1032	6	ABR95185	Human	sec	AbR95185	Human	sec	801	29	64.4	1032	6	ABM01398	Human	sec	Abm01398	Human	sec
729	29	64.4	1032	6	ABR95490	Human	sec	AbR95490	Human	sec	802	29	64.4	1032	6	ABR89000	Human	sec	AbR89000	Human	sec
730	29	64.4	1032	6	ABO21728	Human	sec	Abo21728	Human	sec	803	29	64.4	1032	6	ABM13652	Human	sec	Abm13652	Human	sec
731	29	64.4	1032	6	ABR97992	Human	sec	AbR97992	Human	sec	804	29	64.4	1032	6	ABM21036	Human	sec	Abm21036	Human	sec
732	29	64.4	1032	6	ABR87780	Human	sec	AbR87780	Human	sec	805	29	64.4	1032	6	ABO42167	Human	sec	Abo42167	Human	sec
733	29	64.4	1032	6	ABM77821	Human	sec	Abm77821	Human	sec	806	29	64.4	1032	6	ABO42777	Human	sec	Abo42777	Human	sec
734	29	64.4	1032	6	ABM28051	Human	sec	Abm28051	Human	sec	807	29	64.4	1032	6	ABM10297	Human	sec	Abm10297	Human	sec
735	29	64.4	1032	6	ABM06332	Human	sec	Abm06332	Human	sec	808	29	64.4	1032	6	ABO38812	Human	sec	Abo38812	Human	sec
736	29	64.4	1032	6	ABM03838	Human	sec	Abm03838	Human	sec	809	29	64.4	1032	6	ABM33052	Human	sec	Abm33052	Human	sec
737	29	64.4	1032	6	ABM35289	Human	sec	Abm35289	Human	sec	810	29	64.4	1032	6	ABM22866	Human	sec	Abm22866	Human	sec
738	29	64.4	1032	6	ABM26526	Human	sec	Abm26526	Human	sec	811	29	64.4	1032	6	ABM75077	Human	sec	Abm75077	Human	sec
739	29	64.4	1032	6	ABO48308	Human	sec	Abo48308	Human	sec	812	29	64.4	1032	6	ABR80096	Human	sec	AbR80096	Human	sec
740	29	64.4	1032	6	ABR93050	Human	sec	AbR93050	Human	sec	813	29	64.4	1032	6	ABR96467	Human	sec	AbR96467	Human	sec
741	29	64.4	1032	6	ABO24811	Human	sec	Abo24811	Human	sec	814	29	64.4	1032	6	ABR02618	Human	sec	AbR02618	Human	sec
742	29	64.4	1032	6	ABM11822	Human	sec	Abm11822	Human	sec	815	29	64.4	1032	6	ABR86560	Human	sec	AbR86560	Human	sec
743	29	64.4	1032	6	ABM02923	Human	sec	Abm02923	Human	sec	816	29	64.4	1032	6	ABR86865	Human	sec	AbR86865	Human	sec
744	29	64.4	1032	6	ABM16219	Human	sec	Abm16219	Human	sec	817	29	64.4	1032	6	ABM16829	Human	sec	Abm16829	Human	sec
745	29	64.4	1032	6	ABO27780	Human	sec	Abo27780	Human	sec	818	29	64.4	1032	6	ABM29881	Human	sec	Abm29881	Human	sec
746	29	64.4	1032	6	ABM29271	Human	sec	Abm29271	Human	sec	819	29	64.4	1032	6	ABO29305	Human	sec	Abo29305	Human	sec
747	29	64.4	1032	6	ABM07247	Human	sec	Abm07247	Human	sec	820	29	64.4	1032	6	ABM24086	Human	sec	Abm24086	Human	sec
748	29	64.4	1032	6	ABM21341	Human	sec	Abm21341	Human	sec	821	29	64.4	1032	6	ABM23476	Human	sec	Abm23476	Human	sec
749	29	64.4	1032	6	ABM09687	Human	sec	Abm09687	Human	sec	822	29	64.4	1032	6	ABM22256	Human	sec	Abm22256	Human	sec
750	29	64.4	1032	6	ABO41557	Human	sec	Abo41557	Human	sec	823	29	64.4	1032	6	ABO37897	Human	sec	Abo37897		

828	29	64.4	1032	6	ABM34272	Abm34272 Human sec	901	29	64.4	1032	6	ABR80177	Abr80177 Human sec
829	29	64.4	1032	6	ABM34577	Abm34577 Human sec	902	29	64.4	1032	6	ABM11517	Abm11517 Human sec
830	29	64.4	1032	6	ABO20508	AbO20508 Human sec	903	29	64.4	1032	6	ABO33124	AbO33124 Human PRO
831	29	64.4	1032	6	ABO21423	AbO21423 Human sec	904	29	64.4	1032	6	ABO30830	AbO30830 Human sec
832	29	64.4	1032	6	ABO22338	AbO22338 Human sec	905	29	64.4	1032	6	ABO31135	AbO31135 Human sec
833	29	64.4	1032	6	ABR96772	Abr96772 Human sec	906	29	64.4	1032	6	ABM27441	Abm27441 Human sec
834	29	64.4	1032	6	ABR85950	Abr85950 Human sec	907	29	64.4	1032	6	ABM30186	Abm30186 Human sec
835	29	64.4	1032	6	ABR99932	Abr99932 Human sec	908	29	64.4	1032	6	ABM05722	Abm05722 Human sec
836	29	64.4	1032	6	ABM00483	Abm00483 Human sec	909	29	64.4	1032	6	ABM15787	Abm15787 Human sec
837	29	64.4	1032	6	ABM00788	Abm00788 Human sec	910	29	64.4	1032	6	ABM08772	Abm08772 Human sec
838	29	64.4	1032	6	ABO29915	AbO29915 Human sec	911	29	64.4	1032	6	ABO42472	AbO42472 Human sec
839	29	64.4	1032	6	ABM23781	Abm23781 Human sec	912	29	64.4	1032	6	ABO38202	AbO38202 Human sec
840	29	64.4	1032	6	ABM29576	Abm29576 Human sec	913	29	64.4	1032	6	ABO46112	AbO46112 Human PRO
841	29	64.4	1032	6	ABO38507	AbO38507 Human sec	914	29	64.4	1032	6	ABM66915	Abm66915 Human sec
842	29	64.4	1032	6	ABO45807	AbO45807 Human PRO	915	29	64.4	1032	6	ADB20664	Adb20664 Human sec
843	29	64.4	1032	6	ABM20731	Abm20731 Human sec	916	29	64.4	1032	6	ABM19816	Abm19816 Human sec
844	29	64.4	1032	6	ADA81823	Ada81823 Human sec	917	29	64.4	1032	6	ABO49528	AbO49528 Human sec
845	29	64.4	1032	6	ABO16845	AbO16845 Human sec	918	29	64.4	1032	6	ABO49833	AbO49833 Human sec
846	29	64.4	1032	6	ABO18471	AbO18471 Human sec	919	29	64.4	1032	6	ADA78916	Ada78916 Human sec
847	29	64.4	1032	6	ABO22898	AbO22898 Human PRO	920	29	64.4	1032	6	ABR88390	Abr88390 Human sec
848	29	64.4	1032	6	ABO23203	AbO23203 Human PRO	921	29	64.4	1032	6	ABM27136	Abm27136 Human sec
849	29	64.4	1032	6	ABR92745	Abr92745 Human sec	922	29	64.4	1032	6	ABM03533	Abm03533 Human sec
850	29	64.4	1032	6	ABR81702	Abr81702 Human sec	923	29	64.4	1032	6	ABO40032	AbO40032 Human sec
851	29	64.4	1032	6	ABM78126	Abm78126 Human sec	924	29	64.4	1032	7	ABO50138	AbO50138 Human sec
852	29	64.4	1032	6	ABR89915	Abr89915 Human sec	925	29	64.4	1032	7	ABO51053	AbO51053 Human sec
853	29	64.4	1032	6	ABM26831	Abm26831 Human sec	926	29	64.4	1032	7	ABO05509	AbO05509 Human sec
854	29	64.4	1032	6	ABM13957	Abm13957 Human sec	927	29	64.4	1032	7	ABR74813	Abr74813 Human sec
855	29	64.4	1032	6	ABO28695	AbO28695 Human sec	928	29	64.4	1032	7	ABR77292	Abr77292 Human sec
856	29	64.4	1032	6	ABO30525	AbO30525 Human sec	929	29	64.4	1032	7	ABM18049	Abm18049 Human sec
857	29	64.4	1032	6	ABM07552	Abm07552 Human sec	930	29	64.4	1032	7	ABR96100	Abr96100 Human sec
858	29	64.4	1032	6	ABM04143	Abm04143 Human sec	931	29	64.4	1032	7	ABO22033	AbO22033 Human sec
859	29	64.4	1032	6	ABO37287	AbO37287 Human sec	932	29	64.4	1032	7	ABO20203	AbO20203 Human sec
860	29	64.4	1032	6	ABO41862	AbO41862 Human PRO	933	29	64.4	1032	7	ABO24506	AbO24506 Human sec
861	29	64.4	1032	6	ABO35457	AbO35457 Human PRO	934	29	64.4	1032	7	ABR86255	Abr86255 Human sec
862	29	64.4	1032	6	ABM25306	Abm25306 Human sec	935	29	64.4	1032	7	ABM10907	Abm10907 Human sec
863	29	64.4	1032	6	ABO47698	AbO47698 Human sec	936	29	64.4	1032	7	ABM76906	Abm76906 Human sec
864	29	64.4	1032	6	ABO48003	AbO48003 Human sec	937	29	64.4	1032	7	ABR89610	Abr89610 Human sec
865	29	64.4	1032	6	ABO48613	AbO48613 Human sec	938	29	64.4	1032	7	ABM12737	Abm12737 Human sec
866	29	64.4	1032	6	ABO51663	AbO51663 Human PRO	939	29	64.4	1032	7	ABM06027	Abm06027 Human sec
867	29	64.4	1032	6	ABO51968	AbO51968 Human PRO	940	29	64.4	1032	7	ABO35152	AbO35152 Human PRO
868	29	64.4	1032	6	ABO50748	AbO50748 Human sec	941	29	64.4	1032	7	ABM03228	Abm03228 Human sec
869	29	64.4	1032	6	ABR79872	Abr79872 Human sec	942	29	64.4	1032	7	ABM19206	Abm19206 Human sec
870	29	64.4	1032	6	ABM17134	Abm17134 Human sec	943	29	64.4	1032	7	ABM19511	Abm19511 Human sec
871	29	64.4	1032	6	ABO18166	AbO18166 Human sec	944	29	64.4	1032	7	ABO46722	AbO46722 Human PRO
872	29	64.4	1032	6	ABO21118	AbO21118 Human sec	945	29	64.4	1032	7	ABO49223	AbO49223 Human sec
873	29	64.4	1032	6	ABR97077	Abr97077 Human sec	946	29	64.4	1032	7	ABR69266	Abr69266 Human sec
874	29	64.4	1032	6	ABM12432	Abm12432 Human sec	947	29	64.4	1032	7	ABR89305	Abr89305 Human sec
875	29	64.4	1032	6	ABM16524	Abm16524 Human sec	948	29	64.4	1032	7	ABR72678	Abr72678 Human sec
876	29	64.4	1032	6	ABM24391	Abm24391 Human sec	949	29	64.4	1032	7	ABR74508	Abr74508 Human sec
877	29	64.4	1032	6	ABM14872	Abm14872 Human sec	950	29	64.4	1032	7	ABO18776	AbO18776 Human sec
878	29	64.4	1032	6	ABM04753	Abm04753 Human sec	951	29	64.4	1032	7	ABR80482	Abr80482 Human sec
879	29	64.4	1032	6	ABM06942	Abm06942 Human sec	952	29	64.4	1032	7	ABM01703	Abm01703 Human sec
880	29	64.4	1032	6	ABM09382	Abm09382 Human sec	953	29	64.4	1032	7	ABM02313	Abm02313 Human sec
881	29	64.4	1032	6	ABO39422	AbO39422 Human sec	954	29	64.4	1032	7	ABR87475	Abr87475 Human sec
882	29	64.4	1032	6	ABM75687	Abm75687 Human sec	955	29	64.4	1032	7	ABM13042	Abm13042 Human sec
883	29	64.4	1032	6	ABM25611	Abm25611 Human sec	956	29	64.4	1032	7	ABM30796	Abm30796 Human sec
884	29	64.4	1032	6	ABM20121	Abm20121 Human sec	957	29	64.4	1032	7	ABM24696	Abm24696 Human sec
885	29	64.4	1032	6	ABO47027	AbO47027 Human PRO	958	29	64.4	1032	7	ABO29610	AbO29610 Human sec
886	29	64.4	1032	6	ABO47332	AbO47332 Human PRO	959	29	64.4	1032	7	ABO31440	AbO31440 Human sec
887	29	64.4	1032	6	ADA83621	Ada83621 Human sec	960	29	64.4	1032	7	ABM14567	Abm14567 Human sec
888	29	64.4	1032	6	ABR71763	Abr71763 Human sec	961	29	64.4	1032	7	ABM09992	Abm09992 Human sec
889	29	64.4	1032	6	ABR72373	Abr72373 Human sec	962	29	64.4	1032	7	ABO39117	AbO39117 Human sec
890	29	64.4	1032	6	ABR98712	Abr98712 Human sec	963	29	64.4	1032	7	ABM34882	Abm34882 Human sec
891	29	64.4	1032	6	ABO07082	AbO07082 Human sec	964	29	64.4	1032	7	ABO51358	AbO51358 Human sec
892	29	64.4	1032	6	ABR85035	Abr85035 Human sec	965	29	64.4	1032	7	ABO04184	AbO04184 Human sec
893	29	64.4	1032	6	ABR73593	Abr73593 Human sec	966	29	64.4	1032	7	ABO10654	AbO10654 Human PRO
894	29	64.4	1032	6	ABR76687	Abr76687 Human sec	967	29	64.4	1032	7	ABR77897	Abr77897 Human sec
895	29	64.4	1032	6	ABR73288	Abr73288 Human sec	968	29	64.4	1032	7	ABR79107	Abr79107 Human sec
896	29	64.4	1032	6	ABM18354	Abm18354 Human sec	969	29	64.4	1032	7	ABO24201	AbO24201 Human sec
897	29	64.4	1032	6	ABO20813	AbO20813 Human sec	970	29	64.4	1032	7	ABR93965	Abr93965 Human sec
898	29	64.4	1032	6	ABO25556	AbO25556 Human PRO	971	29	64.4	1032	7	ABM02008	Abm02008 Human sec
899	29	64.4	1032	6	ABO25861	AbO25861 Human PRO	972	29	64.4	1032	7	ABM78431	Abm78431 Human sec
900	29	64.4	1032	6	ABR94270	Abr94270 Human sec	973	29	64.4	1032	7	ABR90220	Abr90220 Human sec



PS Claim 12; Page 30; 77pp; English.  
 XX  
 CC The invention relates to aiding in the diagnosis of a neoplastic  
 CC condition or susceptibility to a neoplastic condition of an animal cell  
 CC or tissue. The method involves determining the amount of expression of an  
 CC eukaryotic translation initiation factor 3 (eIF3) protein in a test  
 CC sample isolated from the cell or tissue, and diagnosing a neoplastic  
 CC condition or susceptibility to a neoplastic condition based on the amount  
 CC of expression of the eIF3 protein. The methods, compounds and kits are  
 CC useful in therapeutics, diagnostic and screening methods for human cancer  
 CC and related malignancies, e.g. ovarian, breast, lung, colon, prostate,  
 CC pancreatic or gastrointestinal cancer, or melanoma. Sequences ABR82213-16  
 CC represent compounds derived from the human antigen eIF3  
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9

Db 1 FLSYDLFVV 9

RESULT 3

ABR80369  
 ID ABR80369 standard; protein; 352 AA.

AC ABR80369;

XX 07-MAY-2002 (first entry)

XX Human cancer antigen eIF3 variant 4 amino acid sequence.

XX Human; melanoma antigen eukaryotic initiation factor 3; eIF3;  
 KW ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;  
 KW anti-cancer; vaccine.  
 XX Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 242 /note= "wild-type Asn is replaced by Phe"  
 FT Domain 242 /note= "HLA-2 binding residue"  
 FT Domain 243 /note= "HLA-2 binding residue"  
 FT Domain 244..249 /note= "T-cell receptor (TCR) binding domain"  
 FT Misc-difference 244 /note= "wild-type Gln is replaced by Ser"  
 FT Misc-difference 245 /note= "wild-type Leu is replaced by Tyr"  
 FT Misc-difference 246 /note= "wild-type Leu is replaced by Asp"  
 FT Misc-difference 247 /note= "wild-type Met is replaced by Leu"  
 FT Misc-difference 248 /note= "wild-type Asp is replaced by Phe"  
 FT Misc-difference 249 /note= "wild-type Arg is replaced by Val"  
 FT Domain 250 /note= "HLA-2 binding residue"

XX WO200192307-A2.

XX 06-DEC-2001.

XX 30-MAY-2001; 2001WO-US017456.

XX 31-MAY-2000; 2000US-0209391P.

XX 17-AUG-2000; 2000US-0226258P.

PR 20-DEC-2000; 2000US-0257008P.

XX (GENZ ) GENZYME CORP.

PA Nicolette CA;

PI MPI; 2002-139606/18.

XX New therapeutic compounds useful against human ovarian cancer, for

PT modulating immune response in a subject, and for generating antibodies  
 PT that specifically recognize and bind to these molecules.

XX Claim 9; Page; 69pp; English.

XX The invention relates to novel therapeutic compounds, that are designed  
 CC to enhance binding to MHC molecules and to enhance immunoregulatory  
 CC properties relative to their natural counterparts. The activity of the  
 CC compounds of the invention may be described as cytostatic and  
 CC immunomodulatory. The compounds are useful against human ovarian cancer,  
 CC for modulating immune response in a subject, and for generating  
 CC antibodies that specifically recognize and bind to these molecules.

CC Compositions comprising the compounds are useful as components of anti-  
 CC cancer vaccines and to expand immune effector cells that are specific for  
 CC cells characterised by expression of antigen eIF3 (melanoma antigen  
 CC eukaryotic initiation factor). The peptides or polypeptides conjugated to  
 CC a detectable agent may be used in diagnostic procedures, such as in the  
 CC detection and purification of antibodies, and as immunogens for  
 CC production of antibodies. The polynucleotides can be used as primers for  
 CC detecting genes or gene transcripts expressed in APC to confirm  
 CC transduction of the polynucleotides into host cells. The current sequence  
 CC represents the human cancer antigen eIF3 variant 4 amino acid sequence.  
 CC Note: This sequence is not present in the specification, but may be  
 CC created from the sequence of the wild-type human cancer antigen eIF3  
 CC sequence given in ABR80360

SQ Sequence 352 AA;

Query Match 100.0%; Score 45; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 0.98;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9

Db 242 FLSYDLFVV 250

RESULT 4

ABR74753  
 ID AAB74753 standard; protein; 51 AA.

XX AAB74753;

XX 12-JUN-2001 (first entry)

XX Human secreted protein sequence encoded by gene 21 SEQ ID NO:62.

XX Human; secreted protein; diagnosis; immunosuppressive; anti-HIV;  
 KW dermatological; immunosuppressive; anti-inflammatory; anti-HIV;  
 KW immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic;  
 KW ophthalmological; neuroprotectant; nootropic; anticonvulsant; vaccine;  
 KW antialzheimer; antiparkinsonian; antimicrobial; vulnery; gene therapy;  
 KW immune disorder; hyperproliferative disorder; cardiovascular disease;  
 KW cancer; angiogenic disorder; neurological disorder; infectious disease;  
 KW wound healing; regeneration; chemotaxis.

XX Homo sapiens.

XX WO200112775-A2.

XX 22-FEB-2001.

XX 16-AUG-2000; 2000WO-US022325.

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PR 17-AUG-1999; 99US-0149182P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Ni J, Florence KA, Fiscella M, Wei P, Baker KP;
PI Birse CB, Young PE, Komatsoulis GA, Moore PA, Soppet DR;
XX WPI: 2001-147550/15.
XX N-PSDB; AAF81807.
XX
XX Nucleic acids encoding 25 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
XX and diabetic retinopathy.
XX
XX Claim 11; Page 471; 485pp; English.
XX
XX AAF81787 to AAF81817 encode the human secreted proteins given in AAB74733
XX to AAB74772. Human secreted proteins can have activities based on the
XX tissues and cells they are expressed in. Example of activities include:
XX immunomodulatory; antisclerotic; dermatological; immunosuppressive;
XX antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant;
XX vascular; anti-angiogenic; ophthalmological; neuroprotectant; neurotropic;
XX anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial; and
XX vaccine. Human secreted proteins can be used in gene therapy and
XX (PEP1) may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate polypeptide expression. For example, NAMI
XX and PEP1 may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patients genome that
XX affect the activity of proteins by expressing inactive proteins or to
XX supplement the patients own production of polypeptides. Disorders that
XX may be prevented, diagnosed and/or treated include immune disorders.
XX hyperproliferative disorders (e.g. cancers), cardiovascular diseases,
XX angioegenic disorders, neurological disorders, infectious diseases and/or
XX for promoting wound healing, regeneration and /or chemotaxis. AAF81778 to
XX AAF81786 and AAB74732 represent sequences used in the exemplification of
XX the present invention
XX
XX Sequence 51 AA;
SQ
Query Match 80.0%; Score 36; DB 4; Length 51;
Best Local Similarity 66.7%; Pred. No. 8.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
DB |:|:|:| |:|
7 FVSYDYFIV 15

RESULT 5
ABG65310
ID ABG65310 standard; protein; 51 AA.
XX AC
XX ABG65310;
XX
XX 27-AUG-2002 (first entry)
XX
XX Human albumin fusion protein #1985.
XX
XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
XX human serum albumin; HSA; cancer; reproductive disorder;
XX digestive disorder; immune disorder; endocrine disorder;
XX haematopoietic disorder; neural disorder; connective disorder;
XX cytostatic; antinfertility; antinflammatory; antitumor;
XX immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
XX neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
XX osteopathic; antiarthritic.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200177137-A1.
XX

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PD 18-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US011988.
XX
XX 12-APR-2000; 2000US-0229358P.
XX 25-APR-2000; 2000US-0199384P.
XX 21-DEC-2000; 2000US-0256931P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Haseltine WA;
XX WPI: 2002-010886/01.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
XX albumin fused to a therapeutic protein.
XX
XX Claim 1; Page 1908; 2102pp; English.
XX
XX The present invention relates to albumin fusion proteins comprising a
XX therapeutic protein X and human albumin (HA, also known as human serum
XX albumin, HSA). The proteins are useful for treating a disease or disorder
XX that may be modulated by therapeutic protein X. The albumin extends the
XX shelf-life of protein X, and may increase its biological in vitro/in vivo
XX activity. The protein is useful for treating and diagnosing disorders
XX such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
XX disease, ulcerative colitis), immune disorders (e.g. acquired
XX immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
XX haematopoietic disorders, neural disorders (e.g. Alzheimer's,
XX Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
XX schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
XX ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
XX Sequence 51 AA;
SQ
Query Match 80.0%; Score 36; DB 5; Length 51;
Best Local Similarity 66.7%; Pred. No. 8.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
DB |:|:|:| |:|
7 FVSYDYFIV 15

RESULT 6
ADL78577
ID ADL78577 standard; protein; 51 AA.
XX AC
XX ADL78577;
XX
XX 20-MAY-2004 (first entry)
XX
XX Albumin fusion protein related therapeutic protein X, SEQ ID No 2059.
XX
XX albumin fusion protein; cytostatic; antianaemic; antiarthritic;
XX antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory;
XX antipsoriatic; antibacterial; osteopathic; dermatologic; antitumor;
XX immunomodulator; antiarrhythmic; cardiant; neurotropic; antilipaemic;
XX nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;
XX antidiabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer;
XX reproductive system disorder; therapeutic protein.
XX
XX Unidentified.
XX
XX US2004010134-A1.
XX
XX 15-JAN-2004.
XX
XX 12-APR-2001; 2001US-00833245.
XX
XX 12-APR-2000; 2000US-0229358P.
XX 25-APR-2000; 2000US-0199384P.
XX 21-DEC-2000; 2000US-0256931P.
XX

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AC AAG01223;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein, SEQ ID NO: 5304.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-00200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 DR WPI; 2000-500381/45.  
 DR N-PSDB; AAC01229.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 XX  
 PS Claim 13; SEQ ID NO 5304; 71pp + Sequence Listing; English.  
 XX  
 CC The present sequence is a polypeptide encoded by one of a large number of  
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
 CC sequences derived from the 5' ends of mRNAs and even in those cases where  
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
 CC are also used in diagnostic, forensic, gene therapy and chromosome  
 CC mapping procedures. They are used to obtain upstream regulatory sequences  
 CC and to design expression and secretion vectors  
 XX  
 SQ Sequence 85 AA;  
 Query Match 77.8%; Score 35; DB 3; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LSYDLFV 8  
 Db |||||  
 18 LSYDLFV 24  
 RESULT 9  
 AAY17226  
 ID AAY17226 standard; protein; 130 AA.  
 XX  
 AC AAY17226;  
 XX  
 DT 09-AUG-1999 (first entry)  
 XX  
 DE Human secreted protein (clone pe204-1).  
 XX  
 KW Secreted protein; kidney; lung; brain; blood; testis; bone marrow;  
 KW nutritional activity; cytokine; cell proliferation; immune stimulation;  
 KW hematopoiesis regulation; tissue growth; thrombolytic; gene therapy;  
 KW anti-inflammatory; tumour invasion.  
 XX  
 OS Homo sapiens.

XX WO9926961-A1.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PF 24-NOV-1998; 98WO-US025149.  
 XX  
 PR 26-NOV-1997; 97US-0066804P.  
 PR 23-NOV-1998; 98US-00197886.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Wong GG, Clark HF;  
 PI Fechtel K;  
 XX  
 DR WPI; 1999-357809/30.  
 DR N-PSDB; AAX60808.  
 XX  
 PT New polynucleotides encoding secreted proteins.  
 XX  
 PS Claim 34; Page 123; 133pp; English.  
 XX  
 CC The invention relates to secreted proteins (AAV17219-228) encoded by  
 CC polynucleotides obtained from human fetal kidney, adult lung, adult  
 CC kidney, adult brain, adult blood, adult testes, and fetal brain and  
 CC murine adult bone marrow cDNA libraries. The secreted protein nucleic acid  
 CC sequences (X8601-811) correspond to clones bd306-7, gj283-6, fk317-3,  
 CC k213-2x, na316-1, nf93-20, np164-1, pe204-1, yal-1 and yb-1, (all clones  
 CC are deposited as ATCC 98599); The PNS and proteins are predicted to have  
 CC biological activities which would make them suitable for treating,  
 CC preventing or ameliorating medical conditions in humans and animals,  
 CC although no supporting data is given. Suggested activities include  
 CC nutritional activity, cytokine and cell proliferation/differentiation  
 CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,  
 CC hematopoiesis regulating activity, tissue growth activity, activin/  
 CC inhibin activity, chemotactic/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cadherin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity. The PNS are also stated to be useful for gene  
 CC therapy  
 XX  
 SQ Sequence 130 AA;  
 Query Match 77.8%; Score 35; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LSYDLFV 8  
 Db |||||  
 18 LSYDLFV 24  
 RESULT 10  
 AAU38996  
 ID AAU38996 standard; protein; 130 AA.  
 XX  
 AC AAU38996;  
 XX  
 DT 16-JAN-2002 (first entry)  
 XX  
 DE Human secreted protein pe241\_1.  
 XX  
 KW Human; secreted protein; antiinflammatory; immunosuppressive; nootropic;  
 KW neuroprotective; antiarthritic; antimicrobial; vulnerary; cytosclastic;  
 KW antidiabetic; virucide; antifertility; anticonvulsant; vasotonic;  
 KW antiparkinsonian; immunostimulant; dermatological; antirheumatic;  
 KW antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective;  
 KW cytokine; cell proliferation; cell differentiation; immune deficiency;  
 KW severe combined immunodeficiency; SCID; tumour; autoimmune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; graft-versus-host disease;  
 KW myeloid deficiency; wound healing; ulcer; periodontal disease;  
 KW osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease;

KW Huntington's disease; infection; cardiac disease; stroke; sepsis;  
 KW inflammatory bowel disease; contraceptive; immunogen; food supplement;  
 KW vaccine.  
 XX Homo sapiens.  
 OS  
 XX WO200175068-A2.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 22-MAR-2001; 2001WO-US009369.  
 XX  
 XX 30-MAR-2000; 2000US-00539330.  
 XX 04-DEC-2000; 2000US-00729674.  
 XX  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 XX Jacobs K, Mccoy JM, Lavallie E, Collins-Racie LA, Evans C;  
 PI Treacy M, Agostino MJ, Steininger RJ, Spaulding V, Wong GG, Clark H;  
 PI Fechtel K, Merberg D;  
 XX  
 XX WPI; 2001-639363/73.  
 XX N-PSDB; AAS59214.  
 XX  
 XX Secreted human proteins, useful as vaccine for treating various diseases  
 XX such as autoimmune disorders (e.g. multiple sclerosis), and nervous  
 XX system disorders (e.g. stroke).  
 XX  
 XX Disclosure; Page 468-469; 619pp; English.  
 XX  
 CC The invention relates to novel human secreted proteins, the nucleic acids  
 CC encoding them. The protein may exhibit cytokine, cell proliferation or  
 CC cell differentiation activity or may induce production of other cytokines  
 CC in certain cell populations and may exhibit immune stimulating or immune  
 CC suppressing activity, which is useful for the treatment of various immune  
 CC deficiencies and disorders e.g. severe combined immunodeficiency (SCID),  
 CC autoimmune disorders e.g. multiple sclerosis, systemic lupus  
 CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation.  
 CC The proteins are also useful in the treatment of diseases and disorders  
 CC including tissue, skin and organ transplantation and in graft-versus-host  
 CC diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid  
 CC cell deficiencies, wound healing and tissue repair, in the treatment of  
 CC burns, incisions and ulcers; as well as in treatment of periodontal  
 CC disease, osteoporosis or osteoarthritis, mediated by inflammatory  
 CC processes, diseases of the peripheral nervous system, Alzheimer's,  
 CC Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and  
 CC central nervous system vessel e.g. stroke, sepsis, inflammatory bowel  
 CC disease, ulcers, bone regeneration. The protein, having activin- or  
 CC inhibin-related activities is useful as a contraceptive based on the  
 CC ability of inhibins to decrease fertility in female mammals and decrease  
 CC spermatogenesis in male mammals. The proteins and nucleic acids are also  
 CC useful as food supplements. The present sequence represents a secreted  
 CC protein of the invention  
 XX  
 XX Sequence 130 AA;  
 Query Match 77.8%; Score 35; DB 4; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LSYDLFV 8  
 Db 18 LSYDLFV 24  
 |||||  
 RESULT 11  
 ABB55705  
 ID ABB55705 standard; protein; 130 AA.  
 XX  
 AC ABB55705;  
 XX  
 DT 14-FEB-2002 (first entry)

XX Human polypeptide SEQ ID NO 16.  
 DE  
 XX Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy;  
 KW immune disorder; bacterial infection; fungal infection; cancer; tumour;  
 KW autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin;  
 KW osteoporosis; osteoarthritis; nervous system disorder; neuropathy;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; activin;  
 KW haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnery;  
 KW ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic;  
 KW Crohn's disease; cytostatic; anti-inflammatory; immunomodulator;  
 KW neuroprotective; haemostatic; thrombolytic; anti-inflammatory.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US2001039335-A1.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 04-DEC-2000; 2000US-00729674.  
 XX  
 XX 26-NOV-1997; 97US-0126425P.  
 XX 04-DEC-1997; 97US-0067454P.  
 XX 20-DEC-1997; 97US-0068379P.  
 XX 02-JAN-1998; 98US-0070346P.  
 XX 07-JAN-1998; 98US-0070643P.  
 XX 08-JAN-1998; 98US-0070755P.  
 XX 13-JAN-1998; 98US-0071304P.  
 XX 22-JAN-1998; 98US-0072134P.  
 XX 30-JAN-1998; 98US-0073095P.  
 XX 18-FEB-1998; 98US-0075038P.  
 XX 23-NOV-1998; 98US-00197886.  
 XX 30-MAR-2000; 2000US-00539330.  
 XX  
 XX (JACO/) JACOBS K.  
 XX (MCCO/) MCCOY J M.  
 XX (LAVA/) LAVALLIE E R.  
 XX (COLL/) COLLINS-RACIE L A.  
 XX (EVAN/) EVANS C.  
 XX (MERB/) MERBERG D.  
 XX (TREA/) TREACY M.  
 XX (AGOS/) AGOSTINO M J.  
 XX (STEI/) STEININGER R J.  
 XX (SPAU/) SPAULDING V.  
 XX (WONG/) WONG G G.  
 XX (CLAR/) CLARK H.  
 XX (FECH/) FECHTEL K.  
 XX  
 XX Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;  
 PI Wong GG, Clark H, Fechtel K;  
 XX  
 XX WPI; 2002-040725/05.  
 XX N-PSDB; ABA90883.  
 XX  
 XX New secreted proteins and encoding polynucleotides, useful in gene  
 PT therapies, particularly for preventing or treating autoimmune disorders,  
 PT cancer, graft-versus-host disease, wound, osteoporosis, stroke or  
 PT inflammations.  
 XX  
 XX Disclosure; Page 189-190; 349pp; English.  
 XX  
 XX The invention relates to isolated polynucleotides (ABA90876-ABA90968 and  
 CC ABA90980) and encoded proteins (ABB55698-ABB55800), especially  
 CC polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and  
 CC proteins SEQ ID NO 2 (ABB55698) and SEQ ID NO 20 (ABB5707) contained in  
 CC clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1  
 CC are deposited with the American Type Culture Collection (ATCC) with  
 CC accession number 98599. The polynucleotides and encoded polypeptides have  
 CC cytostatic, anti-inflammatory, immunomodulator, vulnery,  
 CC neuroprotective, activin, inhibin, chemotactic, haemostatic, thrombolytic  
 CC and anti-inflammatory activity and acting as cytokine modulators,  
 CC haematopoiesis regulators, tissue growth modulators and/or cadherin

CC suppressors. The polypeptides and polynucleotides are useful in gene  
 CC therapies, particularly for preventing, treating or ameliorating any of  
 CC the following diseases: immune deficiency and disorders; e.g. bacterial  
 CC or fungal infections, autoimmune disorders, cancer, systemic lupus  
 CC erythematosus or graft-versus-host disease; myeloid or lymphoid cell  
 CC deficiencies; wound, burns, incisions and ulcers, osteoporosis or  
 CC osteoarthritis; central and peripheral nervous system diseases and  
 CC disease, e.g. Alzheimer's, Parkinson's disease, Huntington's  
 CC disease, amyotrophic lateral sclerosis or Shy-Drager syndrome;  
 CC haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis  
 CC or systemic inflammatory response syndrome, ischaemia-reperfusion injury,  
 CC endotoxin lethality, arthritis, inflammatory bowel disease or Crohn's  
 CC disease; or tumours or cancers, pemphigus vulgaris or pemphigus foliaceus  
 XX  
 XX Sequence 130 AA;

Query Match 77.8%; Score 35; DB 5; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
 |||||  
 Db 18 LSYDLFV 24

## RESULT 12

ADW09103  
 ID ADW09103 standard; protein; 130 AA.

AC ADW09103;

DT 24-MAR-2005 (first entry)

DE Human secreted protein used to treat autoimmune disorders Seq 16.  
 XX  
 XX autoimmune disease; multiple sclerosis; systemic lupus erythematosus;  
 KW rheumatoid arthritis; myasthenia gravis; immunosuppressive;  
 KW neuroprotective; antiinflammatory; antirheumatic; antiarthritic;  
 KW dermatological; genetic marker; DNA fingerprinting.

OS Homo sapiens.

PN US2005003491-A1.

PD 06-JAN-2005.

PF 09-AUG-2004; 2004US-00913553.

PR 26-NOV-1997; 97US-0126425P.

PR 04-DEC-1997; 97US-0067454P.

PR 20-DEC-1997; 97US-0068379P.

PR 02-JAN-1998; 98US-0070346P.

PR 07-JAN-1998; 98US-0070643P.

PR 08-JAN-1998; 98US-0070755P.

PR 13-JAN-1998; 98US-0071304P.

PR 22-JAN-1998; 98US-0072134P.

PR 30-JAN-1998; 98US-0073095P.

PR 18-FEB-1998; 98US-0075038P.

PR 23-NOV-1998; 98US-00197886.

PR 30-NOV-1998; 98US-00203106.

PR 16-DEC-1998; 98US-00212843.

PR 30-DEC-1998; 98US-00222653.

PR 04-JAN-1999; 99US-00225049.

PR 06-JAN-1999; 99US-00225585.

PR 08-JAN-1999; 99US-00227462.

PR 20-JAN-1999; 99US-00235609.

PR 27-JAN-1999; 99US-00237847.

PR 17-FEB-1999; 99US-00251600.

PR 30-MAR-2000; 2000US-00539330.

PR 04-DEC-2000; 2000US-00729674.

(ON0Y ) ONO PHARM CO LTD.

PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;  
 PI Wong GG, Clark H, Fachtel K;  
 XX  
 XX WPI; 2005-065242/07.  
 DR N-PSDB; ADW09102.  
 XX  
 XX New isolated polynucleotide comprises 1534 bp, useful for treating  
 PT autoimmune disorders, e.g. multiple sclerosis, systemic lupus  
 PT erythematosus, rheumatoid arthritis, or myasthenia gravis.

PS Disclosure; SEQ ID NO 16; 351pp; English.

XX  
 XX This invention relates to novel isolated nucleic acid molecules and  
 CC encoded proteins thereof. Specifically, it refers to a full-length human  
 CC secreted protein identified as clone lp347\_4 deposited with the ATCC  
 CC under accession number 98663, and the polynucleotide cDNA insert and  
 CC fragments derived accordingly. The present invention describes  
 CC transformation of a host cell in order to express and purify the protein  
 CC of choice that can in turn be used in preventing, treating, or  
 CC ameliorating a medical condition. In particular, they are useful for  
 CC treating autoimmune disorders, for example multiple sclerosis, systemic  
 CC lupus erythematosus, rheumatoid arthritis or myasthenia gravis. As such,  
 CC compositions derived thereof exhibit immunosuppressive, neuroprotective,  
 CC antiinflammatory, antirheumatic, antarthritic and dermatological  
 CC activities. Furthermore, they can be used as nutritional sources or  
 CC supplements, as well as for molecular biology methods including tissue  
 CC markers, molecular weight markers for Southern gels, chromosome markers  
 CC or to derive primers and probes for genetic fingerprinting. This  
 CC polypeptide is a human secreted protein of the invention.

XX Sequence 130 AA;

Query Match 77.8%; Score 35; DB 9; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
 |||||  
 Db 18 LSYDLFV 24

## RESULT 13

AAV36168

ID AAV36168 standard; protein; 160 AA.

XX AAV36168;

DT 23-SEP-1999 (first entry)

DE Human secreted protein #40.

XX  
 XX Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;  
 KW diagnostic; gene therapy; chromosome mapping; secretion vector.

XX Homo sapiens.

XX WO9925825-A2.

XX 27-MAY-1999.

XX 13-NOV-1998; 98WO-IB001862.

XX 13-NOV-1997; 97US-0066677P.

XX 17-DEC-1997; 97US-0069957P.

XX 09-FEB-1998; 98US-0074121P.

XX 13-APR-1998; 98US-0081563P.

XX 10-AUG-1998; 98US-0096116P.

XX 04-SEP-1998; 98US-0099273P.

XX (GEST ) GENSET.

XX Bougueleret L, Duclert A, Dumas Milne Edwards J;  
 XX



Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
 Db 18 LSYDLFV 24

RESULT 16  
 AAB88605  
 ID AAB88605 standard; protein; 162 AA.  
 XX AAB88605;  
 XX  
 DT 04-JUN-2001 (first entry)  
 XX Human hydrophobic domain containing protein clone HP10773 #129.  
 DE  
 KW Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;  
 KW antianaemic; vulnery; antiulcer; osteopathic; anti-inflammatory;  
 KW cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;  
 KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;  
 KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;  
 KW behavioural characteristic; immune response.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200112660-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 10-AUG-2000; 2000WO-JP005356.  
 XX  
 PR 17-AUG-1999; 99JP-00230344.  
 PR 07-SEP-1999; 99JP-00252551.  
 PR 01-OCT-1999; 99JP-00281132.  
 PR 22-OCT-1999; 99JP-00301624.  
 PR 04-NOV-1999; 99JP-00313877.  
 XX  
 XX (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 XX  
 PI Kato S, Kimura T;  
 XX  
 XX WPI; 2001-160059/16.  
 DR N-PSDB; AAF94505.  
 XX  
 PT Human proteins with hydrophobic domains and the DNAs which encode them  
 PT are useful for treating autoimmune disorders, burns and tumors and for  
 PT screening novel pharmaceuticals.  
 XX  
 PS Claim 1; Page 478-479; 518pp; English.  
 XX  
 PS AAF94417 to AAF94516 encode the human proteins given in AAB88557 to  
 CC AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,  
 CC anti-HIV, neuroprotective, antianaemic, vulnery, antiulcer,  
 CC osteopathic, anti-inflammatory and cytostatic activities, and can be used  
 CC in gene therapy. (I) can be used as pharmaceuticals and as antigens to  
 CC prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes  
 CC for genetic diagnosis and gene sources for gene therapy or for producing  
 CC (I) in large quantities. Cells containing (II) are used for the detection  
 CC of ligands or receptors corresponding to membrane or secretory proteins  
 CC and to screen small molecule novel pharmaceuticals. Antibodies directed  
 CC to (I) can be used for the detection, quantification and purification of  
 CC (I). Activities of (I) may include cytokine and cell  
 CC proliferation/differentiation function, immune stimulating or suppressing  
 CC activity, haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory  
 CC activity. (I) and (II) can be used to treat autoimmune disorders e.g.  
 CC multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,  
 CC inflammatory bowel disease and tumours. (I) and (II) can also be used for  
 CC wound healing, as nutritional sources or supplements e.g. as amino acid,  
 CC carbon or nitrogen source, to effect metabolism, catabolism, anabolism,

CC processing and utilisation of dietary fat, protein, carbohydrate,  
 CC vitamins and minerals, to effect behavioural characteristics, to affect  
 CC appetite, and can act as antigens in vaccines to raise an immune response  
 CC to the protein or another material cross-reactive with the protein  
 XX  
 SQ Sequence 162 AA;

Query Match 77.8%; Score 35; DB 4; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
 Db 18 LSYDLFV 24

RESULT 17  
 ABB89619  
 ID ABB89619 standard; protein; 162 AA.  
 XX ABB89619;  
 AC ABB89619;  
 XX  
 DT 24-MAY-2002 (first entry)  
 XX Human polypeptide SEQ ID NO 1995.  
 DE  
 XX  
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antiulcer;  
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200190304-A2.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 18-MAY-2001; 2001WO-US016450.  
 XX  
 PR 19-MAY-2000; 2000US-0205515P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Birse CB, Rosen CA;  
 XX  
 XX WPI; 2002-122018/16.  
 DR N-PSDB; ABL90028.  
 XX  
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
 PT prevention of neural, immune system, muscular, reproductive,  
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
 PT disorders.  
 XX  
 PS Claim 11; SEQ ID NO 1995; 2081pp + Sequence Listing; English.  
 XX  
 PS The invention relates to novel genes (ABL89449-ABL90853) and proteins  
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, diabetes mellitus, Crohn's disease,  
 CC anaemia, autoimmune thyroiditis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC multiple sclerosis, rheumatoid arthritis and ischaemic colitis; (d) wound healing  
 CC cardiovascular disorders such as myocardial ischaemia; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC ; (e) neurological diseases such as viral, bacterial, fungal and parasitic  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 162 AA;  
 Query Match 77.8%; Score 35; DB 5; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLFV 8  
 Db 18 LSYDLFV 24  
 |||||

RESULT 18  
 ABP65087  
 ID ABP65087 standard; protein; 162 AA.  
 XX  
 AC ABP65087;  
 XX  
 DT 12-NOV-2002 (first entry)  
 XX  
 DE Hypoxia-repressed protein #10.  
 XX  
 KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;  
 KW antiinflammatory; vulnerary; synecological; ophthalmological; vaccine;  
 KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
 KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
 KW preeclampsia; atherosclerosis; inflammatory condition; wound healing;  
 KW inflammation; erythropoiesis; hair loss; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200246465-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PP 10-DEC-2001; 2001WO-GB005458.  
 XX  
 PR 08-DEC-2000; 2000GB-00030076.  
 PR 08-FEB-2001; 2001GB-00003156.  
 PR 25-OCT-2001; 2001GB-00025666.  
 XX  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 PI White J, Mundy CR, Ward NR, Krige D, Kingeman SM, Harris RA;  
 PI Rayner WN;  
 XX  
 DR WPI; 2002-627238/67.  
 XX  
 PT Identifying a gene involved in disease for treating hypoxia-regulated  
 PT conditions, comprises comparing the transcriptome/proteome of two cell  
 PT types under different conditions and identifying a differentially  
 PT regulated gene.  
 XX  
 PS Claim 13; Page 289; 538pp; English.  
 XX  
 CC The present invention relates to methods for identifying genes and  
 CC proteins that are implicated in a specific disease or physiological  
 CC condition. The method comprises comparing the transcriptome/proteome of a  
 CC specialised cell type implicated in a disease or condition with that of a  
 CC second specialised cell type, under two experimental conditions, and  
 CC identifying a gene that is differentially regulated in the two  
 CC specialised cell types under experimental conditions. ABV778116  
 CC and ABP65061-ABP65257 were identified using the methods of the invention.  
 CC The coding sequences and proteins are useful for treating a disease in a  
 CC patient, for manufacture of a medicament for treating hypoxia-regulated  
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,  
 CC biological response to hypoxia conditions, or hypoxic-associated  
 CC pathology in a patient. The coding sequences and proteins are also useful  
 CC for monitoring the therapeutic treatment of a disease or physiological  
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,  
 CC retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory  
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss

XX SQ Sequence 162 AA;  
 Query Match 77.8%; Score 35; DB 5; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLFV 8  
 Db 18 LSYDLFV 24  
 |||||

RESULT 19  
 ADD19028  
 ID ADD19028 standard; protein; 162 AA.  
 XX  
 AC ADD19028;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human disease related protein SeqID517.  
 XX  
 KW human; disease state; cytostatic; antiinflammatory; ophthalmological;  
 KW antiarteriosclerotic; vulnerary; gene therapy;  
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;  
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;  
 KW glucose transportation; catecholamine synthesis; iron transport;  
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;  
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;  
 KW inflammatory condition; wound healing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003018621-A2.  
 XX  
 PD 06-MAR-2003.  
 XX  
 PP 23-AUG-2002; 2002WO-GB003892.  
 XX  
 PR 23-AUG-2001; 2001GB-00020558.  
 PR 05-OCT-2001; 2001GB-00024037.  
 XX  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 PI Kingeman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;  
 PI WPI; 2003-290046/28.  
 XX  
 DR N-PSDB; ADD19029.  
 XX  
 PT New substantially purified polypeptide, useful for diagnosing or treating  
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion  
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or  
 PT wound healing.  
 XX  
 PS Claim 1; SEQ ID NO 517; 424pp; English.  
 XX  
 CC This invention relates to novel human genes and gene product which are  
 CC implicated in certain disease states. Compounds which modulate the  
 CC proteins of the invention may have cytostatic, antiinflammatory, the  
 CC ophthalmological, antiarteriosclerotic or vulnerary activities. The  
 CC sequences of the invention may be useful for gene therapy. The invention  
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,  
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,  
 CC erythropoiesis, or the biological response to hypoxia conditions  
 CC including processes such as glycolysis, gluconeogenesis, glucose  
 CC transportation, catecholamine synthesis, iron transport or nitric oxide  
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion  
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,  
 CC inflammatory conditions or wound healing. The present sequence is that of  
 CC a disease related protein of the invention.  
 XX  
 SQ Sequence 162 AA;  
 Query Match 77.8%; Score 35; DB 7; Length 162;

Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
      |||||  
Db 18 LSYDLFV 24

RESULT 20  
ADJ45973  
ID ADJ45973 standard; protein; 162 AA.  
AC ADJ45973;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Novel human secreted protein-related protein sequence SeqID126.  
XX  
KW secreted protein; upstream regulator; gene therapy; protein purification;  
KW protein synthesis; chromosomal mapping; individual identification;  
KW forensic; hereditary disease; drug reaction; immunoassay;  
KW epitope mapping; vaccine; immune system regulation;  
KW haematopoietic system; tissue growth; reproductive hormone;  
KW cell migration; blood clotting; receptor/ligand interaction;  
KW adhesion molecule; assisted drug delivery;  
KW human glial maturation factor gamma-2; neurite outgrowth;  
KW neurite resprouting; human.  
XX  
OS Homo sapiens.  
XX  
PN US2003144490-A1.  
XX  
PD 31-JUL-2003.  
XX  
PF 10-DEC-2002; 2002US-00319763.  
XX  
PR 13-NOV-1997; 97US-0066677P.  
PR 17-DEC-1997; 97US-0069957P.  
PR 09-FEB-1998; 98US-0074121P.  
PR 13-APR-1998; 98US-0081563P.  
PR 10-AUG-1998; 98US-0096116P.  
PR 04-SEP-1998; 98US-0099273P.  
PR 13-NOV-1998; 98US-00191997.  
PR 15-SEP-2000; 2000US-00663600.  
XX  
(EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLETT A.  
PA (BOUG/) BOUGUELERET L.  
XX  
PI Edwards JDM, Duclert A, Bougueleret L;  
XX  
XX WPI; 2003-851788/79.  
DR N-PSDB; ADJ45926.  
XX  
XX New nucleic acid encoding secreted human polypeptides, useful e.g. in  
PT Gene therapy or diagnosis, also encoded proteins, potential therapeutic  
PT agents.  
XX  
XX Example 28; SEQ ID NO 126; 269pp; English.  
XX  
XX This invention relates to novel purified isolated polynucleotides which  
CC comprise a sequence that encodes at least 10 amino acids (aa) from any of  
CC 48 secreted polypeptide sequences, given in the specification, or  
CC fragments of polypeptides encoded by human cDNA contained in the  
CC corresponding deposited clone. The DNA sequences of the invention encode  
CC secreted proteins (or their fragments) and can be used to  
CC identify/isolate upstream regulators, potentially useful in gene therapy  
CC or protein purification, by controlling protein synthesis, as probes for  
CC chromosomal mapping, identification of individuals, and for diagnosis or  
CC forensics, for example identifying genes associated with hereditary  
CC diseases or drug reactions, for recombinant expression of the encoded  
CC proteins or, where the DNA sequence encodes a signal peptide, for  
CC directing secretion of heterologous polypeptides. Polypeptides encoded by

CC the DNA sequences of the invention can be used to raise antibodies,  
CC useful for detecting the polypeptide, as (ant)agonists, or for preparing  
CC anti-idiotypic antibodies, as tags in for example immunoassays, epitope  
CC mapping or vaccines, also as molecular weight markers, to screen for  
CC agents with biological activity and as therapeutic agents with,  
CC potentially, a very wide range of activities, for example regulation of  
CC the immune or haematopoietic systems, tissue growth, reproductive  
CC hormones, cell migration, blood clotting or receptor/ligand interaction,  
CC also as adhesion molecules for assisted drug delivery. A typical isolated  
CC sequence is human glial maturation factor gamma-2, which stimulates  
CC neurite outgrowth and resprouting. The present sequence is that of a  
CC signal and partial mature sequence of a human secreted protein of the  
CC invention.  
XX  
SQ Sequence 162 AA;

Query Match 77.8%; Score 35; DB 7; Length 162;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
      |||||  
Db 18 LSYDLFV 24

## RESULT 21

ID ADJ46067  
ADJ46067 standard; protein; 162 AA.

AC ADJ46067;

XX 06-MAY-2004 (first entry)

DE Novel human secreted protein-related protein sequence SeqID220.

XX secreted protein; upstream regulator; gene therapy; protein purification;  
KW protein synthesis; chromosomal mapping; individual identification;  
KW forensic; hereditary disease; drug reaction; immunoassay;  
KW epitope mapping; vaccine; immune system regulation;  
KW haematopoietic system; tissue growth; reproductive hormone;  
KW cell migration; blood clotting; receptor/ligand interaction;  
KW adhesion molecule; assisted drug delivery;  
KW human glial maturation factor gamma-2; neurite outgrowth;  
KW neurite resprouting; human.

OS Homo sapiens.

XX US2003144490-A1.

XX 31-JUL-2003.

XX 10-DEC-2002; 2002US-00319763.

XX 13-NOV-1997; 97US-0066677P.

XX 17-DEC-1997; 97US-0069957P.

XX 09-FEB-1998; 98US-0074121P.

XX 13-APR-1998; 98US-0081563P.

XX 10-AUG-1998; 98US-0096116P.

XX 04-SEP-1998; 98US-0099273P.

XX 13-NOV-1998; 98US-00191997.

XX 15-SEP-2000; 2000US-00663600.

XX (EDWA/) EDWARDS J D M.

PA (DUCL/) DUCLETT A.

PA (BOUG/) BOUGUELERET L.

XX Edwards JDM, Duclert A, Bougueleret L;

XX WPI; 2003-851788/79.

XX N-PSDB; ADJ46020.

XX New nucleic acid encoding secreted human polypeptides, useful e.g. in  
PT gene therapy or diagnosis, also encoded proteins, potential therapeutic



PT agents.

PS Claim 11; SEQ ID NO 220; 269pp; English.

XX This invention relates to novel purified isolated polynucleotides which

CC comprise a sequence that encodes at least 10 amino acids (aa) from any of

CC 48 secreted polypeptide sequences, given in the specification, or

CC fragments of polypeptides encoded by human cDNA contained in the

CC corresponding deposited clone. The DNA sequences of the invention encode

CC secreted proteins (or their fragments) and can be used to

CC identify/isolate upstream regulators, potentially useful in gene therapy

CC or protein purification, by controlling protein synthesis, as probes for

CC chromosomal mapping, identification of individuals, and for diagnosis or

CC forensics, for example identifying genes associated with hereditary

CC diseases or drug reactions, for recombinant expression of the encoded

CC proteins or, where the DNA sequence encodes a signal peptide, for

CC directing secretion of heterologous polypeptides. Polypeptides encoded by

CC the DNA sequences of the invention can be used to raise antibodies,

CC useful for detecting the polypeptide, as (ant)agonists, or for preparing

CC anti-idiotypic antibodies, as tags in for example immunoassays, epitope

CC mapping or vaccines, also as molecular weight markers, to screen for

CC agents with biological activity and as therapeutic agents with,

CC potentially, a very wide range of activities, for example regulation of

CC the immune or haematopoietic systems, tissue growth, reproductive

CC hormones, cell migration, blood clotting or receptor/ligand interaction,

CC also as adhesion molecules for assisted drug delivery. A typical isolated

CC sequence is human glial maturation factor gamma-2, which stimulates

CC neurite outgrowth and resprouting. The present sequence is that of a

CC human secreted protein of the invention.

XX SQ Sequence 162 AA;

Query Match 77.8%; Score 35; DB 7; Length 162;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8

Db 18 LSYDLFV 24

RESULT 22

ADP19476

ID ADP19476 standard; protein; 162 AA.

AC ADP19476;

XX 26-AUG-2004 (first entry)

DE Human secreted polypeptide #327.

XX Human; secreted protein; genetic disease.

OS Homo sapiens.

XX US2004110939-A1.

PN 10-JUN-2004.

PD 15-OCT-2001; 2001US-00978360.

XX 17-DEC-1998; 98WO-IB002122.

PR 09-FEB-1999; 99WO-IB000282.

PR 21-JUN-2000; 2000WO-IB000951.

PR 15-SEP-2000; 2000US-00663600.

XX (GEST ) GENSET SA.

PA Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;

PI Duclert A;

XX WPI; 2004-440404/41.

DR N-PSDB; ADP19071.

XX New isolated polynucleotide encoding secreted polypeptide, useful for gene therapy, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes.

PS Claim 2; SEQ ID NO 732; 113pp; English.

XX The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polynucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing human tissues and cells from non-human tissues and cells, and for distinguishing between human tissues and cells that do or do not express the polynucleotides comprising the cDNAs. The polynucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence represents a human secreted polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 162 AA;

Query Match 77.8%; Score 35; DB 8; Length 162;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8

Db 18 LSYDLFV 24

RESULT 23

ADP55495

ID ADP55495 standard; protein; 162 AA.

AC ADP55495;

XX 18-NOV-2004 (first entry)

DE Human PRO protein sequence SEQ ID NO:1471.

XX human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianemic; antiarthritic; antirheumatic; antidiabetic; antiinflammatory; antipsoriatic; antihemostatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy.

XX Homo sapiens.

XX WO2004039956-A2.

PN 13-MAY-2004.

PD 28-OCT-2003; 2003WO-US034381.

PF 29-OCT-2002; 2002US-0422472P.

PR (GETH ) GENENTECH INC.

PA Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;

PI Wood WI, Wu TD;

XX WPI; 2004-376182/35.

DR N-PSDB; ADP55494.

XX New PRO polynucleotides and polypeptides, useful in diagnosing and treating an immune related disease, e.g. systemic lupus

PT erythematous, rheumatoid arthritis, diabetes mellitus or asthma and in  
PT stimulating an immune response.

PS Claim 1; SEQ ID NO 1471; 309pp; English.

XX The present invention describes an isolated PRO nucleic acid (I). Also  
CC described: (1) a vector comprising (I); (2) a host cell comprising the  
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
CC antibody which specifically binds to a polypeptide of (4); (7) a  
CC composition of matter comprising a polypeptide of (4), an agonist or  
CC antagonist of the polypeptide or an antibody that binds to the  
CC polypeptide in combination with a carrier; (8) an article of manufacture  
CC comprising a container, a label on the container and a composition of  
CC matter of (7); (9) a method of treating an immune related disease in a  
CC mammal; (10) a method for determining the presence of a PRO polypeptide  
CC in a sample suspected of having the polypeptide; (11) a method of  
CC diagnosing an immune related disease or an inflammatory immune response  
CC in mammal; (12) a method of identifying a compound that inhibits or  
CC mimics the activity of or expression of a gene encoding a PRO polypeptide  
CC ; and (13) a method of stimulating the immune response in a mammal. The  
CC PRO sequences have anti-allergic, anti-naeemic, antiarthritic,  
CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,  
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,  
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,  
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
CC virucide activities, and can be used in gene therapy. The nucleic acid  
CC (I) and the encoded polypeptides, compositions, kits and methods are  
CC useful in diagnosing and treating an immune related disease and in  
CC stimulating an immune response. The present sequence represents a human  
CC PRO protein from the present invention.

XX SQ Sequence 162 AA;

Query Match 77.8%; Score 35; DB 8; Length 162;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
|||||

RESULT 24  
AAW74871  
ID AAW74871 standard; protein; 163 AA.

XX AC AAW74871;

XX DT 25-JAN-1999 (first entry)

XX DE Human secreted protein encoded by gene 143 clone HBWDM46.

XX KW Human; secreted protein; testis; tumour; foetal brain tissue;  
KW fusion protein; cancer; central nervous system; seizure; diagnosis;  
KW neurodegenerative disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 163 /label= unknown

XX FT W09839448-A2.

XX PN 11-SEP-1998.

XX PF 06-MAR-1998; 98WO-US004493.

XX PR 07-MAR-1997; 97US-0038621P.

XX PR 07-MAR-1997; 97US-0040161P.

XX PR 07-MAR-1997; 97US-0040162P.

PR 07-MAR-1997; 97US-0040163P.  
PR 07-MAR-1997; 97US-0040333P.  
PR 07-MAR-1997; 97US-0040334P.  
PR 07-MAR-1997; 97US-0040336P.  
PR 07-MAR-1997; 97US-0040626P.  
PR 11-APR-1997; 97US-0043311P.  
PR 11-APR-1997; 97US-0043312P.  
PR 11-APR-1997; 97US-0043313P.  
PR 11-APR-1997; 97US-0043314P.  
PR 11-APR-1997; 97US-0043315P.  
PR 11-APR-1997; 97US-0043568P.  
PR 11-APR-1997; 97US-0043569P.  
PR 11-APR-1997; 97US-0043576P.  
PR 11-APR-1997; 97US-0043578P.  
PR 11-APR-1997; 97US-0043580P.  
PR 11-APR-1997; 97US-0043669P.  
PR 11-APR-1997; 97US-0043670P.  
PR 11-APR-1997; 97US-0043671P.  
PR 11-APR-1997; 97US-0043672P.  
PR 11-APR-1997; 97US-0043674P.  
PR 23-MAY-1997; 97US-0047492P.  
PR 23-MAY-1997; 97US-0047500P.  
PR 23-MAY-1997; 97US-0047501P.  
PR 23-MAY-1997; 97US-0047502P.  
PR 23-MAY-1997; 97US-0047503P.  
PR 23-MAY-1997; 97US-0047581P.  
PR 23-MAY-1997; 97US-0047582P.  
PR 23-MAY-1997; 97US-0047583P.  
PR 23-MAY-1997; 97US-0047584P.  
PR 23-MAY-1997; 97US-0047585P.  
PR 23-MAY-1997; 97US-0047586P.  
PR 23-MAY-1997; 97US-0047587P.  
PR 23-MAY-1997; 97US-0047588P.  
PR 23-MAY-1997; 97US-0047589P.  
PR 23-MAY-1997; 97US-0047590P.  
PR 23-MAY-1997; 97US-0047592P.  
PR 23-MAY-1997; 97US-0047593P.  
PR 23-MAY-1997; 97US-0047594P.  
PR 23-MAY-1997; 97US-0047595P.  
PR 23-MAY-1997; 97US-0047596P.  
PR 23-MAY-1997; 97US-0047597P.  
PR 23-MAY-1997; 97US-0047598P.  
PR 23-MAY-1997; 97US-0047599P.  
PR 23-MAY-1997; 97US-0047600P.  
PR 23-MAY-1997; 97US-0047601P.  
PR 23-MAY-1997; 97US-0047612P.  
PR 23-MAY-1997; 97US-0047613P.  
PR 23-MAY-1997; 97US-0047614P.  
PR 23-MAY-1997; 97US-0047615P.  
PR 23-MAY-1997; 97US-0047617P.  
PR 23-MAY-1997; 97US-0047618P.  
PR 23-MAY-1997; 97US-0047632P.  
PR 23-MAY-1997; 97US-0047633P.  
PR 06-JUN-1997; 97US-0048964P.  
PR 06-JUN-1997; 97US-0048974P.  
PR 13-JUN-1997; 97US-0049610P.  
PR 08-JUL-1997; 97US-0051926P.  
PR 16-JUL-1997; 97US-0052874P.  
PR 18-AUG-1997; 97US-0055724P.  
PR 22-AUG-1997; 97US-0056630P.  
PR 22-AUG-1997; 97US-0056631P.  
PR 22-AUG-1997; 97US-0056632P.  
PR 22-AUG-1997; 97US-0056633P.  
PR 22-AUG-1997; 97US-0056634P.  
PR 22-AUG-1997; 97US-0056662P.  
PR 22-AUG-1997; 97US-0056664P.  
PR 22-AUG-1997; 97US-0056845P.  
PR 22-AUG-1997; 97US-0056862P.  
PR 22-AUG-1997; 97US-0056864P.  
PR 22-AUG-1997; 97US-0056872P.  
PR 22-AUG-1997; 97US-0056875P.  
PR 22-AUG-1997; 97US-0056876P.

PR 22-AUG-1997; 97US-0056877P.  
PR 22-AUG-1997; 97US-0056878P.  
PR 22-AUG-1997; 97US-0056879P.  
PR 22-AUG-1997; 97US-0056880P.  
PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
PR 22-AUG-1997; 97US-0056886P.  
PR 22-AUG-1997; 97US-0056887P.  
PR 22-AUG-1997; 97US-0056888P.  
PR 22-AUG-1997; 97US-0056889P.  
PR 22-AUG-1997; 97US-0056892P.  
PR 22-AUG-1997; 97US-0056893P.  
PR 22-AUG-1997; 97US-0056894P.  
PR 22-AUG-1997; 97US-0056903P.  
PR 22-AUG-1997; 97US-0056908P.  
PR 22-AUG-1997; 97US-0056909P.  
PR 22-AUG-1997; 97US-0056910P.  
PR 22-AUG-1997; 97US-0056911P.  
PR 05-SEP-1997; 97US-0057650P.  
PR 05-SEP-1997; 97US-0057669P.  
PR 05-SEP-1997; 97US-0057761P.  
PR 12-SEP-1997; 97US-0058785P.  
PR 02-OCT-1997; 97US-0061060P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;  
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;  
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Eher R, Brewer LA;  
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX  
DR MPI; 1998-506364/43.  
DR N-PSDB; AAV59653.  
XX  
XX  
PT New isolated human genes and the secreted polypeptide(s) they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.  
XX  
PS Claim 1; Page 626-627; 721pp; English.  
XX  
CC This sequence represents a secreted human protein encoded by the nucleic  
CC acid molecule designated Gene 18MDM46 from the human cDNA clone HTRE221  
CC (deposited as clone ATCC 97302 and ATCC 209048). The gene can be used to  
CC generate fusion proteins by linking to the gene to a human immunoglobulin  
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused  
CC protein as compared to the human protein only. The invention relates to  
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-  
CC V59812; amino acid sequences AAW74731-W75026) which are useful for  
CC preventing, treating or ameliorating medical conditions e.g. by protein  
CC or gene therapy. Also, pathological conditions can be diagnosed by  
CC determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new polynucleotides.  
CC Specific uses are described for each of the 186 polynucleotides, based on  
CC which tissues they are most highly expressed in (see AAV59511 for  
CC described uses)  
XX  
SQ Sequence 163 AA;  
Query Match 77.8%; Score 35; DB 2; Length 163;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
RESULT 25  
ABG95322  
ID ABG95322 standard; protein; 163 AA.  
XX  
AC ABG95322;

XX  
DT 15-JAN-2003 (first entry)  
XX Human novel secreted protein #143.  
DE  
XX  
XX Human; secreted protein; autoimmune disease; chemotaxis;  
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;  
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;  
KW nervous system disorders; Alzheimer's disease; infection;  
KW ocular disorder; corneal infection; wound healing; tissue regeneration;  
KW epithelial cell proliferation; organ transplantation; food additive;  
KW preservative; nutritional.  
XX  
OS Homo sapiens.  
XX  
XX US6420526-B1.  
PN  
XX  
XX 16-JUL-2002.  
PD  
XX  
XX 08-SEP-1998; 98US-00149476.  
XX  
PR 07-MAR-1997; 97US-0038621P.  
PR 07-MAR-1997; 97US-0040161P.  
PR 07-MAR-1997; 97US-0040162P.  
PR 07-MAR-1997; 97US-0040163P.  
PR 07-MAR-1997; 97US-0040333P.  
PR 07-MAR-1997; 97US-0040334P.  
PR 07-MAR-1997; 97US-0040336P.  
PR 07-MAR-1997; 97US-0040626P.  
PR 11-APR-1997; 97US-0043311P.  
PR 11-APR-1997; 97US-0043312P.  
PR 11-APR-1997; 97US-0043313P.  
PR 11-APR-1997; 97US-0043314P.  
PR 11-APR-1997; 97US-0043315P.  
PR 11-APR-1997; 97US-0043568P.  
PR 11-APR-1997; 97US-0043569P.  
PR 11-APR-1997; 97US-0043576P.  
PR 11-APR-1997; 97US-0043578P.  
PR 11-APR-1997; 97US-0043580P.  
PR 11-APR-1997; 97US-0043669P.  
PR 11-APR-1997; 97US-0043670P.  
PR 11-APR-1997; 97US-0043671P.  
PR 11-APR-1997; 97US-0043672P.  
PR 11-APR-1997; 97US-0043674P.  
PR 23-MAY-1997; 97US-0047492P.  
PR 23-MAY-1997; 97US-0047500P.  
PR 23-MAY-1997; 97US-0047501P.  
PR 23-MAY-1997; 97US-0047502P.  
PR 23-MAY-1997; 97US-0047503P.  
PR 23-MAY-1997; 97US-0047581P.  
PR 23-MAY-1997; 97US-0047582P.  
PR 23-MAY-1997; 97US-0047583P.  
PR 23-MAY-1997; 97US-0047584P.  
PR 23-MAY-1997; 97US-0047585P.  
PR 23-MAY-1997; 97US-0047586P.  
PR 23-MAY-1997; 97US-0047587P.  
PR 23-MAY-1997; 97US-0047588P.  
PR 23-MAY-1997; 97US-0047589P.  
PR 23-MAY-1997; 97US-0047590P.  
PR 23-MAY-1997; 97US-0047592P.  
PR 23-MAY-1997; 97US-0047593P.  
PR 23-MAY-1997; 97US-0047594P.  
PR 23-MAY-1997; 97US-0047595P.  
PR 23-MAY-1997; 97US-0047596P.  
PR 23-MAY-1997; 97US-0047597P.  
PR 23-MAY-1997; 97US-0047598P.  
PR 23-MAY-1997; 97US-0047599P.  
PR 23-MAY-1997; 97US-0047600P.  
PR 23-MAY-1997; 97US-0047601P.  
PR 23-MAY-1997; 97US-0047612P.  
PR 23-MAY-1997; 97US-0047613P.  
PR 23-MAY-1997; 97US-0047614P.



PR 11-APR-1997; 97US-0043315P.  
 PR 11-APR-1997; 97US-00433568P.  
 PR 11-APR-1997; 97US-00433569P.  
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 XX  
 (RUBE/) RUBEN S M.  
 (ROSE/) ROSEN C A.  
 (SOPP/) SOPPET D R.  
 (CART/) CARTER K C.  
 (BEDN/) BEDNARIK D P.  
 (ENDR/) ENDRESS G A.  
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 (NIJG/) NI J.  
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 (YOUN/) YOUNG P E.  
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 (HUJJ/) HU J.  
 (FLOR/) FLORENCE K A.  
 (OLSE/) OLSEN H S.  
 (FISC/) FISCHER C L.  
 (EBNE/) EBNER R.  
 (BREW/) BREWER L A.  
 (MOOR/) MOORE P A.  
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 (LAF/) LAFLEUR D W.  
 (LIYY/) LI Y.  
 (ZENG/) ZENG Z.  
 (KYAW/) KYAW H.  
 XX  
 Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
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 Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
 Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 WPI: 2003-521800/49.  
 DR N-PSDB; ACD82783.  
 XX  
 New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.  
 PS Claim 3; SEQ ID NO 462; 260pp; English.  
 XX  
 The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The invention also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polynucleotide sequences for the secreted proteins are useful for preventing, treating, ameliorating or diagnosing medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive disorders, blood-related disorders (e.g. haemophilia or thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease, multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma), viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina

CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
 CC disorders, neurological disorders (e.g. Alzheimer's disease or  
 CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
 CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
 CC ABO34374-ABO34815 represent human secreted proteins or their fragments.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC USPTO web site at seqdata.uspto.gov/paipatIDEntry.html  
 XX  
 SQ Sequence 163 AA;

Query Match 77.8%; Score 35; DB 6; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
 |||||  
 Db 18 LSYDLFV 24

## RESULT 27

AD123177  
 ID AD123177 standard; protein; 163 AA.

AC  
 AD123177;

DT 22-APR-2004 (first entry)

DE Novel human secreted protein seq id 462.

XX cytotstatic; gene therapy; cancer; human; secreted protein.

XX Homo sapiens.

XX US2003175858-A1.

XX 18-SEP-2003.

XX 18-JUN-2001; 2001US-00882171.

XX 07-MAR-1997; 97US-0038621P.

XX 07-MAR-1997; 97US-0040162P.

XX 07-MAR-1997; 97US-0040163P.

XX 07-MAR-1997; 97US-0040333P.

XX 07-MAR-1997; 97US-0040334P.

XX 07-MAR-1997; 97US-0040336P.

XX 07-MAR-1997; 97US-0040626P.

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 PR 22-AUG-1997; 97US-0056881P.  
 PR 22-AUG-1997; 97US-0056882P.  
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 PR 22-AUG-1997; 97US-0056888P.  
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 PR 06-MAR-1998; 98WO-US004493.  
 PR 08-SEP-1998; 98WO-00149476.  
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 PR 16-MAR-2001; 2001US-00809391.  
 (RUBE/) RUBEN S M.  
 (ROSE/) ROSEN C A.

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PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX  
DR WPI; 2003-898535/82.  
DR N-PSDB; ADI22868.  
XX  
XX  
PT New nucleic acid molecule, useful for preparing a medicament for  
PT diagnosing, preventing, treating or ameliorating a medical condition  
PT e.g., cancer.  
XX  
PS Claim 11; SEQ ID NO 462; 256pp; English.  
XX  
CC The invention describes an isolated nucleic acid comprising a sequence  
CC having 95 % identity with: a polynucleotide fragment of a sequence not  
CC given in the specification, or its allelic variant; a polynucleotide  
CC fragment of the cDNA sequence; a polynucleotide sequence encoding a  
CC polypeptide, or its fragment, domain, epitope or species homologue; or a  
CC polynucleotide that hybridises under stringent conditions to any one of  
CC the sequences of (a)-(c). The nucleic acid is useful for preparing a  
CC medicament for diagnosing, preventing, treating or ameliorating a medical  
CC condition e.g., cancer. The is the amino acid sequence of a novel human  
CC secreted protein of the invention.  
XX  
SQ Sequence 163 AA;  
Query Match 77.8%; Score 35; DB 7; Length 163;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
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RESULT 28  
ADH74179  
ID ADH74179 standard; protein; 163 AA.  
XX  
AC ADH74179;  
XX  
XX 25-MAR-2004 (first entry)  
XX  
XX Human secreted protein #143.  
XX human; secreted protein; cancer; haematopoietic disorder;  
XX endocrine disorder; immune system disease; inflammatory disorder.  
XX  
OS Homo sapiens.  
XX US2003225248-A1.  
XX  
XX 04-DEC-2003.  
XX  
XX 10-JUN-2002; 2002US-00164861.  
XX  
XX 07-MAR-1997; 97US-0038621P.  
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XX 16-JUL-1997; 97US-0052874P.  
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XX 22-AUG-1997; 97US-0056631P.  
XX 22-AUG-1997; 97US-0056632P.

PR 22-AUG-1997; 97US-0056636P.  
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PR 22-AUG-1997; 97US-0056662P.  
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PR 22-AUG-1997; 97US-0056874P.  
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PR 22-AUG-1997; 97US-0056879P.  
PR 22-AUG-1997; 97US-0056880P.  
PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
PR 22-AUG-1997; 97US-0056886P.  
PR 22-AUG-1997; 97US-0056887P.  
PR 22-AUG-1997; 97US-0056888P.  
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PR 05-SEP-1997; 97US-0057761P.  
PR 12-SEP-1997; 97US-0058785P.  
PR 02-OCT-1997; 97US-0061060P.  
PR 06-MAR-1998; 98WO-US004493.  
PR 08-SEP-1998; 98US-00149476.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Rosen CA, Carter DR, Soppet DR, Bednarik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX  
DR WPI; 2004-131264/13.  
DR N-PSDB; ADH73870.  
XX  
PT Isolated nucleic acid molecules encoding human secreted proteins, useful  
PT for preventing, diagnosing and treating disorders associated with  
PT aberrant expression and activity.  
XX  
PS Claim 11; SEQ ID NO 462; 142pp; English.  
XX  
CC The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and its complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbant assay (ELISA)). The present sequence  
CC represents the amino acid sequence of a human secreted protein.

XX SQ Sequence 163 AA;  
SQ  
Query Match 77.8%; Score 35; DB 8; Length 163;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFV 8  
DB 18 LSYDLFV 24  
RESULT 29  
ABB97496  
ID ABB97496 standard; protein; 177 AA.  
XX ABB97496;  
XX 27-JUN-2002 (first entry)  
XX Novel human protein SEQ ID NO: 764.  
XX Human; antianaemic; vulnary; antiinflammatory; immunomodulator;  
KW antifertility; cerebroprotective; cytostatic; rheumatic; gene therapy;  
KW neuroprotective; antiparkinsonian; protein therapy; EST;  
KW expressed sequence tag.  
XX Homo sapiens.  
XX WO200222660-A2.  
XX 21-MAR-2002.  
XX 10-SEP-2001; 2001WO-US026015.  
XX 11-SEP-2000; 2000US-00659671.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX WPI; 2002-292408/33.  
DR N-PSDB; ABR32682.  
XX  
PT An isolated polynucleotide for treating diseases associated with its  
PT encoded polypeptide such as cancer and multiple sclerosis.  
XX  
PS Claim 20; SEQ ID NO 764; 509pp; English.  
XX  
CC The present invention provides the protein and coding sequences of 444  
CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke  
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.  
CC rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC Parkinson's disease. The present sequence is a protein of the invention  
XX  
SQ Sequence 177 AA;  
SQ  
Query Match 77.8%; Score 35; DB 5; Length 177;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFV 8  
DB 18 LSYDLFV 24  
RESULT 30



```

AAE25673
ID  AAE25673 standard; protein; 203 AA.
XX
AC  AAE25673;
XX
XX  29-AUG-2003 (revised)
DT  04-NOV-2002 (first entry)
DT
DE  Bacillus stearothermophilus BstYI endonuclease protein.
DE
DE  Recombinant DNA; BstYI restriction endonuclease; BstY methylase;
KW  purification; enzyme.
KW
XX  Geobacillus stearothermophilus.
OS
XX  US6403354-B1.
XX
XX  11-JUN-2002.
XX
XX  19-JAN-2001; 2001US-00766055.
XX
XX  19-JAN-2001; 2001US-00766055.
XX
XX  (NEWE ) NEW ENGLAND BIOLABS INC.
XX
XX  Xu S, Samuelson J, Pelletier J, Sibley M, Wilson GG;
PI  WPI; 2002-536039/57.
XX
XX  N-PSDB; AAD42119.
DR
XX
XX  Novel DNA encoding BstYI restriction endonuclease and BstY methylase,
PT  useful for producing recombinant BstY restriction endonuclease.
PT
XX  Disclosure; Col 19-20; 18pp; English.
XX
XX  The invention relates to recombinant DNA encoding BstYI restriction
CC  endonuclease and BstY methylase. The invention also relates to methods
CC  for purification of the recombinant BstYI restriction endonuclease and
CC  BstY methylase. Host cell transformed by the recombinant DNA of the
CC  invention is useful for producing recombinant BstY restriction
CC  endonuclease. The DNA of the invention is an useful tool for creating
CC  recombinant molecules in the laboratory. The present sequence is Bacillus
CC  stearothermophilus BstYI endonuclease protein. (Updated on 29-AUG-2003 to
CC  standardise OS field)
XX
XX  Sequence 203 AA;
SQ
Query Match 77.8%; Score 35; DB 5; Length 203;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
DB 136 FVAYDLFV 143

RESULT 31
ABR62959
ID  ABR62959 standard; protein; 203 AA.
XX
AC  ABR62959;
XX
XX  04-DEC-2003 (first entry)
DT
XX
DE  BstYI restriction endonuclease.
XX
XX  BstYI; restriction endonuclease; enzyme.
XX
XX  Bacillus stearothermophilus.
OS
XX  WO2003060152-A2.
XX
XX  24-JUL-2003.
XX

```

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XX
XX  09-JAN-2003; 2003WO-US000542.
XX
XX  10-JAN-2002; 2002US-0347403P.
XX
XX  (NEWE ) NEW ENGLAND BIOLABS INC.
XX
XX  Samuelson JC, Xu S;
PI
XX
XX  WPI; 2003-587289/55.
DR  N-PSDB; ACF79289.
XX
XX  Altering an endonuclease recognition site specificity, comprises
PT  subjecting a mutagenized endonuclease gene library to a genetic selection
PT  in prokaryotic host cells expressing one or more non-cognate DNA
PT  methyltransferases.
XX
XX  Disclosure; Fig 2; 51pp; English.
XX
XX  The present sequence is the protein sequence of the BstYI restriction
CC  endonuclease of Bacillus stearothermophilus Y406. BstYI was used in an
CC  example of the method of the invention, which involves altering the DNA
CC  recognition and cleavage characteristics of an endonuclease. The method
CC  can be used without prior knowledge of the endonuclease's three-
CC  dimensional structure and/or the amino acid residues responsible for
CC  activity and/or specificity. It involves selection in prokaryotic cells
CC  endonuclease gene library to a genetic selection in mutagenised
CC  expressing one or more non-cognate DNA methyltransferases. Genetic
CC  selection selects for viable cells in the population, and viable cells
CC  that express as active mutated endonuclease with an altered recognition
CC  site specificity are identified. A claimed modified BstYI enzyme has the
CC  recognition site 5'-AGATCT-3', altered from 5'-RGATCY-3' for the native
CC  enzyme
XX
XX  Sequence 203 AA;
SQ
Query Match 77.8%; Score 35; DB 7; Length 203;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
DB 136 FVAYDLFV 143

RESULT 32
AAO08931
ID  AAO08931 standard; protein; 51 AA.
XX
XX  AAO08931;
AC
XX
XX  06-NOV-2001 (first entry)
DT
XX
DE  Human polypeptide SEQ ID NO 22823.
DE
XX
XX  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX  vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW  tissue growth factor; immunomodulatory; cancer; leukaemia;
KW  nervous system disorders; arthritis; inflammation.
XX
XX  Homo sapiens.
OS
XX  WO200164835-A2.
XX
XX  07-SEP-2001.
PD
XX
XX  26-FEB-2001; 2001WO-US004927.
PF
XX
XX  28-FEB-2000; 2000US-00515126.
PR
XX  18-MAY-2000; 2000US-00577409.
XX
XX  (HYSE-) HYSEQ INC.
XX
XX

```

PI Tang YT, Liu C, Drmanac RT;  
 XX WPI; 2001-514838/56.  
 DR N-PSDB; AA18862.  
 XX  
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 XX  
 PS Claim 20; SEQ ID NO 22823; 1399pp + Sequence Listing; English.  
 XX  
 CC The invention relates to human polynucleotides (AA179941-AA193841) and  
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 51 AA;  
 Query Match 75.6%; Score 34; DB 4; Length 51;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FLSYDLFVV 9  
 DB 42 FLPYDIFTV 50  
 RESULT 33  
 ABP64088  
 ID ABP64088 standard; protein; 55 AA.  
 XX  
 AC ABP64088;  
 XX  
 DT 04-NOV-2002 (first entry)  
 XX  
 DE Human ORF459.  
 XX  
 KW Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulneryary;  
 KW Antinflammatory; gene therapy; human; ORFX; atherogenic; platelet;  
 KW human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;  
 KW cancer; cardiovascular disease; allergy; autoimmune disease;  
 KW wound healing; blood coagulation disorder; inflammatory disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002082206-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX  
 XX 30-MAY-2001; 2001US-00867550.  
 PF  
 XX 30-MAY-2000; 2000US-0208427P.  
 PR  
 XX (LEAC/) LEACH M D.  
 PA (MEHR/) MEHRABAN F.  
 PA (CONL/) CONLEY P B.  
 PA (TOPP/) TOPPER J N.  
 PA (LAWD/) LAW D.  
 XX  
 XX Leach MD, Mehraban F, Conley PB, Topper JN, Law D;  
 PI WPI; 2002-626554/67.  
 XX N-PSDB; ABQ98651.  
 DR  
 XX New polypeptide designated ORFX are present in human atherogenic cells

PT and are useful to prevent and treat ORFX-associated disorders including  
 PT cancer, allergy, wound healing or autoimmune, cardiovascular or  
 PT inflammatory disease.  
 XX  
 PS Claim 10; SEQ ID NO 916; 78pp; English.  
 XX  
 CC The present invention relates to novel human ORFX polypeptides and their  
 CC coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences  
 CC were discovered in human atherogenic cells, in particular in platelets  
 CC and human umbilical vein endothelial cells (HUVEC) and are expressed in  
 CC many other tissues as well. Atherogenic cells are cells which have the  
 CC nucleic acids are useful for treating or preventing a pathological  
 CC condition associated with an ORFX-associated disorder, e.g. cancer,  
 CC cardiovascular disease, allergy, autoimmune disease, wound healing, blood  
 CC coagulation disorders or inflammatory disorders. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/sequence.html?DocID=20020082206  
 XX  
 SQ Sequence 55 AA;  
 Query Match 75.6%; Score 34; DB 5; Length 55;  
 Best Local Similarity 77.8%; Pred. No. 24;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLSYDLFVV 9  
 DB 16 FLSLDLFLV 24  
 RESULT 34  
 AAG73909  
 ID AAG73909 standard; protein; 98 AA.  
 XX  
 AC AAG73909;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE Human colon cancer antigen protein SEQ ID NO:4673.  
 XX  
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200122920-A2.  
 PD  
 XX 05-APR-2001.  
 XX  
 XX 28-SEP-2000; 2000WO-US026524.  
 PF  
 XX 29-SEP-1999; 99US-0157137P.  
 PR  
 XX 03-NOV-1999; 99US-0163280P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
 PI WPI; 2001-235357/24.  
 DR N-PSDB; AAH33340.  
 XX  
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers.  
 PT  
 XX Claim 11; Page 6473-6474; 9803pp; English.  
 PS  
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
 CC proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene therapy  
 CC and vaccine production. N and P may be used in the prevention, diagnosis  
 CC and treatment of diseases associated with inappropriate P expression. For

CC example, N and P may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of P by expressing inactive proteins or to  
 CC supplement the patient's own production of P. Additionally, N may be used  
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the proteins. N and P  
 CC can be used in the prevention, diagnosis and treatment of colorectal  
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
 CC sequences used in the exemplification of the present invention. N.B.  
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
 CC to 1052, 7921 and 7922

XX SQ Sequence 98 AA;

Query Match 75.6%; Score 34; DB 4; Length 98;  
 Best Local Similarity 77.8%; Pred. No. 45;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFPV 9  
 ||| ||||:  
 Db 16 FLSLDLFLVL 24

RESULT 35  
 ADC32867  
 ID ADC32867 standard; protein; 160 AA.

XX AC ADC32867;

XX DT 18-DEC-2003 (first entry)

XX DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:2949.

XX KW Human; diagnostic; drug screening; forensics; gene mapping;  
 KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;  
 KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;  
 KW ulcers; osteoporosis; autoimmune disease; cancer;  
 KW molecular weight marker; food supplement; antiparkinsonian; nootropic;  
 KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnary;  
 KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;  
 KW gene therapy; chromosome X.

XX OS Homo sapiens.

XX PN WO2003029271-A2.

XX XX 10-APR-2003.

XX PF 24-SEP-2002; 2002WO-US030474.

XX PR 24-SEP-2001; 2001US-0324631P.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;  
 PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;  
 PI Haley-Vicente D, Drmanac RT;

XX DR WPI; 2003-371981/35.  
 DR N-PSDB; ADC32100.

XX PT New polynucleotide and polypeptide useful for diagnosing, preventing or  
 PT treating conditions such as neurodegenerative diseases, anemias, platelet  
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
 PT cancer.

XX PS Example 2; SEQ ID NO 2949; 1185pp; English.

XX CC The invention relates to 971 novel human cDNA sequences (ADC29919-  
 CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The  
 CC invention also relates to nucleic acid sequences over 99% identical with  
 CC the novel human cDNAs. The invention additionally encompasses expression

CC vectors and host cells comprising a nucleic acid of the invention; the  
 CC recombinant production of a polypeptide of the invention; an antibody  
 CC against a polypeptide of the invention; a method of detecting  
 CC polynucleotides or polypeptides of the invention; and methods of  
 CC identifying a compound which binds to a polypeptide of the invention. The  
 CC invention further discloses methods of preventing, treating or  
 CC ameliorating a medical condition; kits comprising polynucleotide probes  
 CC and/or monoclonal antibodies for carrying out the methods of the  
 CC invention; methods for the identification of compounds that modulate the  
 CC expression or activity of the polynucleotide and/or polypeptide; and 767  
 CC contig sequences corresponding to the cDNA sequences of the invention  
 CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628  
 CC -ADC33394). The nucleic acids and polypeptides of the invention are  
 CC useful in diagnostics, drug screening, forensics, gene mapping, in the  
 CC identification of mutations responsible for genetic disorders or other  
 CC traits, for assessing biodiversity, and in producing many other types of  
 CC data and products dependent on DNA and amino acid sequences. They are  
 CC also used for treating diseases such as Parkinson's disease, Alzheimer's  
 CC disease and other neurodegenerative diseases, anaemia, platelet  
 CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
 CC cancer. The nucleic acids may also be used as hybridisation probes or  
 CC primers, and in the recombinant production of a protein. The polypeptides  
 CC are also useful in generating antibodies, as molecular weight markers,  
 CC and as food supplements. The present sequence represents a human contig-  
 CC encoded polypeptide sequence used in an example of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 160 AA;

Query Match 75.6%; Score 34; DB 7; Length 160;  
 Best Local Similarity 77.8%; Pred. No. 75;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFPV 9  
 ||| ||||:  
 Db 78 FLSLDLFLVL 86

RESULT 36

ADM04330

ID ADM04330 standard; protein; 247 AA.

XX AC ADM04330;

XX DT 20-MAY-2004 (first entry)

XX DE Human protein of the invention SEQ ID NO:3015.

XX KW human; gene therapy; diagnostic marker; pharmaceutical.

XX OS Homo sapiens.

XX PN EP1347046-A1.

XX PD 24-SEP-2003.

XX PF 12-APR-2002; 2002EP-00008400.

XX PR 22-MAR-2002; 2002JP-00137785.

XX XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 PI WPI; 2003-723558/69.  
 DR N-PSDB; ADM01887.

XX PT New polynucleotides and polypeptides are useful in gene therapy, for  
 PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.  
 XX  
 PS Claim 1; SEQ ID NO 3015; 305pp; English.  
 XX  
 CC The invention relates to a novel human polynucleotide and the encoded  
 CC polypeptide. A polynucleotide of the invention may have a use in gene  
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
 CC as a primer for synthesizing the polynucleotide or as a probe for  
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
 CC useful in gene therapy, for developing a diagnostic marker or medicines  
 CC for regulating their expression and activity, or as a target of gene  
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
 CC are useful as pharmaceutical agents. The present sequence represents a  
 CC protein sequence of the invention.  
 XX  
 SQ Sequence 247 AA;  
 Query Match 75.6%; Score 34; DB 7; Length 247;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLSYDLFVV 9  
 |||:|:|:  
 Db 47 FLSFDLMVI 55  
 RESULT 37  
 ADA34406  
 ID ADA34406 standard; protein; 363 AA.  
 XX  
 AC ADA34406;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Acinetobacter baumannii protein #1567.  
 XX  
 KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;  
 KW plant biocontrol agent.  
 XX  
 OS Acinetobacter baumannii.  
 XX  
 PN US6562958-B1.  
 XX  
 PD 13-MAY-2003.  
 XX  
 PF 04-JUN-1999; 99US-00328352.  
 XX  
 PR 09-JUN-1998; 98US-0088701P.  
 XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 PI Breton G, Bush D;  
 XX  
 DR WPI: 2003-576092/54.  
 DR N-PSDB; ADA30280.  
 XX  
 PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents  
 PT for diagnosing a bacterial disease, as components of antibacterial  
 PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for  
 PT plants.  
 XX  
 PS Example; SEQ ID NO 5693; 328pp; English.  
 XX  
 CC The invention relates to isolated Acinetobacter baumannii nucleic acids.  
 CC The A. baumannii nucleic acids and polypeptides are useful as reagents  
 CC for diagnosing a bacterial disease, as components of antibacterial  
 CC vaccines, as targets for antibacterial drugs, to detect the presence of  
 CC A. baumannii and other Acinetobacter species in a sample, in screening  
 CC compounds for the ability to interfere with the A. baumannii life cycle  
 CC or to inhibit A. baumannii infection, and as biocontrol agents for  
 CC plants. The present sequence represents the amino acid sequence of an A.  
 CC baumannii protein.

SQ Sequence 363 AA;  
 Query Match 75.6%; Score 34; DB 6; Length 363;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLSYDLFVV 9  
 |||:|:|:  
 Db 39 FLVYDIFWV 47  
 RESULT 38  
 AAW98765  
 ID AAW98765 standard; protein; 412 AA.  
 XX  
 AC AAW98765;  
 XX  
 DT 31-MAR-1999 (first entry)  
 XX  
 DE H. pylori GHPO 1113 protein.  
 XX  
 KW GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;  
 KW peptic ulcer disease.  
 XX  
 OS Helicobacter pylori.  
 XX  
 PN WO9843478-A1.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PF 01-APR-1998; 98WO-US006371.  
 XX  
 PR 01-APR-1997; 97US-00833457.  
 PR 24-JUN-1997; 97US-00881227.  
 PR 29-JUL-1997; 97US-00902615.  
 XX  
 PA (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Kleanthous H, Al-Garawi A, Miller C, Tomb J, Oomen RP;  
 XX  
 DR WPI: 1998-542293/46.  
 DR N-PSDB; AAX14484.  
 XX  
 PT New isolated Helicobacter polynucleotides - used to develop products for  
 PT the diagnosis, prevention and treatment of Helicobacter infections and  
 PT gastrointestinal diseases.  
 XX  
 PS Claim 8; Page 1651-1653; 2054pp; English.  
 XX  
 CC This sequence represents a Helicobacter pylori GHPO protein of the  
 CC invention. The polypeptides can be used for preventing or treating  
 CC Helicobacter infections, and gastroduodenal diseases associated with  
 CC these infections, including acute, chronic, and atrophic gastritis, and  
 CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be  
 CC used for the production of antibodies. The products can also be used for  
 CC detection and diagnosis  
 XX  
 SQ Sequence 412 AA;  
 Query Match 75.6%; Score 34; DB 2; Length 412;  
 Best Local Similarity 77.8%; Pred. No. 2.1e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLSYDLFVV 9  
 |||:|:|:  
 Db 253 FLKDKIFWV 261  
 RESULT 39  
 ABB93691  
 ID ABB93691 standard; protein; 516 AA.  
 XX



PT New polynucleotides encoding full-length polypeptides, e.g. secretory  
 PT and/or membrane proteins, useful for developing medicines for diseases in  
 PT which the gene is involved, or as target molecules for gene therapy.

XX Claim 14; SEQ ID NO 2686; 205pp; English.

XX The present invention relates to novel human secretory or membrane  
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
 CC ADA54071). The coding sequences are useful in the gene therapy of  
 CC diseases caused by abnormalities of the proteins, e.g. cancer,  
 CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 674 AA;

Query Match 75.6%; Score 34; DB 6; Length 674;  
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
 |||:|:|  
 Db 474 FLSFDLWVI 482

RESULT 42

ADM72293  
 ID ADM72293 standard; protein; 1031 AA.

XX AC ADM72293;

DT 17-JUN-2004 (first entry)

XX DE Equine TLR9 polypeptide.

XX KW TLR9; toll-like receptor 9; CpG; TLR9 signaling; equine.

XX OS Equus caballus.

XX PN WO2004026888-A2.

XX PD 01-APR-2004.

XX PF 19-SEP-2003; 2003WO-US029577.

XX PR 19-SEP-2002; 2002US-0412479P.

XX PA (COLE-) COLEY PHARM GMBH.

XX PA (UYSA-) UNIV SASKATCHEWAN.

XX PA (QIAG-) QIAGEN GMBH.

PI Lipford GB, Mookherjee N, Babiuk L, Brownlie R, Griebel P;

PI Mutwiri G, Hecker R;

XX WPI; 2004-295374/27.

DR N-PSDB; ADM72295.

XX New polypeptide, useful for identifying key amino acids in a TLR9 of a  
 PT first species which confer specificity for CpG DNA optimized for TLR9 of  
 PT the first species.

XX Claim 1; SEQ ID NO 13; 170pp; English.

XX The invention relates to novel Toll-like receptor 9 (TLR9) polypeptides  
 CC and encoding polynucleotides. It provides methods for (i) identifying key  
 CC amino acids in a TLR9 of a first species which confer specificity for CpG  
 CC DNA optimized for TLR9 of the first species; (ii) identifying key amino  
 CC acids in human TLR9 which confer specificity for CpG DNA optimized for  
 CC human TLR9; (iii) identify a TLR9 ligand; and (iv) identify species-  
 CC specific CpG-motif preference of the isolated polypeptide. The screening  
 CC method to identify species-specific CpG-motif preference of the isolated  
 CC polypeptide comprises: contacting an isolated polypeptide with a CpG DNA  
 CC comprising a hexamer sequence consisting of GACGTT, AACGTT, CACGTT,  
 CC TACGTT, GGCCTT, GTCGTT, GATGTT, GAAGTT, GAGCTT, GACATT, GACCTT,  
 CC GACTTT, GACGCT, GACGAT, GACGCT, GACGTC, GACGTA and GACGTG; measuring a

CC signal in response to the contacting; and identifying a species-specific  
 CC CpG-motif preference when the signal in response to the contacting is  
 CC consistent with TLR9 signaling. The signal comprises expression of a  
 CC reporter gene responsive to TLR/IL-1R signal transduction pathway. The  
 CC CpG DNA is an oligodeoxynucleotide having a sequence consisting of  
 CC sequences selected from ADM72319- ADM72337. The polypeptide is useful for  
 CC identifying key amino acids in a TLR9 of a first species which confer  
 CC specificity for CpG DNA optimized for TLR9 of the first species. The  
 CC present sequence represents an equine TLR9 polypeptide.

XX Sequence 1031 AA;

Query Match 75.6%; Score 34; DB 8; Length 1031;  
 Best Local Similarity 87.5%; Pred. No. 5.6e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSYDLFVV 9  
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 Db 866 LSYDAFVV 873

RESULT 43

AAG38087

ID AAG38087 standard; protein; 90 AA.

XX AC AAG38087;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 46934.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 23-APR-1999; 99US-0130891P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-MAY-1999; 99US-0132407P.

XX PR 05-MAY-1999; 99US-0132484P.

XX PR 06-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

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PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
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PR 01-JUL-1999; 99US-0141842P.  
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PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145313P.  
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PR 28-JUL-1999; 99US-0145351P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
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PR 03-AUG-1999; 99US-0147038P.  
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PR 04-AUG-1999; 99US-0147302P.  
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PR 25-AUG-1999; 99US-0150566P.  
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PR 27-AUG-1999; 99US-0151065P.  
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PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
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PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
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PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
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PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
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PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160982P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.

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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 73.3%; Score 33; DB 3; Length 90;
Best Local Similarity 55.6%; Pred. No. 65;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLSYDLFV 9
   :|||:|
Db 70 FSYDVFSE 78

RESULT 44
ID ADF04479 standard; protein; 103 AA.
AC ADF04479;
XX
XX DT 12-FEB-2004 (first entry)
XX DE Bacterial polypeptide #592.
XX KW Proteus mirabilis infection; bacterial infection; antibacterial;
XX immunostimulant.
XX OS Proteus mirabilis.
XX PN US6605709-B1.
XX PD 12-AUG-2003.
XX PF 05-APR-2000; 2000US-00543681.
XX PR 09-APR-1999; 99US-0128706P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Breton GL;
XX DR WPI; 2003-895291/82.
XX N-PSDB; ADF00307.
XX PT New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX PS Disclosure; SEQ ID NO 4764; 870pp; English.
XX CC The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunizing an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX SQ Sequence 103 AA;

Query Match 73.3%; Score 33; DB 7; Length 103;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLFV 8
   :|||||
```

```
Db 39 ISYDLFV 45

RESULT 45
ID AAG14935 standard; protein; 119 AA.
XX AC AAG14935;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 14984.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
XX PR 25-MAR-1999; 99US-0126264P.
XX PR 29-MAR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 06-APR-1999; 99US-0128234P.
XX PR 08-APR-1999; 99US-0128714P.
XX PR 16-APR-1999; 99US-0129845P.
XX PR 19-APR-1999; 99US-0130077P.
XX PR 21-APR-1999; 99US-0130449P.
XX PR 23-APR-1999; 99US-0130510P.
XX PR 23-APR-1999; 99US-0130891P.
XX PR 28-APR-1999; 99US-0131449P.
XX PR 30-APR-1999; 99US-0132048P.
XX PR 30-APR-1999; 99US-0132407P.
XX PR 04-MAY-1999; 99US-0132484P.
XX PR 05-MAY-1999; 99US-0132485P.
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XX PR 14-MAY-1999; 99US-0134370P.
XX PR 18-MAY-1999; 99US-0134768P.
XX PR 19-MAY-1999; 99US-0134941P.
XX PR 20-MAY-1999; 99US-0135124P.
XX PR 21-MAY-1999; 99US-0135353P.
XX PR 24-MAY-1999; 99US-0135629P.
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XX PR 27-MAY-1999; 99US-0136392P.
XX PR 28-MAY-1999; 99US-0136782P.
XX PR 01-JUN-1999; 99US-0137222P.
XX PR 03-JUN-1999; 99US-0137528P.
XX PR 04-JUN-1999; 99US-0137502P.
XX PR 07-JUN-1999; 99US-0137724P.
XX PR 08-JUN-1999; 99US-0138094P.
XX PR 10-JUN-1999; 99US-0138540P.
XX PR 10-JUN-1999; 99US-0138847P.
XX PR 14-JUN-1999; 99US-0139119P.
XX PR 16-JUN-1999; 99US-0139452P.
XX PR 16-JUN-1999; 99US-0139453P.
XX PR 17-JUN-1999; 99US-0139492P.
XX PR 18-JUN-1999; 99US-0139454P.
XX PR 18-JUN-1999; 99US-0139455P.
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PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	27-AUG-1999;	99US-0151103P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
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PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
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PR	12-OCT-1999;	99US-0158232P.
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PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	22-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	25-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
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PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161922P.
PR	28-OCT-1999;	99US-0161993P.
PR	28-OCT-1999;	99US-0162142P.

RESULT 47  
ADH32233  
ID ADH32233 standard; protein; 211 AA.

RESULT 48	
ABB55172	
ID	ABB55172 standard; protein; 304 AA.
XX	
XX	AC ABB55172;
XX	
DT	29-AUG-2003 (revised)
DT	16-MAY-2002 (first entry)
XX	
DE	Lactococcus lactis protein yslB.

KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
XX Lactococcus lactis; IL1403.  
XX FR2807446-A1.  
PN 12-OCT-2001.  
XX  
XX 11-APR-2000; 2000FR-00004630.  
XX  
XX 11-APR-2000; 2000FR-00004630.  
PR (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
XX  
XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
XX WPI; 2002-043418/06.  
XX  
XX New nucleotide sequence useful in the identification or Lactococcus  
PT lactis and related species.  
XX  
XX Claim 6; SEQ ID NO 1874; 2504pp; French.  
XX  
XX The present invention is related to a Lactococcus lactis nucleotide  
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
CC acid sequence is useful in the detection and/or amplification of nucleic  
CC acid sequence, particularly to identify Lactococcus lactis or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO200177334 (published 18-OCT-2001) which is available in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
CC standardise OS field)  
XX  
XX Sequence 304 AA;  
SQ  
Query Match 73.3%; Score 33; DB 5; Length 304;  
Best Local Similarity 62.5%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLSYDLFV 8  
Db |||||:  
155 FLMDIFI 162  
RESULT 49  
ADN19667  
ID ADN19667 standard; protein; 573 AA.  
XX  
XX ADN19667;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Bacterial polypeptide #2320.  
XX  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
XX Bacteria.  
XX  
XX US2003233675-A1.  
PN  
XX 18-DEC-2003.  
PD  
XX  
XX 20-FEB-2003; 2003US-00369493.  
XX

PR 21-FEB-2002; 2002US-0360039P.  
XX  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
PI WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 2320; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
XX Sequence 573 AA;  
SQ  
Query Match 73.3%; Score 33; DB 8; Length 573;  
Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SYDLFV 9  
Db |||||:  
59 SYDLFII 65  
RESULT 50  
ADN19661  
ID ADN19661 standard; protein; 573 AA.  
XX  
XX ADN19661;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Bacterial polypeptide #2314.  
XX  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
XX Bacteria.

XX US2003233675-A1.  
XX 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 2314; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
XX Sequence 573 AA;

Query Match 73.3%; Score 33; DB 8; Length 573;  
Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 SYDLFVV 9  
Db 59 SYDLFII 65  
|||||::

Search completed: May 9, 2006, 02:14:51  
Job time : 135.4 sec

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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:17:29 ; Search time 16.4 Seconds  
(without alignments)  
52.802 Million cell updates/sec

Title: US-09-870-216C-9  
Perfect score: 45  
Sequence: 1 FLSYDLFW 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	91.1	247	2 A82921	protein phosphatas
2	37	82.2	259	2 C89964	truncated transpos
3	36	80.0	131	2 F72277	hypothetical prote
4	34	75.6	95	2 A10315	conserved hypothet
5	34	75.6	412	2 C64712	ubiquinol-cytochro
6	34	75.6	412	2 D71803	ubiquinol-cytochro
7	34	75.6	452	2 C72295	hypothetical prote
8	33	73.3	70	2 S01213	NADH2 dehydrogenas
9	33	73.3	203	2 I40517	spag protein - Bac
10	33	73.3	274	2 T39166	inorganic phosphat
11	33	73.3	305	2 G86852	oxidoreductase ysj
12	33	73.3	333	2 T17712	hypothetical prote
13	33	73.3	370	2 T47504	mitogen-activated
14	33	73.3	370	2 S40469	mitogen-activated
15	33	73.3	559	2 S62503	inorganic phosphat
16	33	73.3	572	2 T50404	probable inorganic
17	33	73.3	583	2 T41275	probable inorganic
18	33	73.3	849	2 T20422	hypothetical prote
19	32	71.1	137	2 A83852	hypothetical prote
20	32	71.1	288	2 I78556	membrane glycoprot
21	32	71.1	309	2 G69796	lactose permease h
22	32	71.1	346	2 B90243	aminomethyltransfe
23	32	71.1	397	2 B98293	mannonate dehydrat
24	32	71.1	397	2 AG2990	mannonate dehydrat
25	32	71.1	413	2 D86920	probable UNP-galac
26	32	71.1	586	2 T19075	hypothetical prote
27	32	71.1	614	2 T05387	hypothetical prote
28	32	71.1	726	1 S73915	virulence-associat
29	32	71.1	800	2 T38032	hypothetical prote

hypothetical prote  
hypothetical prote  
chloroplast outer  
chloroplast outer  
apolipoprotein B -  
apolipoprotein B -  
protein P282.10 [i  
hypothetical prote  
probable membrane  
hypothetical prote  
hypothetical prote  
myfB protein precu  
Lactococcus lactis  
yabT protein - Bac  
hypothetical prote  
hypothetical prote  
serine/threonine-p  
hypothetical prote  
hypothetical prote  
geranylgeranyl-bac  
GTP-binding protei  
probable membrane  
hypothetical prote  
cytochrome-c oxida  
hypothetical prote  
probable oligopept  
hypothetical prote  
probable ABC-trans  
hypothetical prote  
probable Na+/H+ an  
hypothetical prote  
hypothetical prote  
DNA-directed RNA p  
nonstructural poly  
hypothetical prote  
protein T23G18.2 [i  
lipoprotein homolo  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable membrane  
dynein light chain  
partial transposas  
hypothetical prote  
probable signal pe  
probable calcium b  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable dipeptide  
probable dipeptide  
dipeptide transpor  
peptide ABC transp  
probable ABC trans  
hypothetical prote  
hypothetical prote  
oligopeptide ABC t  
oligopeptide ABC t  
probable oligopept  
ABC ATPase dipept1  
peptide ABC transp  
dipeptide transpor  
dipeptide trans  
oligopeptide trans  
hypothetical prote  
dipeptide transpor  
hypothetical prote  
hypothetical prote

103	30	66.7	335	2	AG0486	dipeptide transpor	176	29	64.4	311	2	AD2979	hypothetical prote
104	30	66.7	337	2	AI0983	dipeptide transpor	177	29	64.4	314	2	E84518	probable spliceoso
105	30	66.7	344	2	AG3617	oligopeptide trans	178	29	64.4	319	2	B53290	oligopeptide trans
106	30	66.7	370	2	C90504	amino-end of forma	179	29	64.4	326	2	G75117	dipeptide abc tran
107	30	66.7	384	2	C72371	oligopeptide ABC t	180	29	64.4	329	2	G71014	probable dipeptide
108	30	66.7	385	1	CBNC	ubiquinol-cytochro	181	29	64.4	335	2	T44211	hypothetical prote
109	30	66.7	387	2	C86640	multidrug efflux t	182	29	64.4	335	2	B36769	11R protein - huma
110	30	66.7	395	2	AD3354	hypothetical cytos	183	29	64.4	338	2	C83653	oligopeptide ABC t
111	30	66.7	413	2	H72293	probable valine-py	184	29	64.4	341	2	B72300	oligopeptide ABC t
112	30	66.7	458	2	I39477	glutathione-disulf	185	29	64.4	347	2	A72618	probable oligopept
113	30	66.7	459	2	AH2426	glutathione reduct	186	29	64.4	354	2	A70255	immunogenic protei
114	30	66.7	464	2	AG2774	glutathione-disulf	187	29	64.4	363	2	B84565	probable spliceoso
115	30	66.7	464	2	E97554	glutathione-disulf	188	29	64.4	381	2	C96657	hypothetical prote
116	30	66.7	471	2	H90502	phosphate transpor	189	29	64.4	386	2	A99503	hypothetical prote
117	30	66.7	483	2	AF3373	glutathione-disulf	190	29	64.4	387	2	A86302	hypothetical prote
118	30	66.7	492	2	AS9105	hypothetical prote	191	29	64.4	398	2	AC3322	membrane-bound lyt
119	30	66.7	496	2	T03766	probable glutathio	192	29	64.4	401	2	S74793	succinate-CoA liga
120	30	66.7	505	2	T37975	probable alanine a	193	29	64.4	408	2	E72353	extracellular poly
121	30	66.7	516	2	S34525	hypothetical prote	194	29	64.4	419	2	T04215	hypothetical prote
122	30	66.7	533	2	H95949	hypothetical prote	195	29	64.4	432	2	F64484	probable transamin
123	30	66.7	536	2	D83419	probable ATP-bind	196	29	64.4	438	2	A55185	hypothetical prote
124	30	66.7	536	2	B83389	probable ATP-bind	197	29	64.4	438	2	A98052	oxidoreductase (Me
125	30	66.7	539	2	B82393	ABC transporter, A	198	29	64.4	459	2	T16632	hypothetical prote
126	30	66.7	551	2	H98306	hypothetical prote	199	29	64.4	464	2	T33249	hypothetical prote
127	30	66.7	551	2	AC2976	hypothetical prote	200	29	64.4	476	2	S60927	hypothetical prote
128	30	66.7	555	2	C45868	glycerol-3-phospha	201	29	64.4	511	2	AD3079	hypothetical prote
129	30	66.7	555	2	AH3236	hypothetical prote	202	29	64.4	527	2	G84626	arginate O-acetyla
130	30	66.7	569	2	C69422	hydrogenase (EC 1.	203	29	64.4	530	2	C82442	probable peptide A
131	30	66.7	583	2	T00091	rgpC protein - St	204	29	64.4	530	2	AD0155	probable ABC trans
132	30	66.7	611	2	S19434	probable transport	205	29	64.4	544	2	B98311	probable ATP-bind
133	30	66.7	617	2	F84681	hypothetical prote	206	29	64.4	544	2	AH2971	hypothetical prote
134	30	66.7	627	2	AB2403	ABC transporter AT	207	29	64.4	548	2	H70788	probable peptider
135	30	66.7	632	2	C71327	probable phosphogl	208	29	64.4	549	1	D30010	cytochrome-c oxida
136	30	66.7	650	2	S75333	oligopeptide trans	209	29	64.4	549	2	AH2599	hypothetical prote
137	30	66.7	741	2	S73827	hypothetical prote	210	29	64.4	549	2	A37382	probable ATP-bind
138	30	66.7	817	2	T51787	hypothetical prote	211	29	64.4	550	2	AD3494	oligopeptide trans
139	30	66.7	837	2	T19074	hypothetical prote	212	29	64.4	551	2	E98207	ABC transporter, A
140	30	66.7	846	2	A85663	aminopeptidase N [	213	29	64.4	555	2	AD3130	hypothetical prote
141	30	66.7	846	2	JN0324	lysine aminopeptid	214	29	64.4	555	2	D95918	probable oligopept
142	30	66.7	846	2	D23157	membrane alanyl am	215	29	64.4	570	2	E98157	ABC transporter, A
143	30	66.7	873	2	T50171	hypothetical prote	216	29	64.4	571	2	C84356	hypothetical prote
144	30	66.7	904	2	S53896	DNA mismatch repai	217	29	64.4	580	2	F83927	Na+/myo-inositol c
145	30	66.7	923	1	MBBY7C	probable membrane	218	29	64.4	612	2	A70756	probable ABC-type
146	30	66.7	1194	2	C59436	KIAA1391 protein [	219	29	64.4	633	2	AC3634	norD protein limpo
147	30	66.7	1444	2	S57335	cleavage and polya	220	29	64.4	653	2	S67035	probable membrane
148	30	66.7	1737	2	T00209	MEGF8 protein - hu	221	29	64.4	660	2	F98020	hypothetical prote
149	30	66.7	3944	2	T19997	hypothetical prote	222	29	64.4	662	2	H97834	cytochrome c-type
150	30	66.7	3971	2	T44806	mycosubtilin synth	223	29	64.4	670	2	C71630	cytochrome C-type
151	29	64.4	48	2	D81975	hypothetical prote	224	29	64.4	703	2	D84604	hypothetical prote
152	29	64.4	93	2	AG0092	probable membrane	225	29	64.4	703	2	T39420	conserved hypothet
153	29	64.4	98	2	H96953	hypothetical prote	226	29	64.4	711	2	T27358	hypothetical prote
154	29	64.4	103	2	A05200	hypothetical prote	227	29	64.4	821	2	B84509	probable Na/H anti
155	29	64.4	104	2	E96779	probable ribosomal	228	29	64.4	837	2	F90191	integral membrane
156	29	64.4	108	2	T38079	very hypothetical	229	29	64.4	844	2	S77383	hypothetical prote
157	29	64.4	142	2	T25224	hypothetical prote	230	29	64.4	879	2	I64133	phosphoenolpyruvat
158	29	64.4	195	2	A90467	hypothetical prote	231	29	64.4	889	2	T40557	probable inositol
159	29	64.4	197	2	B86697	hypothetical prote	232	29	64.4	962	2	C43274	N-methyl D-asparta
160	29	64.4	208	2	T52450	ribosomal protein	233	29	64.4	993	2	C55226	cytM protein - Ent
161	29	64.4	210	2	D89606	protein B0416.3 [i	234	29	64.4	1023	2	AE1280	ATP-dependent dsDN
162	29	64.4	245	2	T18616	hypothetical prote	235	29	64.4	1034	2	S60051	sodium channel alp
163	29	64.4	257	2	F70166	hypothetical prote	236	29	64.4	1034	2	S60060	sodium channel alp
164	29	64.4	258	2	A33953	enterotoxin D prec	237	29	64.4	1138	2	H84529	hypothetical prote
165	29	64.4	262	2	F95280	hypothetical prote	238	29	64.4	1203	2	I55466	N-methyl-D-asparta
166	29	64.4	263	2	H87296	aminomethyltransfe	239	29	64.4	1206	2	D84542	probable chloropia
167	29	64.4	268	2	A71952	dipeptide transpor	240	29	64.4	1239	2	I49705	glutamate receptor
168	29	64.4	268	2	F64557	dipeptide transpor	241	29	64.4	1250	1	B45219	N-methyl-D-asparta
169	29	64.4	269	2	A34727	Surf-4 protein - m	242	29	64.4	1323	2	S72224	N-methyl-D-asparta
170	29	64.4	271	2	A99949	hypothetical prote	243	29	64.4	1323	2	I78557	N-methyl-D-asparta
171	29	64.4	281	2	AG3062	hypothetical prote	244	29	64.4	1356	1	C45219	N-methyl-D-asparta
172	29	64.4	281	2	H98223	hypothetical prote	245	29	64.4	1820	2	A33299	sodium channel pro
173	29	64.4	282	2	AG3545	dipeptide transpor	246	29	64.4	1846	2	T42047	insulin receptor h
174	29	64.4	283	2	JQ2324	hypothetical ABC t	247	29	64.4	2108	2	S72458	sodium channel pro
175	29	64.4	311	2	A98304	oligopeptide ABC t	248	29	64.4	2269	2	T18472	hypothetical prote



249	29	64.4	6260	2	T30228	polyketide synthas	322	28	62.2	325	2	G70421	probable endoglucanase
250	29	64.4	8563	2	T30226	polyketide synthas	323	28	62.2	326	2	T37874	probable mitochondrion
251	29	64.4	10223	2	T30225	polyketide synthas	324	28	62.2	327	2	E70343	transporter (OppBC)
252	28	62.2	40	2	S45689	glutathione transf	325	28	62.2	328	2	H90889	hypothetical prote
253	28	62.2	40	2	S45690	glutathione transf	326	28	62.2	328	2	G64901	ABC-type transport
254	28	62.2	65	2	AC0779	hypothetical prote	327	28	62.2	328	2	A85728	hypothetical prote
255	28	62.2	67	2	E81108	hypothetical prote	328	28	62.2	330	2	T49002	hypothetical prote
256	28	62.2	95	2	A29104	chitinase (EC 3.2.	329	28	62.2	331	2	T18618	hypothetical prote
257	28	62.2	130	2	H95034	ribosomal protein	330	28	62.2	336	2	S15997	chitinase (EC 3.2.
258	28	62.2	130	2	H97905	30S ribosomal prot	331	28	62.2	338	2	AE0917	lysophospholipase
259	28	62.2	153	2	G95988	conserved hypotet	332	28	62.2	340	1	PSCL2	lysophospholipase
260	28	62.2	160	2	T47370	hypothetical prote	333	28	62.2	340	1	A86070	lysophospholipase
261	28	62.2	161	2	A30338	myosin regulatory	334	28	62.2	340	2	C91223	lysophospholipase
262	28	62.2	166	2	T07949	calcium binding pr	335	28	62.2	340	2	A13134	hypothetical prote
263	28	62.2	169	2	G71944	hypothetical prote	336	28	62.2	342	2	A71957	flagellar P-ring p
264	28	62.2	171	2	E64655	hypothetical prote	337	28	62.2	342	2	F64550	flagellar basal-bo
265	28	62.2	172	2	T04498	AlG2 protein homol	338	28	62.2	344	2	A69507	conserved hypotet
266	28	62.2	183	2	H83983	C4-dicarboxylate t	339	28	62.2	346	2	G75380	peptide ABC transp
267	28	62.2	186	2	B64391	hypothetical prote	340	28	62.2	347	2	F22845	hypothetical prote
268	28	62.2	195	2	A97332	transcription regu	341	28	62.2	349	2	S51267	probable galactosy
269	28	62.2	202	2	H95329	protein [imported	342	28	62.2	349	2	C98153	oligopeptide ABC t
270	28	62.2	206	2	D97285	ribosomal protein	343	28	62.2	352	2	T22019	hypothetical prote
271	28	62.2	215	2	C72722	probable amatinas	344	28	62.2	357	2	H70346	undecaprenyl-phosp
272	28	62.2	218	2	B64365	hypothetical prote	345	28	62.2	361	2	T33728	hypothetical prote
273	28	62.2	222	2	AF0395	probable amino aci	346	28	62.2	363	2	T33731	hypothetical prote
274	28	62.2	222	2	E71652	hypothetical prote	347	28	62.2	366	2	B64413	hypothetical prote
275	28	62.2	222	2	F97797	hypothetical prote	348	28	62.2	367	2	F95159	prephenate dehydro
276	28	62.2	223	2	F83703	hypothetical prote	349	28	62.2	367	2	F98025	prephenate dehydro
277	28	62.2	224	2	T04358	glutathione transf	350	28	62.2	373	2	AC0199	conserved hypotet
278	28	62.2	227	2	A39267	superoxide dismuta	351	28	62.2	374	2	G69119	probable aspartat
279	28	62.2	229	2	T38618	probable splicosom	352	28	62.2	375	2	E83954	flagella-associate
280	28	62.2	233	2	C71645	ferric transport A	353	28	62.2	376	1	C64135	ribonucleoside-dip
281	28	62.2	233	2	A97861	zinc ABC transport	354	28	62.2	376	2	AH0148	ribonucleoside-dip
282	28	62.2	235	2	S69757	hypothetical prote	355	28	62.2	378	2	E83373	adenylate cyclase
283	28	62.2	236	2	S65985	yybL protein - Bac	356	28	62.2	378	2	D83381	hypothetical prote
284	28	62.2	239	2	S55931	cellulase (EC 3.2.	357	28	62.2	387	2	E81306	probable transmemb
285	28	62.2	243	2	JC5918	chitinase (EC 3.2.	358	28	62.2	389	2	S41748	heat shock protein
286	28	62.2	243	2	JN0884	chitinase (EC 3.2.	359	28	62.2	389	2	G84245	NADH dehydrogenase
287	28	62.2	252	2	T16405	hypothetical prote	360	28	62.2	391	2	S17818	bacteriochlorophyl
288	28	62.2	253	2	S20738	chitinase (EC 3.2.	361	28	62.2	392	2	A70243	multidrug-efflux t
289	28	62.2	253	2	G81713	RNA polymerase sig	362	28	62.2	402	2	S58477	rdxL protein - fis
290	28	62.2	253	2	G71560	probable sigma-28/	363	28	62.2	402	2	D82980	hypothetical prote
291	28	62.2	257	2	A28179	enterotoxin E prec	364	28	62.2	410	2	T11064	NADH2 dehydrogenas
292	28	62.2	257	2	G70937	hypothetical prote	365	28	62.2	416	2	AH0543	gamma-glutamyl pho
293	28	62.2	260	2	AB3457	conserved hypotet	366	28	62.2	416	2	A89996	probable ammonium
294	28	62.2	261	2	A82952	hypothetical prote	367	28	62.2	425	2	F97108	probable glycoeylt
295	28	62.2	261	2	C98331	hypothetical prote	368	28	62.2	433	2	T19607	hypothetical prote
296	28	62.2	266	2	A38664	probable peptide A	369	28	62.2	434	2	AD0197	NADH2 dehydrogenas
297	28	62.2	266	2	JC7816	chitinase (EC 3.2.	370	28	62.2	447	2	S52437	CDP-diacylglycerol
298	28	62.2	269	2	AD0804	probable membrane	371	28	62.2	453	2	B83427	para-aminobenzoate
299	28	62.2	271	2	C96015	probable hydroxyty	372	28	62.2	453	2	B95135	MATE efflux family
300	28	62.2	274	2	E83909	oligopeptide ABC t	373	28	62.2	453	2	D98003	conserved hypotet
301	28	62.2	276	2	C88650	protein C09G12.3 l	374	28	62.2	457	2	D89840	hypothetical prote
302	28	62.2	276	2	T33493	hypothetical prote	375	28	62.2	458	1	Q8EGC4	p53C intron protei
303	28	62.2	278	2	C69854	conserved hypotet	376	28	62.2	461	2	S52777	probable mannosyl
304	28	62.2	283	2	C88469	protein C2H8.7 [i	377	28	62.2	468	2	S57013	superoxide-produci
305	28	62.2	288	2	A05235	hypothetical prote	378	28	62.2	472	2	B90095	hypothetical prote
306	28	62.2	290	2	AC1235	Lactococcus lactis	379	28	62.2	474	2	F86819	dipeptidase [impor
307	28	62.2	294	2	AB1388	cell-division prot	380	28	62.2	496	2	T11376	cytochrome-c oxida
308	28	62.2	294	2	AD1763	cell-division prot	381	28	62.2	501	1	FWEMA	H+-transporting tw
309	28	62.2	302	2	JC2071	chitinase (EC 3.2.	382	28	62.2	503	1	PWYBA	H+-transporting tw
310	28	62.2	304	2	F95268	probable ABC trans	383	28	62.2	503	2	S36965	H+-transporting tw
311	28	62.2	308	2	JC2253	chitinase (EC 3.2.	384	28	62.2	503	2	F78321	H+-transporting tw
312	28	62.2	309	1	GTBPT4	gene 13 protein -	385	28	62.2	504	1	PWMTA	H+-transporting tw
313	28	62.2	309	2	F89980	manganese-dependen	386	28	62.2	504	2	JC7782	Cl- pump-associate
314	28	62.2	312	2	AH2791	conserved hypotet	387	28	62.2	505	1	PWYCA	H+-transporting tw
315	28	62.2	315	2	H97570	hypothetical 34.4X	388	28	62.2	505	2	S39520	H+-transporting tw
316	28	62.2	317	2	S63358	hypothetical prote	389	28	62.2	505	2	T06910	H+-transporting tw
317	28	62.2	318	2	T04403	probable chitinase	390	28	62.2	505	2	S13330	fixL protein - Bra
318	28	62.2	318	2	S14948	chitinase (EC 3.2.	391	28	62.2	506	2	AE1807	ATP synthase chain
319	28	62.2	319	2	JC2252	chitinase (EC 3.2.	392	28	62.2	506	2	G31090	H+-transporting tw
320	28	62.2	323	2	T03614	chitinase (EC 3.2.	393	28	62.2	507	1	PWLVA	H+-transporting tw
321	28	62.2	325	2	JC7560	cellulase (EC 3.2.	394	28	62.2	507	1	PWNTA	H+-transporting tw

395	28	62.2	507	1	PWRZA	H+-transporting tw	468	28	62.2	1051	2	T13174	gpi150 protein - fr
396	28	62.2	507	1	PWSPA	H+-transporting tw	469	28	62.2	1097	2	J00301	hypothetical 127K
397	28	62.2	507	1	PWZNA	H+-transporting tw	470	28	62.2	1097	2	T40678	hypothetical prote
398	28	62.2	512	2	JH0098	anthranilate synth	471	28	62.2	1148	2	JC5984	CAMP-dependent cel
399	28	62.2	516	2	E71957	ABC transporter, A	472	28	62.2	1162	2	T37889	probable nuclear p
400	28	62.2	516	2	B64551	oligopeptide ABC t	473	28	62.2	1238	2	T15824	hypothetical prote
401	28	62.2	521	2	S67491	phosphate transpor	474	28	62.2	1238	2	T42405	sax-3 protein - Ca
402	28	62.2	522	2	AF0893	methyl-accepting c	475	28	62.2	1291	2	T17242	hypothetical prote
403	28	62.2	529	2	AB2069	hypothetical prote	476	28	62.2	1581	2	T12963	hypothetical prote
404	28	62.2	532	2	JC1392	monophenol monooxy	477	28	62.2	1583	2	T14176	probable phosphati
405	28	62.2	534	2	D83775	hypothetical prote	478	28	62.2	2004	2	T30185	hypothetical prote
406	28	62.2	539	1	S39988	cytochrome-c oxida	479	27.5	61.1	445	2	E22845	hypothetical prote
407	28	62.2	539	1	S49495	cytochrome-c oxida	480	27	60.0	30	2	C82592	hypothetical prote
408	28	62.2	539	2	S77595	cytochrome-c oxida	481	27	60.0	42	2	T07248	hypothetical prote
409	28	62.2	539	2	A95345	FixN1 Heme b / cop	482	27	60.0	57	2	D82395	hypothetical prote
410	28	62.2	539	2	B95313	cytochrome-c oxida	483	27	60.0	66	2	T17015	metallothionein-li
411	28	62.2	541	2	AF3447	cytochrome-c oxida	484	27	60.0	76	2	T28248	ORF MSV087 probabl
412	28	62.2	545	2	S67621	hypothetical prote	485	27	60.0	83	2	T44124	hypothetical prote
413	28	62.2	548	2	B87423	cytochrome-c oxida	486	27	60.0	83	2	D64845	hypothetical prote
414	28	62.2	551	2	A13601	oligopeptide trans	487	27	60.0	85	2	T44083	hypothetical prote
415	28	62.2	568	2	T43734	phosphate transpor	488	27	60.0	86	2	C71960	hypothetical prote
416	28	62.2	569	2	T19483	hypothetical prote	489	27	60.0	88	2	A82803	hypothetical prote
417	28	62.2	570	2	AH2765	cytochrome-c oxida	490	27	60.0	90	2	T14922	hypothetical prote
418	28	62.2	571	2	S70773	cytochrome b245 be	491	27	60.0	100	2	A70424	hypothetical prote
419	28	62.2	571	2	T20359	hypothetical prote	492	27	60.0	107	2	S09879	hypothetical prote
420	28	62.2	583	2	A83540	exoenzymes regulat	493	27	60.0	108	2	AC1255	hypothetical prote
421	28	62.2	587	2	S54061	probable inorganic	494	27	60.0	111	2	T31580	hypothetical prote
422	28	62.2	598	2	E97546	cytochrome c oxida	495	27	60.0	112	2	H69537	conserved hypoteth
423	28	62.2	600	2	G83081	conserved hypoteth	496	27	60.0	118	2	S38608	ribosomal protein
424	28	62.2	603	2	AG3137	hypothetical prote	497	27	60.0	119	2	T19321	hypothetical prote
425	28	62.2	606	2	C98174	hypothetical ABC t	498	27	60.0	120	2	F81802	probable transcrip
426	28	62.2	606	2	AB3113	hypothetical prote	499	27	60.0	121	2	S18751	chitinase (EC 3.2.
427	28	62.2	609	2	D87049	hypothetical prote	500	27	60.0	136	2	PN0529	G protein-coupled
428	28	62.2	611	2	F98325	hypothetical ABC t	501	27	60.0	137	2	AF1148	hypothetical prote
429	28	62.2	611	2	AH2957	hypothetical prote	502	27	60.0	137	2	E64845	ycdV protein - Esc
430	28	62.2	612	2	E64820	probable oligopept	503	27	60.0	138	2	AF1507	hypothetical prote
431	28	62.2	612	2	D90742	hypothetical prote	504	27	60.0	142	2	S53808	hypothetical prote
432	28	62.2	612	2	G85592	hypothetical prote	505	27	60.0	143	2	C81065	transcription regu
433	28	62.2	616	2	A13102	hypothetical prote	506	27	60.0	144	2	S66938	probable membrane
434	28	62.2	616	2	A98184	hypothetical ABC t	507	27	60.0	147	2	T44120	conserved hypoteth
435	28	62.2	622	2	E72754	probable phosphoen	508	27	60.0	148	2	AG2200	two-component syst
436	28	62.2	623	2	A33622	SAC1 protein - yea	509	27	60.0	150	2	E90281	hypothetical prote
437	28	62.2	623	2	AD0603	hypothetical ABC t	510	27	60.0	156	2	AH2229	hypothetical prote
438	28	62.2	629	2	E72297	methionine-tRNA li	511	27	60.0	157	2	T44645	glycosyl transfera
439	28	62.2	636	2	S76730	hypothetical prote	512	27	60.0	157	2	S60084	ywd protein - Bac
440	28	62.2	642	2	E98150	hypothetical ABC t	513	27	60.0	161	2	S63061	probable membrane
441	28	62.2	648	2	A54892	Na+-dependent nucl	514	27	60.0	165	2	B84464	hypothetical prote
442	28	62.2	663	2	C71551	probable DNA ligas	515	27	60.0	172	2	T12904	hypothetical prote
443	28	62.2	667	2	T33526	hypothetical prote	516	27	60.0	174	1	H64007	hypothetical prote
444	28	62.2	673	2	C82326	MSHA biogenesis pr	517	27	60.0	184	2	D87234	probable secreted
445	28	62.2	677	2	T11231	NADH2 dehydrogenas	518	27	60.0	193	2	E82171	DNA-3-methyladenin
446	28	62.2	681	2	C75395	methionyl-tRNA syn	519	27	60.0	195	2	D71019	probable NADH-ubiq
447	28	62.2	705	2	D88536	acidic protein - C	520	27	60.0	195	2	A75114	NADH dehydrogenase
448	28	62.2	705	2	S27786	acidic protein - C	521	27	60.0	198	2	C97638	hypothetical prote
449	28	62.2	717	2	S09069	probable membrane	522	27	60.0	198	2	AD2861	hypothetical prote
450	28	62.2	717	1	VGBE11	glycoprotein H pre	523	27	60.0	199	2	A69859	hypothetical prote
451	28	62.2	725	1	E64211	virulence-associat	524	27	60.0	200	2	T47531	hypothetical prote
452	28	62.2	742	2	AH2166	hypothetical prote	525	27	60.0	205	2	D69804	conserved hypoteth
453	28	62.2	744	2	A45622	surface antigen gp	526	27	60.0	214	1	RGBSCA	regulatory protein
454	28	62.2	790	2	S63138	probable protein k	527	27	60.0	216	2	C90456	hypothetical prote
455	28	62.2	825	2	I46078	endothelin convert	528	27	60.0	216	2	D82921	conserved hypoteth
456	28	62.2	833	2	S50225	potassium transpor	529	27	60.0	217	2	T33652	hypothetical prote
457	28	62.2	840	2	B86901	mismatch repair pr	530	27	60.0	219	2	C69439	sugar fermentation
458	28	62.2	841	2	T38703	hypothetical prote	531	27	60.0	224	2	G82913	conserved hypoteth
459	28	62.2	843	2	T41237	conserved hypoteth	532	27	60.0	232	2	G84954	adenosylhomocystei
460	28	62.2	865	2	A83946	DNA mismatch repai	533	27	60.0	232	2	S47846	rfaY protein - Esc
461	28	62.2	870	2	B40121	Grpase-activating	534	27	60.0	235	2	T26489	hypothetical prote
462	28	62.2	874	2	T29548	hypothetical prote	535	27	60.0	237	2	D95938	hypothetical membr
463	28	62.2	906	2	E84948	NADH2 dehydrogenas	536	27	60.0	239	2	D89969	enterotoxin SEM i
464	28	62.2	919	2	JC5934	exostose-related p	537	27	60.0	240	2	G89991	extracellular ente
465	28	62.2	1038	2	JT0663	ras Grpase-activat	538	27	60.0	241	2	AH1941	extracellular ente
466	28	62.2	1044	2	S01966	Grpase-activating	539	27	60.0	242	2	C89969	hypothetical prote
467	28	62.2	1047	2	A40121	Grpase-activating	540	27	60.0	244	2	E70905	hypothetical prote

541	27	60.0	245	2	F64465	hypothetical prote	614	27	60.0	324	2	T10802	chitinase (EC 3.2.
542	27	60.0	247	2	S37342	chitinase (EC 3.2.	615	27	60.0	326	2	B98967	hypothetical prote
543	27	60.0	247	2	G82202	hypothetical prote	616	27	60.0	327	1	JQ0965	chitinase (EC 3.2.
544	27	60.0	250	2	S51588	chitinase (EC 3.2.	617	27	60.0	329	2	T24217	hypothetical prote
545	27	60.0	251	2	T09980	H+-transporting tw	618	27	60.0	332	1	S41003	protein kinase (EC
546	27	60.0	252	2	S48848	chitinase (EC 3.2.	619	27	60.0	332	2	B64184	oligopeptide trans
547	27	60.0	252	2	B95082	amino acid ABC tra	620	27	60.0	333	2	A02066	oligopeptide trans
548	27	60.0	252	2	F97949	hypothetical prote	621	27	60.0	334	1	QREBOF	oligopeptide trans
549	27	60.0	253	1	A40582	type IV prepilin p	622	27	60.0	334	2	C06651	oligopeptide trans
550	27	60.0	253	2	S37343	chitinase (EC 3.2.	623	27	60.0	334	2	C90847	hypothetical prote
551	27	60.0	253	2	S51589	chitinase (EC 3.2.	624	27	60.0	334	2	B85705	hypothetical prote
552	27	60.0	253	2	A34801	pathogenesis-relat	625	27	60.0	334	2	B64872	oligopeptide trans
553	27	60.0	253	2	B34801	pathogenesis-relat	626	27	60.0	334	2	F69495	conserved hypothet
554	27	60.0	253	2	S20737	chitinase (EC 3.2.	627	27	60.0	335	2	B75057	glycerate dehydrog
555	27	60.0	253	2	D82273	leader peptidase T	628	27	60.0	335	2	AB0776	probable exported
556	27	60.0	253	2	H81391	amino-acid ABC tra	629	27	60.0	335	2	G72258	conserved hypothet
557	27	60.0	254	2	S20741	chitinase (EC 3.2.	630	27	60.0	336	2	F82242	oligopeptide ABC t
558	27	60.0	255	2	B82813	hypothetical prote	631	27	60.0	336	2	B64499	hypothetical prote
559	27	60.0	256	2	S48847	chitinase (EC 3.2.	632	27	60.0	338	2	B72424	oligopeptide ABC t
560	27	60.0	259	1	TPBPPR	terminal protein -	633	27	60.0	338	2	D69052	phosphoribosylamin
561	27	60.0	261	2	T40773	hypothetical prote	634	27	60.0	342	1	CPFM	plastoquinol-plast
562	27	60.0	261	2	T20264	hypothetical prote	635	27	60.0	343	2	E75172	probable threonine
563	27	60.0	261	2	G72470	probable ABC trans	636	27	60.0	343	2	H96703	probable RING zinc
564	27	60.0	263	2	S72528	chitinase (EC 3.2.	637	27	60.0	344	2	D86597	outer membrane pro
565	27	60.0	264	2	S22600	ste4 protein - fis	638	27	60.0	344	2	H72027	major outer membra
566	27	60.0	264	2	AE2274	hypothetical prote	639	27	60.0	346	2	T41913	G protein-coupled
567	27	60.0	266	2	A99369	hypothetical prote	640	27	60.0	346	2	T19629	hypothetical prote
568	27	60.0	266	2	G64538	conserved hypothet	641	27	60.0	349	2	T27204	hypothetical prote
569	27	60.0	271	2	D71230	hypothetical prote	642	27	60.0	351	2	A38528	outer membrane por
570	27	60.0	272	2	D75626	glycerol-3-phospha	643	27	60.0	354	2	B72688	probable high-affi
571	27	60.0	273	2	PC4153	monophenol monooxy	644	27	60.0	357	2	T33507	hypothetical prote
572	27	60.0	274	2	F75161	homoserine kinase	645	27	60.0	358	2	B64309	hypothetical prote
573	27	60.0	275	2	T03032	chitinase (EC 3.2.	646	27	60.0	361	2	G64354	hypothetical prote
574	27	60.0	275	2	T40345	probable autophago	647	27	60.0	361	2	A64507	hypothetical prote
575	27	60.0	275	2	H70881	probable PR protei	648	27	60.0	362	2	B90461	hypothetical prote
576	27	60.0	277	2	T29611	hypothetical prote	649	27	60.0	362	2	S74433	GDP-D-mannose dehy
577	27	60.0	278	1	A47404	alpha-tocopherol t	650	27	60.0	363	2	H64378	hypothetical prote
578	27	60.0	278	2	T03440	probable chitinase	651	27	60.0	364	2	T34221	lir-1 protein - Ca
579	27	60.0	278	2	S54352	alpha-tocopherol t	652	27	60.0	367	2	AD1315	prephenate dehydro
580	27	60.0	279	2	T24606	hypothetical prote	653	27	60.0	367	2	AD1687	prephenate dehydro
581	27	60.0	280	2	T24579	hypothetical prote	654	27	60.0	372	2	T24569	hypothetical prote
582	27	60.0	280	2	C86881	hypothetical prote	655	27	60.0	373	2	T21955	hypothetical prote
583	27	60.0	288	2	T28209	triacylglycerol li	656	27	60.0	374	2	H83471	probable glycosyl
584	27	60.0	289	2	E97185	polysaccharide dea	657	27	60.0	376	1	RDEC2R	ribonucleoside-dip
585	27	60.0	290	2	E70141	oligopeptide trans	658	27	60.0	376	2	A71175	probable dehydroge
586	27	60.0	290	2	E72676	hypothetical prote	659	27	60.0	376	2	AD0791	ribonucleoside-dip
587	27	60.0	292	2	T10106	chitinase (EC 3.2.	660	27	60.0	376	2	H85862	ribonucleoside-dip
588	27	60.0	294	2	G90032	hypothetical prote	661	27	60.0	376	2	F91018	ribonucleoside-dip
589	27	60.0	298	2	H81422	proteinase Cj0068	662	27	60.0	376	2	AC3535	dipeptide transpor
590	27	60.0	300	2	T32697	hypothetical prote	663	27	60.0	377	2	A64426	hypothetical prote
591	27	60.0	302	2	T10810	chitinase (EC 3.2.	664	27	60.0	378	2	D70324	hypothetical prote
592	27	60.0	302	2	D81435	probable iron-upta	665	27	60.0	379	2	G87046	probable acyltrans
593	27	60.0	308	2	G98084	hypothetical prote	666	27	60.0	380	2	G97969	hypothetical prote
594	27	60.0	308	2	G95220	hypothetical prote	667	27	60.0	380	2	F95101	aminotransferase,
595	27	60.0	308	2	S11151	amid protein - Str	668	27	60.0	383	2	T15043	fungal elicitor-in
596	27	60.0	308	2	S11153	oligopeptide trans	669	27	60.0	383	2	F70752	hypothetical prote
597	27	60.0	308	2	E95220	hypothetical prote	670	27	60.0	383	2	A26768	opsin, R7 photorec
598	27	60.0	308	2	G84104	oligopeptide ABC t	671	27	60.0	383	2	E81928	probable glycosyl
599	27	60.0	311	2	T27203	hypothetical prote	672	27	60.0	386	1	A64433	probable hydro-lya
600	27	60.0	313	2	T11160	NADH2 dehydrogenas	673	27	60.0	388	2	D72200	ornithine decarbox
601	27	60.0	313	2	B23701	olfactory receptor	674	27	60.0	394	1	S43915	maltoase permease -
602	27	60.0	314	2	T43132	hypothetical prote	675	27	60.0	397	2	AG1426	transport protein
603	27	60.0	315	2	C72687	hypothetical prote	676	27	60.0	397	2	C95221	hypothetical prote
604	27	60.0	317	2	AE0580	lysr-family transc	677	27	60.0	397	2	B98085	hypothetical prote
605	27	60.0	318	2	T50039	beta-1,4-galactosy	678	27	60.0	399	1	E70888	probable glf prote
606	27	60.0	318	2	T28941	hypothetical prote	679	27	60.0	399	2	B70349	hypothetical prote
607	27	60.0	319	2	T32696	hypothetical prote	680	27	60.0	400	2	D64462	hypothetical prote
608	27	60.0	320	2	S59947	chitinase (EC 3.2.	681	27	60.0	401	2	B75395	aminotransferase,
609	27	60.0	321	2	S57482	chitinase class 1	682	27	60.0	401	2	AF1800	transport protein
610	27	60.0	322	2	S59953	chitinase (EC 3.2.	683	27	60.0	401	2	AE3537	oligopeptide trans
611	27	60.0	322	2	E84105	oligopeptide ABC t	684	27	60.0	402	2	T37694	hypothetical prote
612	27	60.0	322	2	A57516	DNA supercoiling f	685	27	60.0	403	2	E71309	conserved hypothet
613	27	60.0	323	2	E98084	hypothetical prote	686	27	60.0	405	2	H71620	aspartate transami

687	27	60.0	405	2	T09359	hypothetical prote	760	27	60.0	559	2	AC1512	hypothetical prote
688	27	60.0	414	2	S75052	hypothetical prote	761	27	60.0	566	2	T50536	succinate dehydrog
689	27	60.0	414	2	T21954	hypothetical prote	762	27	60.0	566	2	D30250	glycogen synthase
690	27	60.0	414	2	S70138	probable membrane	763	27	60.0	571	2	E36550	hypothetical prote
691	27	60.0	415	2	I56251	GTP binding protei	764	27	60.0	578	2	H82355	peptide ABC transp
692	27	60.0	418	2	S30134	hypothetical prote	765	27	60.0	578	2	I56215	interleukin-10 rec
693	27	60.0	420	2	AF2464	hypothetical prote	766	27	60.0	578	2	T15077	hypothetical prote
694	27	60.0	422	2	A55587	ketosynthase - Str	767	27	60.0	589	2	T23881	hypothetical prote
695	27	60.0	424	2	S70399	zona pellucida gly	768	27	60.0	589	2	F95292	probable ABC trans
696	27	60.0	430	2	D90535	DNA-damage repair	769	27	60.0	591	1	WMBPQ2	gene P2 protein -
697	27	60.0	432	2	H64709	hypothetical prote	770	27	60.0	592	2	T51712	threonine ammonia-
698	27	60.0	432	2	A34413	atrial gland granu	771	27	60.0	609	2	S04757	NADH2 dehydrogen
699	27	60.0	432	2	E89954	conserved hypotet	772	27	60.0	613	2	A69535	aldehyde ferredoxi
700	27	60.0	433	2	T21989	hypothetical prote	773	27	60.0	617	2	S77332	NADH2 dehydrogen
701	27	60.0	435	2	S23580	probable protein k	774	27	60.0	617	2	T23082	hypothetical prote
702	27	60.0	440	2	A84387	oligopeptide ABC t	775	27	60.0	617	2	AF1284	5-methyltetrahydro
703	27	60.0	444	2	T12297	NADH2 dehydrogen	776	27	60.0	617	2	A11655	5-methyltetrahydro
704	27	60.0	445	2	D84385	oligopeptide ABC t	777	27	60.0	624	2	B71810	probable type I re
705	27	60.0	445	2	E64388	conserved hypotet	778	27	60.0	639	2	T06735	hypothetical prote
706	27	60.0	450	2	F96816	hypothetical prote	779	27	60.0	648	2	F69848	transcription anti
707	27	60.0	452	2	A84196	acyl-CoA dehydrog	780	27	60.0	652	2	T39722	serine/threonine p
708	27	60.0	457	2	C97341	uncharacterized FA	781	27	60.0	658	2	G81727	conserved hypotet
709	27	60.0	458	2	T20441	hypothetical prote	782	27	60.0	662	2	JC7906	sucrose 1F-fructos
710	27	60.0	458	2	E72244	conserved hypotet	783	27	60.0	674	2	G72204	hypothetical prote
711	27	60.0	459	2	B84905	hypothetical prote	784	27	60.0	674	2	E82954	conserved hypotet
712	27	60.0	460	2	E64019	hypothetical prote	785	27	60.0	676	1	W2VZ18	I8 protein - vacci
713	27	60.0	461	2	A53370	arginine catabolis	786	27	60.0	676	2	T37345	NPH-II, helicase -
714	27	60.0	461	2	C72357	conserved hypotet	787	27	60.0	676	2	D42511	I8R protein - vacc
715	27	60.0	463	2	T04686	hypothetical prote	788	27	60.0	676	2	F36843	ATP/GTP-binding pr
716	27	60.0	463	2	AG2162	hypothetical prote	789	27	60.0	676	2	T28500	hypothetical prote
717	27	60.0	470	2	A37854	para-aminobenzoate	790	27	60.0	682	2	D72158	L8R protein - vari
718	27	60.0	472	2	T33800	hypothetical prote	791	27	60.0	735	2	D96737	AR1-like protein,
719	27	60.0	474	1	T05239	acid phosphatase (	792	27	60.0	736	2	T26006	hypothetical prote
720	27	60.0	475	2	T26460	hypothetical prote	793	27	60.0	737	2	AE2245	hypothetical prote
721	27	60.0	479	2	H86465	FI2G12.1 protein -	794	27	60.0	747	2	F64127	DNA topoisomerase
722	27	60.0	481	2	H96729	probable alanine a	795	27	60.0	747	2	C75545	phosphoribosylform
723	27	60.0	486	2	S51503	NADH2 dehydrogen	796	27	60.0	749	2	H82691	topoisomerase IV s
724	27	60.0	486	2	H72321	glycogen synthase	797	27	60.0	752	2	AF0888	topoisomerase IV c
725	27	60.0	486	2	B83661	para-aminobenzoate	798	27	60.0	752	2	A65089	DNA topoisomerase
726	27	60.0	487	2	H97304	uncharacterized co	799	27	60.0	752	2	A45582	DNA topoisomerase
727	27	60.0	493	2	B42519	Al8R protein - vac	800	27	60.0	752	2	G85961	DNA topoisomerase
728	27	60.0	493	2	C36415	56K abortive late	801	27	60.0	752	2	G91116	DNA topoisomerase
729	27	60.0	493	2	T37405	DNA helicase - vac	802	27	60.0	754	2	G83025	topoisomerase IV s
730	27	60.0	493	2	A36850	Al8R protein - var	803	27	60.0	757	2	AB0083	DNA topoisomerase
731	27	60.0	493	2	T28560	hypothetical prote	804	27	60.0	760	2	T24521	hypothetical prote
732	27	60.0	493	2	H72165	Al9R protein - var	805	27	60.0	761	2	F82078	topoisomerase IV,
733	27	60.0	494	2	AD0751	cytoplasmic alpha-	806	27	60.0	761	2	T43788	DNA topoisomerase
734	27	60.0	495	1	A45738	alpha-amylase (EC	807	27	60.0	768	2	G82506	hypothetical prote
735	27	60.0	495	2	B85810	cytoplasmic alpha-	808	27	60.0	772	2	T16474	hypothetical prote
736	27	60.0	495	2	B90962	cytoplasmic alpha-	809	27	60.0	791	2	E90566	conserved hypotet
737	27	60.0	495	2	T33548	hypothetical prote	810	27	60.0	793	2	A12712	organic solvent to
738	27	60.0	501	2	B83662	lysyl-tRNA synthet	811	27	60.0	793	2	G57494	gene fused protein
739	27	60.0	502	2	T01996	nucleoid DNA-bind	812	27	60.0	795	2	JC4234	outer envelope mem
740	27	60.0	503	2	JN0524	tcptf protein - Vib	813	27	60.0	818	2	T12975	probable NADH2 deh
741	27	60.0	503	2	F82275	toxin co-regulated	814	27	60.0	820	2	C81252	hypothetical prote
742	27	60.0	504	2	S73163	H+-transporting tw	815	27	60.0	838	2	F97768	probable chromomet
743	27	60.0	505	2	C84949	NADH2 dehydrogen	816	27	60.0	839	2	G96719	endopeptidase Clp
744	27	60.0	505	2	S26962	H+-transporting tw	817	27	60.0	857	1	D35905	ClpB protein (heat
745	27	60.0	505	2	AE1451	hypothetical prote	818	27	60.0	857	2	A10831	heat shock protein
746	27	60.0	508	2	T22836	hypothetical prote	819	27	60.0	857	2	G91060	Clp ATPase [import
747	27	60.0	509	2	E83315	NADH2 dehydrogen	820	27	60.0	857	2	A10397	taste receptor T1R
748	27	60.0	527	2	S46155	probable serine/th	821	27	60.0	858	2	JC7683	heat shock protein
749	27	60.0	529	1	YRHU1	monophenol monooxy	822	27	60.0	861	2	E85905	mismatch repair pr
750	27	60.0	531	2	T11074	NADH2 dehydrogen	823	27	60.0	863	2	H84177	hypothetical prote
751	27	60.0	533	1	YRMSCS	monophenol monooxy	824	27	60.0	881	2	T25786	hypothetical prote
752	27	60.0	534	2	S41735	cholesterol estera	825	27	60.0	896	2	G96946	probable vacuolar
753	27	60.0	540	2	B45665	adult-specific 61.	826	27	60.0	905	2	T38314	uncharacterized co
754	27	60.0	541	2	F96776	hypothetical prote	827	27	60.0	906	2	B96901	DNA polymerase I (
755	27	60.0	541	2	G90516	ABC transporter at	828	27	60.0	908	2	C70168	multiple banded an
756	27	60.0	546	2	JN0551	cytochrome-c oxida	829	27	60.0	913	2	D82885	vril protein - Dic
757	27	60.0	549	2	JN0551	triacetylgllycerol li	830	27	60.0	929	2	T17392	DNA polymerase I N
758	27	60.0	551	2	B95390	probable ABC Trans	831	27	60.0	938	2	G81020	DNA-directed DNA p
759	27	60.0	557	2	H72400	excinuclease ABC c	832	27	60.0	938	2	F81963	

833	27	60.0	940	2	B81852	probable type III	906	26	57.8	149	2	F81304	hypothetical prote
834	27	60.0	943	2	G84402	dipeptide ABC tran	907	26	57.8	151	2	S52598	coagulation factor
835	27	60.0	959	2	F72763	probable DNA-dirc	908	26	57.8	152	2	JC4690	hypothetical prote
836	27	60.0	981	2	T05505	hypothetical prote	909	26	57.8	155	2	C81150	hypothetical prote
837	27	60.0	991	2	C96764	hypothetical prote	910	26	57.8	158	2	T46080	hypothetical prote
838	27	60.0	1001	2	T13807	potassium channel	911	26	57.8	160	2	C34285	NADH2 dehydrogenas
839	27	60.0	1003	2	H82883	hypothetical prote	912	26	57.8	161	2	F82322	conserved hypotnet
840	27	60.0	1004	2	JH0470	Na+/K+-exchanging	913	26	57.8	163	2	F84059	hypothetical prote
841	27	60.0	1007	2	D71490	probable exodeoxyr	914	26	57.8	163	2	C86323	protein F14D16.7 [
842	27	60.0	1007	2	JC8066	138K protein - Tet	915	26	57.8	164	2	F83798	hypothetical prote
843	27	60.0	1025	2	H81751	exodeoxyribonuclea	916	26	57.8	166	2	T47266	ribosomal protein
844	27	60.0	1045	2	B30239	hydroxymethylgluta	917	26	57.8	168	2	A75113	hypothetical prote
845	27	60.0	1062	2	D96540	hypothetical prote	918	26	57.8	169	2	P69353	conserved hypotnet
846	27	60.0	1068	1	A43322	1-phosphatidylinos	919	26	57.8	169	2	S19459	hypothetical prote
847	27	60.0	1068	1	I38110	1-phosphatidylinos	920	26	57.8	170	2	F82908	conserved hypotnet
848	27	60.0	1093	2	H84126	cation efflux syst	921	26	57.8	172	2	S18871	2S-like storage pr
849	27	60.0	1119	2	T16720	hypothetical prote	922	26	57.8	178	2	B81872	hypothetical prote
850	27	60.0	1173	2	T30308	rexA protein - Lac	923	26	57.8	179	2	A12056	polypeptide deform
851	27	60.0	1203	2	D86625	subunit A of ATP-d	924	26	57.8	182	2	AE2355	hypothetical prote
852	27	60.0	1240	2	T48800	SMT4 related prote	925	26	57.8	186	2	B29835	Tras protein - Esc
853	27	60.0	1248	2	A53588	adenylate cyclase	926	26	57.8	187	2	S75402	hypothetical prote
854	27	60.0	1256	1	A43829	muramidase-release	927	26	57.8	188	2	G82333	conserved hypotnet
855	27	60.0	1270	2	T26720	hypothetical prote	928	26	57.8	190	2	T39556	hypothetical prote
856	27	60.0	1299	2	T42589	hypothetical prote	929	26	57.8	191	2	T32278	hypothetical prote
857	27	60.0	1315	2	G96722	hypothetical prote	930	26	57.8	193	2	AH2035	hypothetical prote
858	27	60.0	1336	2	T18288	ABC transport prot	931	26	57.8	194	2	T15115	hypothetical prote
859	27	60.0	1345	2	T29090	surface layer-asso	932	26	57.8	195	2	T49012	calmodulin-like pr
860	27	60.0	1413	2	G84790	probable ABC trans	933	26	57.8	196	2	T28253	hypothetical prote
861	27	60.0	1430	2	T21910	hypothetical prote	934	26	57.8	202	2	T21165	hypothetical prote
862	27	60.0	1442	2	C82898	DNA polymerase III	935	26	57.8	202	2	H97247	S-adenosylmethioni
863	27	60.0	1450	2	T45888	ABC transporter-I1	936	26	57.8	203	2	A43856	major fibmbrial pro
864	27	60.0	1553	2	T18502	hypothetical prote	937	26	57.8	203	2	B83854	hypothetical prote
865	27	60.0	1628	2	T38055	hypothetical prote	938	26	57.8	206	2	T27766	hypothetical prote
866	27	60.0	1646	1	WMTWS2	186K protein - cuc	939	26	57.8	208	2	E97899	hypothetical prote
867	27	60.0	1780	2	T17272	hypothetical prote	940	26	57.8	210	2	S52050	cytochrome-c oxida
868	27	60.0	1817	2	D71606	hypothetical prote	941	26	57.8	211	2	C97223	probable S-adenosy
869	27	60.0	1883	2	G82875	hypothetical prote	942	26	57.8	213	2	F95198	hypothetical prote
870	27	60.0	1905	2	T18267	multidrug resistan	943	26	57.8	213	2	F86310	protein F1L3.8 [im
871	27	60.0	1994	2	D86452	protein F6N18.13 [	944	26	57.8	216	2	AC1155	probable transaldo
872	27	60.0	2013	2	C71610	probable membrane	945	26	57.8	216	2	AF1513	probable transaldo
873	27	60.0	2244	2	F90563	hypothetical prote	946	26	57.8	218	2	B28946	glutathione transf
874	27	60.0	3106	1	S53868	laminin alpha-2 ch	947	26	57.8	218	2	S33860	glutathione transf
875	27	60.0	3135	2	A48584	transmission block	948	26	57.8	218	2	A29794	glutathione transf
876	27	60.0	3600	2	D86161	F1003.12 protein -	949	26	57.8	218	2	B29231	glutathione transf
877	27	60.0	3724	2	T18427	hypothetical prote	950	26	57.8	221	2	C96974	acyl carrier prote
878	26.5	58.9	268	2	T15693	hypothetical prote	951	26	57.8	222	2	AF3133	hypothetical prote
879	26.5	58.9	885	2	C83441	two-component sens	952	26	57.8	223	1	F64404	hypothetical prote
880	26	57.8	30	2	B95126	hypothetical prote	953	26	57.8	224	1	D69217	hypothetical prote
881	26	57.8	63	2	A99951	hypothetical prote	954	26	57.8	225	1	MMIH68	E1 membrane glycop
882	26	57.8	66	2	D90144	hypothetical prote	955	26	57.8	225	2	A35295	glutathione transf
883	26	57.8	68	2	S52051	hypothetical prote	956	26	57.8	225	2	D75118	uridylyate kinase (
884	26	57.8	80	2	E70310	host factor I - Aq	957	26	57.8	226	2	G86641	hypothetical prote
885	26	57.8	85	2	A42056	ribosomal protein	958	26	57.8	227	2	C58932	channel subunit of
886	26	57.8	90	2	T25304	hypothetical prote	959	26	57.8	228	2	S09772	hypothetical prote
887	26	57.8	99	2	A44866	major merozoite su	960	26	57.8	229	2	T40148	hypothetical prote
888	26	57.8	104	2	AG2357	hypothetical prote	961	26	57.8	230	2	S34975	polysaccharide cha
889	26	57.8	107	2	S41542	membrane alanyl am	962	26	57.8	231	2	D96718	hypothetical prote
890	26	57.8	108	2	B40085	ubiquitin carboxyl	963	26	57.8	232	2	H96702	hypothetical prote
891	26	57.8	108	2	B99318	hypothetical prote	964	26	57.8	233	1	H71040	probable phosphoes
892	26	57.8	109	2	G81059	hypothetical prote	965	26	57.8	234	2	A75587	probable urea/ehor
893	26	57.8	115	2	S39393	glutathione transf	966	26	57.8	235	2	G65212	hypothetical 26.7K
894	26	57.8	119	2	A71229	hypothetical prote	967	26	57.8	240	2	F64676	biotin synthesis p
895	26	57.8	119	2	H71610	hypothetical prote	968	26	57.8	242	2	G75029	hypothetical prote
896	26	57.8	122	2	E71540	hypothetical prote	969	26	57.8	243	2	E90042	hypothetical prote
897	26	57.8	124	2	C69335	succinate dehydrog	970	26	57.8	243	2	B97344	ABC-type polar ami
898	26	57.8	124	2	S09802	hypothetical prote	971	26	57.8	243	2	F98154	glutamine ABC tran
899	26	57.8	143	2	S41017	hypothetical prote	972	26	57.8	243	2	AD2748	hypothetical prote
900	26	57.8	146	2	D95092	conserved hypotnet	973	26	57.8	243	2	C97529	glutamine ABC tran
901	26	57.8	147	2	A97960	conserved hypotnet	974	26	57.8	243	2	C95295	probable ABC trans
902	26	57.8	147	2	AH0495	probable membrane	975	26	57.8	245	2	JC7893	prostate-specific
903	26	57.8	147	2	AI2142	hypothetical prote	976	26	57.8	247	2	D83671	amino acid ABC tra
904	26	57.8	148	1	OTBWL3	cytochrome-c oxida	977	26	57.8	249	2	S07917	Rf3 protein - yeast
905	26	57.8	149	1	W6YL35	E6 protein - human	978	26	57.8	251	2	B64501	hypothetical prote

979 26 57.8 253 2 D71446 hypothetical prote  
980 26 57.8 253 2 H83874 oligopeptide ABC t  
981 26 57.8 254 2 G90031 hypothetical prote  
982 26 57.8 255 2 E71967 hypothetical prote  
983 26 57.8 256 2 S37893 csGA protein homol  
984 26 57.8 256 2 A35340 H+-transporting tw  
985 26 57.8 258 2 G89968 extracellular ente  
986 26 57.8 260 2 S78160 ymf16 protein - Re  
987 26 57.8 262 2 S78172 probable transpor  
988 26 57.8 263 2 A44229 interferon-gamma r  
989 26 57.8 265 1 OT0B3M cytochrome-c oxida  
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991 26 57.8 265 2 S20801 cytochrome-c oxida  
992 26 57.8 265 2 A70944 hypothetical prote  
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994 26 57.8 266 2 H90286 hypothetical prote  
995 26 57.8 267 2 C90411 ketopantoate hydro  
996 26 57.8 267 2 B82694 copper homeostasis  
997 26 57.8 268 2 H97256 probable membrane  
998 26 57.8 269 2 T37210 hypothetical prote  
999 26 57.8 271 2 T11386 cytochrome-c oxida  
1000 26 57.8 271 2 B82295 prolipoprotein dia

## ALIGNMENTS

RESULT 1  
A82921  
protein phosphatase UU215 [imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 05-Oct-2004  
C:Accession: A82921  
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
submitted to GenBank, February 2000  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min  
A:Reference number: A82870  
A:Accession: A82921  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-247 <GLA>  
A:Cross-references: UNIPARC:UPI00000C1BD0; GB:AE002120; GB:AF222894; NID:G6899167; PIDN:  
A:Experimental source: serovar 3; biovar 1  
C:Genetics:  
A:Gene: ptcl; UU215  
A:Genetic code: SGC3  
C:Superfamily: conserved hypothetical protein yloO

Query Match 91.1%; Score 41; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0

QY 1 FLSYDLFV 8  
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Db 176 FLSYDLFV 183

RESULT 2  
C89964  
truncated transposase [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: C89964  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: C89964  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-259 <KUR>

A:Cross-references: UNIPROT:Q9782; UNIPARC:UPI00000CAB88; GB:BA000018; PID:g13701580;  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: truncated-SA

Query Match 82.2%; Score 37; DB 2; Length 259;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLF 7  
|||||||  
Db 12 FLSYDLF 18

RESULT 3  
F72277  
hypothetical protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: F72277  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
C.M.

Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: F72277  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-191 <ARN>  
A:Cross-references: UNIPROT:Q9X0X9; UNIPARC:UPI00000C12CB; GB:AE001780; GB:AE000512; NID  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM1252

Query Match 80.0%; Score 36; DB 2; Length 191;  
Best Local Similarity 66.7%; Pred. No. 8.2;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
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Db 44 FLSYDLFVV 52

RESULT 4  
A10315  
conserved hypothetical protein YPO2589 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: A10315  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB00001; MUID:21470413; PMID:11586360  
A:Accession: A10315  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-95 <KUR>  
A:Cross-references: UNIPROT:Q8ZDH9; UNIPARC:UPI00000DC6C5; GB:AL590842; PIDN:CAC91389.1,  
C:Genetics:  
A:Gene: YPO2589

Query Match 75.6%; Score 34; DB 2; Length 95;  
Best Local Similarity 85.7%; Pred. No. 10;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
|||||||  
Db 36 LSYDLFV 42

```

RESULT 5
C64712
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Helicobacter pylori (strain
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: C64712
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64712
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-412 <TOM>
A:Cross-references: UNIPROT:Q26064; UNIPARC:UPI00000D31AD; GB:AE000652; GB:AE000511; NID
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C:Keywords: electron transfer; heme; iron; metalloprotein; oxidoreductase
F:21-370/Domain: cytochrome b6 homology <CB6>
F:21-223/Domain: cytochrome b6 homology <CB6>
F:250-370/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F:94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:108,210/Binding site: heme iron (His) (axial ligands) (high potential) #status predict

Query Match 75.6%; Score 34; DB 2; Length 412;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
||| |:|||
Db 253 FLKSDIFV 261

RESULT 6
D71803
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Helicobacter pylori (strain
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: D71803
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923362
A:Accession: D71803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-412 <ARN>
A:Cross-references: UNIPROT:Q92J55; UNIPARC:UPI00000D374F; GB:AE001568; GB:AE001439; NID
A:Experimental source: strain J99
C:Genetics:
A:Gene: petB
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C:Keywords: electron transfer; heme; iron; metalloprotein; oxidoreductase
F:21-370/Domain: cytochrome b6 homology <CB6>
F:21-223/Domain: cytochrome b6 homology <CB6>
F:250-370/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F:94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:108,210/Binding site: heme iron (His) (axial ligands) (high potential) #status predict

Query Match 75.6%; Score 34; DB 2; Length 412;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
||| |:|||
Db 253 FLKSDIFV 261

RESULT 7
C64712
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Helicobacter pylori (strain
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: C64712
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64712
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-412 <TOM>
A:Cross-references: UNIPROT:Q26064; UNIPARC:UPI00000D31AD; GB:AE000652; GB:AE000511; NID
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C:Keywords: electron transfer; heme; iron; metalloprotein; oxidoreductase
F:21-370/Domain: cytochrome b6 homology <CB6>
F:21-223/Domain: cytochrome b6 homology <CB6>
F:250-370/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F:94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:108,210/Binding site: heme iron (His) (axial ligands) (high potential) #status predict

Query Match 75.6%; Score 34; DB 2; Length 412;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
||| |:|||
Db 253 FLKSDIFV 261

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C72295
hypothetical protein TW1105 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72295
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se-
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-452 <ARN>
A:Cross-references: UNIPROT:O9X019; UNIPARC:UPI00000D392D; GB:AE001769; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TW1105
C:Superfamily: [NiFe]-hydrogenase-3-type complex, large membrane subunit
C:Keywords: [NiFe]-hydrogenase-3-type complex, large membrane subunit

Query Match 75.6%; Score 34; DB 2; Length 452;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLF 7
||| |:|||
Db 102 FVSYDLF 108

RESULT 8
S01213
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - brine shrimp mitochondrion (fra
C:Species: mitochondrion Artemia sp. (brine shrimp)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Jun-2002
C:Accession: S01213
R:Batuecas, B.; Garesse, R.; Calleja, M.; Valverde, J.R.; Marco, R.
Nucleic Acids Res. 16, 6515-6529, 1988
A:Title: Genome organization of Artemia mitochondrial DNA.
A:Reference number: S01207; MUID:88289417; PMID:3135541
A:Accession: S01213
A:Molecule type: DNA
A:Residues: 1-31,32-70 <BAT>
A:Cross-references: UNIPARC:UPI000016D4B8; UNIPARC:UPI000016D4B9; EMBL:X07665
A:Note: The translation of residues 1-8 is inconsistent with the nucleotide sequence
C:Genetics:
A:Gene: mitochondrion
A:Genetic code: SGC4
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 73.3%; Score 33; DB 2; Length 70;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
||| |:|||
Db 33 FLSYPLFI 40

RESULT 9
I40517
spag protein - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40517
R:Klein, C.; Entian, K.D.
Appl. Environ. Microbiol. 60, 2793-2801, 1994
A:Title: Genes involved in self-protection against the lantibiotic subtilin produced by
A:Reference number: I40511; MUID:94368094; PMID:8085823
A:Accession: I40517
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

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A;Residues: 1-203 <RES>  
A;Cross-references: UNIPROT:Q45405; UNIPARC:UPI00000B9FE1; EMBL:U09819; NID:g2702240; PI  
C;Genetics:  
A;Gene: spa

Query Match 73.3%; Score 33; DB 2; Length 203;  
Best Local Similarity 62.5%; Pred. No. 35;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFVV 9  
|||::|:  
Db 78 LSYDIFIM 85

RESULT 10  
T39166  
inorganic phosphate transporter [similarity] - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jun-2000  
C;Accession: T50381; T39166  
R;Connor, R.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, February 1998  
A;Reference number: Z21832  
A;Accession: T50381  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-274 <CO2>  
A;Cross-references: UNIPARC:UPI0000162112; EMBL:AL021815; PIDN:CAA16994.1; GSPDB:GN000067  
A;Experimental source: strain 972h-; cosmid c8E4  
C;Genetics:  
A;Gene: SPDB:SPAC8B4.01c  
A;Map position: 2  
C;Superfamily: probable inorganic phosphate transport protein PHO84

Query Match 73.3%; Score 33; DB 2; Length 274;  
Best Local Similarity 71.4%; Pred. No. 47;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
|||::|:  
Db 59 SYDLFII 65

RESULT 11  
G86852  
oxidoreductase ysjB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: G86852  
R;Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: G86852  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-305 <STO>  
A;Cross-references: UNIPROT:Q9CEL4; UNIPARC:UPI00000C6B27; GB:AE005176; PID:g12724851; H  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: ysjB

Query Match 73.3%; Score 33; DB 2; Length 305;  
Best Local Similarity 62.5%; Pred. No. 52;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
|||::|:  
Db 155 FLMYDIFI 162

RESULT 12  
T17712

hypothetical protein A222R - Chlorella virus PBCV-1  
C;Species: Chlorella virus PBCV-1  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T17712  
R;Graves, M.V.; Van Etten, J.L.  
submitted to the EMBL Data Library, May 1999  
A;Reference number: Z18806  
A;Accession: T17712  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-333 <GRA>  
A;Cross-references: UNIPROT:Q84542; UNIPARC:UPI0000179461; EMBL:U42580; NID:g4028896; PI  
A;Experimental source: specific host Chlorella strain NC64A  
C;Genetics:  
A;Note: A222R  
C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A222R

Query Match 73.3%; Score 33; DB 2; Length 333;  
Best Local Similarity 75.0%; Pred. No. 57;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
|||::|:  
Db 254 FFSFDLFV 261

RESULT 13  
T47504  
mitogen-activated protein kinase 3 - Arabidopsis thaliana  
N;Alternate names: protein F9K21.220  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T47504  
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.  
submitted to the Protein Sequence Database, February 2000  
A;Reference number: Z24467  
A;Accession: T47504  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-370 <JOR>  
A;Cross-references: UNIPROT:Q39023; UNIPARC:UPI0000001AE1; EMBL:AL138657  
A;Experimental source: cultivar Columbia; BAC clone F9K21  
C;Genetics:  
A;Map position: 3  
A;Introns: 53/2; 96/3; 142/3; 253/3; 315/1  
A;Note: F9K21.220  
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 73.3%; Score 33; DB 2; Length 370;  
Best Local Similarity 71.4%; Pred. No. 63;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 7  
|||::|:  
Db 21 FISYDIF 27

RESULT 14  
S40469  
mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 06-Oct-1994 #sequence\_revision 19-Jan-1996 #text\_change 09-Jul-2004  
C;Accession: S40469  
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.  
FEBS Lett. 336, 440-444, 1993  
A;Title: ATPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.  
A;Reference number: S40469; MUID:94109583; PMID:8282107  
A;Accession: S40469  
A;Molecule type: mRNA  
A;Residues: 1-370 <MIZ>  
A;Cross-references: UNIPROT:Q39023; UNIPARC:UPI000014C688; EMBL:D21839; NID:g4573797; PID  
C;Genetics:  
A;Gene: MPK3



C;Superfamily: kinase-related transforming protein; protein kinase homology  
 C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
 F;35-324/Domain: protein kinase homology <KIN>  
 F;44-52/Region: protein kinase ATP-binding motif

Query Match 73.3%; Score 33; DB 2; Length 370;  
 Best Local Similarity 71.4%; Pred. No. 63;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLSYDLF 7  
 |::|::|  
 Db 21 FISYDIF 27

## RESULT 15

S62503 inorganic phosphate transporter - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe  
 C;Date: 16-May-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C;Accession: T38287; S62503  
 R;Niilet, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, October 1995

A;Reference number: Z21783

A;Accession: T38287

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-559 <NI2>

A;Cross-references: UNIPROT:Q09852; UNIPARC:UPI000013A05C; EMBL:Z64354; NID:g1039338; PI

A;Experimental source: strain 972h-; cosmid c23D3

C;Genetics:

A;Gene: SPDB:SPAC23D3.12

A;Map position: IR

C;Superfamily: probable inorganic phosphate transporter protein PHO84

Query Match 73.3%; Score 33; DB 2; Length 559;

Best Local Similarity 71.4%; Pred. No. 94;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYDLFVV 9  
 |::|::|  
 Db 57 SYDLFII 63

## RESULT 16

T50404 probable inorganic phosphate transporter [imported] - fission yeast (Schizosaccharomyces

C;Species: Schizosaccharomyces pombe

C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004

C;Accession: T50404

R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, January 2000

A;Reference number: Z25068

A;Accession: T50404

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-572 <RIE>

A;Cross-references: UNIPROT:Q42885; UNIPARC:UPI000013A3B7; EMBL:AL137099; PIDN:CAB68656.

A;Experimental source: strain 972h(-); clone p1 p4G3

C;Genetics:

A;Gene: SPBC884.01c; SPDB:SPBP4G3.01

A;Map position: 2

C;Superfamily: probable inorganic phosphate transporter protein PHO84

Query Match 73.3%; Score 33; DB 2; Length 572;

Best Local Similarity 71.4%; Pred. No. 96;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYDLFVV 9  
 |::|::|  
 Db 59 SYDLFII 65

## RESULT 17

## T41275

probable inorganic phosphate transporter - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T41275

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.

submitted to the EMBL Data Library, March 1999

A;Reference number: Z21962

A;Accession: T41275

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-583 <LYN>

A;Cross-references: UNIPROT:Q9Y7Q9; UNIPARC:UPI000006C72C; EMBL:AL049567; PIDN:CAB40203

A;Experimental source: strain 972h-; cosmid c2H8

C;Genetics:

A;Gene: SPDB:SPCC2H8.02

A;Map position: 3

C;Superfamily: probable inorganic phosphate transporter protein PHO84

Query Match 73.3%; Score 33; DB 2; Length 583;

Best Local Similarity 71.4%; Pred. No. 98;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYDLFVV 9  
 |::|::|  
 Db 53 SYDLFII 59

## RESULT 18

T20422

hypothetical protein E02H4.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T20422

R;Barlow, K.

submitted to the EMBL Data Library, November 1995

A;Reference number: Z19273

A;Accession: T20422

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-849 <WIL>

A;Cross-references: UNIPROT:Q19040; UNIPARC:UPI0000082463; EMBL:Z68003; PIDN:CAA91977.1

A;Experimental source: clone E02H4

C;Genetics:

A;Gene: CESP:E02H4.4

A;Map position: X

A;Introns: 19/1; 69/3; 100/2; 135/1; 234/1; 337/3; 380/3; 406/2; 441/2; 509/1; 576/3; 5

Query Match 73.3%; Score 33; DB 2; Length 849;

Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLSYDLFVV 9  
 |::|::|  
 Db 315 FITHDIFVV 323

## RESULT 19

A83852

hypothetical protein BH1617 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C;Accession: A83852

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: A83852

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-137 <STO>

A;Cross-references: UNIPROT:Q9KCF4; UNIPARC:UPI000000C3C51; GB:AP001512; GB:BA000004; NI

A;Experimental source: strain C-125

C:Genetics:  
A:Gene: BH1617

Query Match 71.1%; Score 32; DB 2; Length 137;  
Best Local Similarity 75.0%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
||:|:|  
Db 59 FLAYSFLV 66

RESULT 20

I78556  
membrane glycoprotein M6 - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I78556  
R:Yan, Y.; Lagenaur, C.; Narayanan, V.  
Neuron 11, 423-431, 1993  
A:Title: Molecular cloning of M6: identification of a P1P/DW20 gene family.  
A:Reference number: 158150; MUID:94000809; PMID:8398137  
A:Accession: I78556  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-288 <RES>  
A:Cross-references: UNIPARC:UPI0000008C2; GB:S65737; NID:9425586; PIDN:AB28351.1; PID:  
C:Superfamily: myelin proteolipid protein  
C:Keywords: glycoprotein

Query Match 71.1%; Score 32; DB 2; Length 288;  
Best Local Similarity 55.6%; Pred. No. 78;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
::||:|  
Db 219 YMSYHLFIV 227

RESULT 21

G69796  
lactose permease homolog yesp - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: G69796  
R:Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertel  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huilo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; rognoni, K.; rosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: G69796  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-309 <KUN>  
A:Cross-references: UNIPROT:Q31519; UNIPARC:UPI0000060053; GB:Z99107; GB:AL009126; NID:9  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yesp  
C:Superfamily: inner membrane protein ugpA

Query Match 71.1%; Score 32; DB 2; Length 309;  
Best Local Similarity 85.7%; Pred. No. 83;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7  
|:|:|  
Db 49 FTSYDLF 55

RESULT 22

B90243  
aminomethyltransferase [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: B90243  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.  
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: B90243  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-346 <KUR>  
A:Cross-references: UNIPROT:Q97217; UNIPARC:UPI00000642DF; GB:AE006641; NID:gl3814101; F  
C:Genetics:  
A:Gene: SSO0919  
C:Superfamily: aminomethyltransferase

Query Match 71.1%; Score 32; DB 2; Length 346;  
Best Local Similarity 44.4%; Pred. No. 93;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
|:|:|  
Db 167 FMGYDVFLI 175

RESULT 23

B98293  
mannonate dehydratase (d-mannonate hydrolase) [imported] - Agrobacterium tumefaciens (str  
C:Species: Agrobacterium tumefaciens  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: B98293  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, B.  
A.; Liu, F.; Woliam, C.; Allinger, M.; Doughcy, D.; Scott, C.; Lappas, C.; Markelz, B.  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: B98293  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-397 <KUR>  
A:Cross-references: UNIPROT:Q8UA46; UNIPARC:UPI00000D2233; GB:AE007870; PIDN:AAK89868.1,  
C:Genetics:  
A:Gene: AGR\_L 2605  
A:Map position: linear chromosome

Query Match 71.1%; Score 32; DB 2; Length 397;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
|:|:|:|  
Db 133 FVAYDVFIL 141

RESULT 24

AG2990  
mannonate dehydratase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AG2990  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

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erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, K.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.; E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2990
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <KUR>
A:Cross-references: UNIPROT:Q8UA46; UNIPARC:UPI00000D2233; GB:AE008689; PIDN:AAL44341.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: uxuA
A:Map position: linear chromosome

Query Match 71.1%; Score 32; DB 2; Length 397;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFWV 9
DB 133 FVAYDVFIL 141
:::|:::

RESULT 25
D86920
probable UDP-galactopyranose mutase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: D86920
R:Coile, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H.C.; Davies, R.M.; Devlin, K.; Duthoy, S.; Peltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, R.; Davies, R.M.; Rutherford, K.M.
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: D86920
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-413 <STO>
A:Cross-references: UNIPROT:Q9CDB8; UNIPARC:UPI00000C6C35; GB:AL450380; NID:gl3092474; F.
C:Genetics:
A:Gene: glf
C:Superfamily: Methanobacterium thermoautotrophicum UDP-galactopyranose mutase

Query Match 71.1%; Score 32; DB 2; Length 413;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFWV 9
DB 3 VSFDFWV 10
:::|:::

RESULT 26
T19075
hypotheical protein C08B6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19075
R:Wilkinson, J.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19070
A:Accession: T19075
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-586 <WIL>
A:Cross-references: UNIPROT:Q17813; UNIPARC:UPI0000178B9A; EMBL:Z72502; PIDN:CAA96584.1;
A:Experimental source: clone C08B6
C:Genetics:

```

## RESULT 29

T38032 Hypothetical protein SPAC1B3.13 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T38032

R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z21763

A:Accession: T38032

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-800 &lt;MUR&gt;

A:Cross-references: UNIPROT:O13878; UNIPARC:UPI000006B48C; EMBL:Z98598; PIDN:CAB11248.1;

A:Experimental source: strain 972h-; cosmid c1B3

C:Genetics:

A:Gene: SPDB:SPAC1B3.13

A:Map position: 1

A:Introns: 39/2

Query Match 71.1%; Score 32; DB 2; Length 800;

Best Local Similarity 62.5%; Pred. No. 2.1e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8

|||||:

Db 42 FLTDTFTI 49

## RESULT 30

G86189

Hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: G86189

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G86189

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-855 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9SYD9; UNIPARC:UPI00000A7611; GB:AE005172; NID:g4836908; PI

C:Genetics:

A:Map position: 1

Query Match

Best Local Similarity 71.1%; Score 32; DB 2; Length 855;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFV 9

|||||:

Db 734 SYDLVYV 740

## RESULT 31

A85032

Hypothetical protein AT4G02510 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Dec-2004

C:Accession: A85032

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin

Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: A85032

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-865 &lt;STO&gt;

A:Cross-references: UNIPROT:O22774; UNIPARC:UPI00000502B1; GB:NC\_001268; NID:g7269011; I

C:Genetics:

A:Gene: AT4G02510

A:Map position: 4

C:Superfamily: chloroplast outer membrane protein

Query Match

Best Local Similarity 71.1%; Score 32; DB 2; Length 865;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8

|||||:

Db 358 LSYDVFFV 364

## RESULT 32

S49910

chloroplast outer envelope protein OEP86 precursor - garden pea

N:Alternate names: chloroplast import-associated protein IAP86, GTP-binding

C:Species: Pisum sativum (garden pea)

C:Date: 26-Jan-1995 #sequence\_revision 10-Feb-1995 #text\_change 31-Dec-2004

C:Accession: S49910; A55386; A55171

R:Hirsch, S.; Soll, J.

submitted to the EMBL Data Library, March 1994

A:Reference number: S49910

A:Accession: S49910

A:Molecule type: mRNA

A:Residues: 1-879 &lt;HIR&gt;

A:Cross-references: UNIPROT:Q41010; UNIPARC:UPI00000AABB4; EMBL:Z31581; NID:g599957; PI

R:Hirsch, S.; Muckel, E.; Heemeyer, F.; von Heijne, G.; Soll, J.

Science 266, 1989-1992, 1994

A:Title: A receptor component of the chloroplast protein translocation machinery.

A:Reference number: A55386; MUID:95099324; PMID:7801125

A:Accession: A55386

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-137,'Q',139-875,877-879 &lt;HI2&gt;

A:Cross-references: UNIPARC:UPI000017A044

R:Kessler, F.; Blobel, G.; Patel, H.A.; Schnell, D.J.

Science 266, 1035-1039, 1994

A:Title: Identification of two GTP-binding proteins in the chloroplast protein import m

A:Reference number: A55171; MUID:95063938; PMID:7973656

A:Accession: A55171

A:Molecule type: mRNA

A:Residues: 1-372,'EQQ',376-879 &lt;KES&gt;

A:Cross-references: UNIPARC:UPI000016DP27; GB:IJ5857; NID:g576508; PIDN:AAAS3276.1; PID

C:Superfamily: chloroplast outer membrane protein

C:Keywords: chloroplast; GTP binding; membrane protein; nucleotide binding; P-loop

F:245-253/Region: nucleotide-binding motif A (P-loop)

Query Match

Best Local Similarity 71.1%; Score 32; DB 2; Length 879;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8

|||||:

Db 379 LSYDVFFV 385

## RESULT 33

T01098

chloroplast outer envelope protein OEP86 homolog T10P11.19 - Arabidopsis thaliana

N:Alternate names: chloroplast import-associated protein, GTP-binding; protein T14P8.24

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 31-Dec-2004

C:Accession: T01098; T01299

R:Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, S.; de la Bastide, I

hi, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McCombie, W.R.

submitted to the EMBL Data Library, November 1998

A;Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.

A;Reference number: Z14248

A;Accession: T01098

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1503 <MAP>

A;Cross-references: UNIPROT:O81283; UNIPARC:UPI00000A553E; EMBL:AC002330; NID:G2262135;

A;Experimental source: cultivar Columbia

R;Kalicki, J.; Elliott, G.; Cloud, J.

submitted to the EMBL Data Library, May 1998

A;Description: The sequence of A. thaliana T14P8.

A;Reference number: Z14290

A;Accession: T01299

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1503 <MAP>

A;Cross-references: UNIPARC:UPI00000A553E; EMBL:AF069298; NID:g3193282; PID:g3193301

A;Experimental source: cultivar Columbia

C;Genetics:

A;Map position: 4

A;Introns: 22/1

A;Note: T10P11.19; T14P8.24

C;Superfamily: chloroplast outer membrane protein

C;Keywords: chloroplast; GTP binding; membrane protein; nucleotide binding; P-loop

F;862-869/Region: nucleotide-binding motif A (P-loop)

Query Match

Best Local Similarity 71.1%; Score 32; DB 2; Length 1503;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8

Db 996 LSYDVVF 1002

RESULT 34

JT0382

apolipoprotein B - pig (fragments)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Dec-2004

C;Accession: JT0382; I46567; I46568

R;Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.; Attie, A.D.; Rapacz

Gene 70, 213-229, 1988

A;Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atherosclerosis

A;Reference number: JT0382; MUID:89108006; PMID:2905887

A;Accession: JT0382

A;Molecule type: DNA

A;Residues: 1-1778 <MAP>

A;Cross-references: UNIPROT:Q29433; UNIPARC:UPI0000177795

R;Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.O.; Attie, A.D.; Rapacz

Gene 69, 213-229, 1988

A;Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atherosclerosis

A;Reference number: I46567

A;Accession: I46567

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-8,'S',10-238 <MA2>

A;Cross-references: UNIPARC:UPI0000087121; GB:M22646; NID:gl64366; PIDN:AAA30996.1; PID:

A;Accession: I46568

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 239-1778 <MA3>

A;Cross-references: UNIPARC:UPI0000087AFF; GB:M22647; NID:gl64367; PIDN:AAA30997.1; PID:

C;Comment: Apolipoprotein B is the predominant protein component of the low-density lipoprotein

C;Genetics:

A;Gene: apoB

A;Introns: 39/3; 88/3; 159/2; 238/3; 1133/1; 1171/2; 1232/3

A;Note: the list of introns may be incomplete

C;Keywords: atherosclerosis; cholesterol metabolism; LDL; lipid binding; lipoprotein

Query Match

71.1%; Score 32; DB 2; Length 1778;

Best Local Similarity 77.8%; Pred. No. 4.6e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9

Db 1126 FLEYDLNVV 1134

RESULT 35

I46569

apolipoprotein B - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004

C;Accession: I46569

R;Furterell, C.; Maeda, N.; Ebert, D.L.; Kaiser, M.; Lund-Katz, S.; Sturley, S.L.; Kodoyi

J.; Lipid Res. 34, 1323-1335, 1993

A;Title: Nucleotide sequence encoding the carboxyl-terminal half of apolipoprotein B fr

A;Reference number: I46569; MUID:94014802; PMID:8409766

A;Accession: I46569

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2629 <PUR>

A;Cross-references: UNIPROT:Q29021; UNIPARC:UPI000008862B; GB:L11235; NID:gl64371; PIDN

C;Genetics:

A;Gene: APOB

A;Introns: 1984/1; 2022/2; 2083/3

C;Superfamily: apolipoprotein B

Query Match

Best Local Similarity 71.1%; Score 32; DB 2; Length 2629;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9

Db 1977 FLEYDLNVV 1985

RESULT 36

D86353

protein F2E2.10 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: D86353

R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: AB6141; MUID:21016719; PMID:11130712

A;Accession: D86353

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-68 <STO>

A;Cross-references: UNIPROT:Q9LM56; UNIPARC:UPI00000A4428; GB:AE005172; NID:g9280678; P

C;Genetics:

A;Gene: F2E2.10

A;Map position: 1

Query Match

68.9%; Score 31; DB 2; Length 68;

Best Local Similarity 75.0%; Pred. No. 30;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSYDLFVV 9

Db 24 LRYDVVV 31

RESULT 37

D98006  
hypothetical protein laxX-truncation [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: D98006  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
y, P.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
e, R.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; E  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:111544234  
A:Accession: D98006  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <KUR>  
A:Cross-references: UNIPROT:Q8DPN8; UNIPARC:UPI00000E35B7; GB:AE007317; PIDN:AAK99880.1;  
C:Genetics:  
A:Gene: laxX-truncation

Query Match 68.9%; Score 31; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLF 7  
|||  
Db 19 LSYDLF 24

RESULT 38  
F81339  
probable membrane protein Cj0691 [imported] - Campylobacter jejuni (strain NCTC 11168)  
C:Species: Campylobacter jejuni  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: F81339  
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barr  
Nature 403, 665-668, 2000  
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A:Reference number: A81250; MUID:20150912; PMID:10688204  
A:Accession: F81339  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-163 <PAR>  
A:Cross-references: UNIPROT:Q9PPL6; UNIPARC:UPI00000C1CER; GB:AL139076; GB:AL111168; NID  
A:Experimental source: serotype O2, strain NCTC 11168  
C:Genetics:  
A:Gene: Cj0691  
C:Superfamily: Campylobacter jejuni probable membrane protein Cj0691

Query Match 68.9%; Score 31; DB 2; Length 163;  
Best Local Similarity 55.6%; Pred. No. 71;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLSYDLFW 9  
|:|:|  
Db 95 FIGYDIFKV 103

RESULT 39  
G95247  
hypothetical protein SP2117 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: G95247  
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
son, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Lofcus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: G95247

D98112  
 C:Species: Streptococcus pneumoniae  
 C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
 C:Accession: D98112  
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B  
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
 y, P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 183, 5709-5717, 2001  
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
 A:Reference number: A97872; MUID:21429245; PMID:11544234  
 A:Accession: D98112  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-246 <KUR>  
 A:Cross-references: UNIPROT:Q8CY72; UNIPARC:UPI0000084785; GB:AE007317; PIDN:AAL00729.1;  
 C:Genetics:  
 A:Gene: spr1927

Query Match 68.9%; Score 31; DB 2; Length 246;  
 Best Local Similarity 77.8%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
 |||: |||  
 Db 133 FLSFLFVV 141

RESULT 43  
 S39364  
 myfB protein precursor - Yersinia enterocolitica  
 C:Species: Yersinia enterocolitica  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
 C:Accession: S39364; S39362  
 R:Iriarte, M.  
 submitted to the EMBL Data Library, March 1993  
 A:Reference number: S39364  
 A:Accession: S39364  
 A:Molecule type: DNA  
 A:Residues: 1-267 <IRI>  
 A:Cross-references: UNIPROT:P33407; UNIPARC:UPI000012FB1E; EMBL:Z21953; NID:g402169; PID  
 R:Iriarte, M.; Vanoteghem, J.C.; Delor, I.; Diaz, R.; Knutton, S.; Cornelis, G.R.  
 Mol. Microbiol. 9, 507-520, 1993  
 A:Title: The Myf fibrillae of Yersinia enterocolitica.  
 A:Reference number: S36206; MUID:94018646; PMID:8105362  
 A:Accession: S39362  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 35-267 <IR2>  
 A:Cross-references: UNIPARC:UPI00001781FA; EMBL:Z21953  
 C:Genetics:  
 A:Gene: myfB  
 C:Superfamily: chaperone protein papD  
 F:1-34/Domain: signal sequence #status predicted <SIG>  
 F:35-267/Product: myfB protein #status predicted <MAT>

Query Match 68.9%; Score 31; DB 2; Length 267;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 8  
 |: |||:  
 Db 9 FLSYDLFVV 16

RESULT 44  
 AIL597  
 Lactococcus lactis LacX protein homolog lin1322 [imported] - Listeria innocua (strain C)  
 C:Species: Listeria innocua  
 C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: AIL597  
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Ducaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihi, H.  
 D.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001  
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M  
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland  
 A:Title: Comparative genomics of Listeria species.  
 A:Reference number: AB1077; MUID:21537279; PMID:11679669  
 A:Accession: AIL597  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-290 <GLA>  
 A:Cross-references: UNIPROT:Q92C69; UNIPARC:UPI00000CC523; GB:AL592022; PIDN:CAC96553.1  
 A:Experimental source: strain Clp11262  
 C:Genetics:  
 A:Gene: lin1322

Query Match 68.9%; Score 31; DB 2; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLF 7  
 |||: |||  
 Db 195 LSYDLF 200

RESULT 45  
 S66096  
 yabT protein - Bacillus subtilis  
 C:Species: Bacillus subtilis  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 15-Oct-1999  
 C:Accession: S66096; C69740  
 R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.  
 DNA Res. 1, 1-14, 1994  
 A:Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chr  
 A:Reference number: S65967; MUID:96051385; PMID:7584024  
 A:Accession: S66096  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-297 <OGA>  
 A:Cross-references: UNIPARC:UPI000005FDF0; EMBL:D26185; NID:g467326; PIDN:BAA05301.1;  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993

R:Kunst, P.; Ogasawara, N.; Woszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
 C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F  
 Kostter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
 y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Seguchi, J.; Sekowska, A.; Sero  
 akeuchi, M.; Tamakoehi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosaato, V.; Uchiyama  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377

Query Match 68.9%; Score 31; DB 2; Length 297;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
 |||: |||

Db 159 SYDLFAV 165

RESULT 46

G90564

hypothetical protein MYPV 4230 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C:Accession: G90564

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis

A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: G90564

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-297 <KUR>

A:CROSS-references: UNIPROT:Q980E3; UNIPARC:UPI00000D45R0; GB:AL445566; PID:gl4089837; E

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPV 4230

A:Genetic code: SGC3

Query Match 68.9%; Score 31; DB 2; Length 297;

Best Local Similarity 55.6%; Pred. No. 1.3e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9

|||||

Db 215 FLSFDFFII 223

RESULT 47

T23362

hypothetical protein K06B4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T23362

R:Lloyd, C.

submitted to the EMBL Data Library, December 1996

A:Reference number: Z19732

A:Accession: T23362

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-298 <WIL>

A:CROSS-references: UNIPROT:Q45663; UNIPARC:UPI0000075013; EMBL:283233; PIDN:CAB05758.1;

A:Experimental source: clone K06B4

C:Genetics:

A:Gene: CESP:K06B4.4

A:Map position: 5

A:Introns: 41/3; 75/1; 103/2; 130/3; 142/3; 193/3; 218/3; 247/1; 274/2

C:Superfamily: Caenorhabditis elegans hypothetical protein K06B4.4

Query Match 68.9%; Score 31; DB 2; Length 298;

Best Local Similarity 55.6%; Pred. No. 1.3e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9

|||||

Db 34 FLSFNLFAI 42

RESULT 48

T21907

hypothetical protein F37B12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T21907

R:Thomas, K.

submitted to the EMBL Data Library, September 1995

A:Reference number: Z19486

A:Accession: T21907

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-315 <WIL>

A:CROSS-references: UNIPROT:Q20116; UNIPARC:UPI000007EC55; EMBL:Z54218; PIDN:CAA90954.1

A:Experimental source: clone F37B12

C:Genetics:

A:Gene: CESP:F37B12.1

A:Map position: 2

A:Introns: 50/2; 191/3; 230/2

C:Superfamily: Caenorhabditis elegans hypothetical protein F37B12.1

Query Match 68.9%; Score 31; DB 2; Length 315;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDL 6

|||||

Db 281 FLSYDL 286

RESULT 49

H83659

serine/threonine-protein kinase BH0080 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C:Accession: H83659

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai, Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: H83659

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-327 <STO>

A:CROSS-references: UNIPROT:Q9KG11; UNIPARC:UPI00000C37A8; GB:AP001507; GB:BA000004; NII

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0080

Query Match 68.9%; Score 31; DB 2; Length 327;

Best Local Similarity 85.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYDLFVV 9

|||||

Db 199 SYDLFAV 205

RESULT 50

T33242

hypothetical protein H27D07.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T33242

R:Goela, D.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid H27D07.

A:Reference number: Z21307

A:Accession: T33242

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-361 <GOE>

A:CROSS-references: UNIPROT:O61908; UNIPARC:UPI000007DC35; EMBL:AF067950; PIDN:AAC18400.1

A:Experimental source: strain Bristol N2; clone H27D07

C:Genetics:

A:Gene: CESP:H27D07.2

A:Map position: 5

A:Introns: 30/2; 229/3; 304/2; 351/3

Query Match 68.9%; Score 31; DB 2; Length 361;

Best Local Similarity 71.4%; Pred. No. 1.5e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7



Db       || || || || ||  
          179 FLEYDIF 185

Search completed: May 9, 2006, 02:24:32  
Job time : 41.4 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:06:12 ; Search time 99.6 Seconds  
(without alignments)  
63.753 Million cell updates/sec

Title: US-09-870-216C-9  
Perfect score: 45  
Sequence: 1 FLSYDLFVV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	91.1	247	2	Q9PQ87_UREPA
2	38	84.4	69	2	Q7BHL0_9FUSO
3	38	84.4	534	2	Q60J25_CAEER
4	37	82.2	259	2	Q99T82_STAAM
5	36	80.0	31	2	Q4XPX6_PLACH
6	36	80.0	191	2	Q9X0X9_THEWA
7	35	77.8	101	2	Q9D9A8_MOUSE
8	35	77.8	161	2	Q5JPE1_HUMAN
9	35	77.8	162	2	Q9NP10_HUMAN
10	35	77.8	162	2	Q9D6G5_MOUSE
11	35	77.8	163	2	Q4HI01_CAMCO
12	35	77.8	132	2	Q812F8_PLAF7
13	35	77.8	203	2	Q84AF2_BACST
14	35	77.8	506	2	Q59WS4_CANAL
15	35	77.8	673	2	Q4UN00_RICPE
16	35	77.8	1066	2	Q4N4P9_THEPA
17	34	75.6	35	2	Q88216_PSESM
18	34	75.6	95	2	Q8ZDH9_YERPE
19	34	75.6	95	2	Q66DG3_YERPE
20	34	75.6	182	2	Q6ACA3_LEIXX
21	34	75.6	184	2	Q6L299_PICTO
22	34	75.6	340	2	Q4UGS8_THEAN
23	34	75.6	363	2	Q4V194_BACZ2
24	34	75.6	382	2	Q9ZPF4_ARATH
25	34	75.6	399	1	UXUA_BACTN
26	34	75.6	394	1	UXUA_RHILO
27	34	75.6	409	2	Q7VHG1_HELHP
28	34	75.6	411	2	Q7MTQ1_WOLSU
29	34	75.6	412	2	Q26064_HELFP
30	34	75.6	412	2	Q9ZJ55_HELFB
31	34	75.6	452	2	Q9X019_THEMA

32	34	75.6	516	2	Q9ZWT3_ARATH	Q9zwt3 arabidopsis
33	34	75.6	590	2	Q8Y105_RALSO	Q8y105 ralstonia s
34	34	75.6	618	2	Q7NIU9_GLOVI	Q7niu9 gloeobacter
35	34	75.6	659	2	Q4N0P8_THEPA	Q4n0p8 theileria p
36	34	75.6	674	1	KBT86_HUMAN	Q86v97 homo sapien
37	34	75.6	674	2	Q5T8Y8_HUMAN	Q5t8y8 homo sapien
38	34	75.6	694	2	Q4UCZ7_THEAN	Q4ucz7 theileria a
39	34	75.6	729	2	Q91183_WSSV	Q91183 white spot
40	34	75.6	924	1	ATG11_YARLI	Q6cfr0 yarrowia li
41	34	75.6	1111	2	Q4UEU7_THEAN	Q4ueu7 theileria a
42	34	75.6	1559	2	Q8IDC3_PLAF7	Q8idc3 plasmodium
43	34	75.6	1807	2	Q55GM7_DICDI	Q55gm7 dictyosteli
44	33.5	74.4	2422	2	Q51BD7_ENTHI	Q51bd7 entamoeba h
45	33	73.3	70	1	NU3M_ARTSA	P19043 artemia sal
46	33	73.3	189	2	Q4Q8H5_LEIMA	Q4q8h5 leishmania
47	33	73.3	203	2	Q45405_BACSV	Q45405 bacillus su
48	33	73.3	262	2	Q5UR23_MIMIV	Q5ur23 mimivirus
49	33	73.3	305	2	Q9CEL4_LACLA	Q9cel4 lactococcus
50	33	73.3	310	2	Q4Z603_PLABE	Q4z603 plasmodium
51	33	73.3	332	2	Q4JYK0_STREN	Q4jyk0 streptococ
52	33	73.3	332	2	Q5SHH0_THET8	Q5shh0 thermus the
53	33	73.3	332	2	Q72HT6_THET2	Q72ht6 thermus the
54	33	73.3	355	2	Q8RD34_THETN	Q8rd34 thermoanaer
55	33	73.3	356	2	Q512Y3_ENTHI	Q512y3 entamoeba h
56	33	73.3	369	2	Q5PZV2_9BRAS	Q5pzv2 chorispora
57	33	73.3	370	1	MPK3_ARATH	Q39023 arabidopsis
58	33	73.3	370	2	Q51V18_BRANA	Q51v18 brassica na
59	33	73.3	455	2	Q5PB18_ANANM	Q5pb18 anaplasma m
60	33	73.3	479	2	Q9DHK3_YLDV	Q9dhk3 yaba-like d
61	33	73.3	559	1	YAECS_SCHPO	Q9852 schizosacch
62	33	73.3	572	1	YBN1_SCHPO	Q42885 schizosacch
63	33	73.3	573	1	YBD1_SCHPO	Q9p619 schizosacch
64	33	73.3	583	2	Q9Y7Q9_SCHPO	Q9y7q9 schizosacch
65	33	73.3	607	2	Q8A4J7_BACTN	Q8a4j7 bacteroides
66	33	73.3	635	2	Q6RJV2_CANGA	Q6rfj2 candida gla
67	33	73.3	654	2	Q59P53_CANAL	Q59p53 candida alb
68	33	73.3	664	2	Q4N5M4_THEPA	Q4n5m4 theileria p
69	33	73.3	677	2	Q84542_PBCV1	Q84542 parametium
70	33	73.3	702	2	Q54UH7_DICDI	Q54uh7 dictyosteli
71	33	73.3	723	2	Q4PG33_USTWA	Q4pg33 ustilago ma
72	33	73.3	849	2	Q19040_CAEEL	Q19040 caenorhabdi
73	33	73.3	877	2	Q6BZ57_DEBHA	Q6bz57 debaryomyce
74	33	73.3	1040	2	Q5GRJ2_WOLTR	Q5grj2 wolbachia s
75	33	73.3	1076	2	Q4UDW9_THEAN	Q4udw9 theileria a
76	33	73.3	1482	2	Q6MT15_MYCMS	Q6mt15 mycoplasma
77	32	71.1	22	2	Q4VYP2_PLABE	Q4vyp2 plasmodium
78	32	71.1	80	2	Q4Z466_PLABE	Q4z466 plasmodium
79	32	71.1	89	2	Q8X459_ECOS7	Q8x459 escherichia
80	32	71.1	96	2	Q4MU20_BACCE	Q4mu20 bacillus ce
81	32	71.1	96	2	Q813M1_BACCR	Q813m1 bacillus ce
82	32	71.1	110	2	Q4XBK6_PLACH	Q4xbk6 plasmodium
83	32	71.1	117	2	Q8PY01_METWA	Q8py01 methanosarc
84	32	71.1	137	2	Q9KCF4_BACHD	Q9kcf4 bacillus ha
85	32	71.1	165	2	Q82NQ3_STRAM	Q82nj3 streptomyce
86	32	71.1	225	2	Q8MOW6_9CRUS	Q8mow6 kanadaceae
87	32	71.1	231	2	Q9KIM7_PSEFL	Q9kim7 pseudomonas
88	32	71.1	232	2	Q68203_ECOLI	Q68203 escherichia
89	32	71.1	246	2	Q5R5S8_PONPY	Q5r5s8 pongo pygma
90	32	71.1	246	2	Q5RD89_PONPY	Q5rd89 pongo pygma
91	32	71.1	246	2	Q98ST2_XENLA	Q98st2 xenopus lae
92	32	71.1	265	1	QPM6B_HUMAN	Q13491 homo sapien
93	32	71.1	265	2	Q5R603_PONPY	Q5r603 pongo pygma
94	32	71.1	265	2	Q9JJK1_RAT	Q9jjk1 rattus norv
95	32	71.1	269	2	Q5R415_PONPY	Q5r415 pongo pygma
96	32	71.1	269	2	Q5EES2_CHICK	Q5ees2 gallus gall
97	32	71.1	269	2	Q98ST3_XENLA	Q98st3 xenopus lae
98	32	71.1	269	2	Q6AZU1_XENLA	Q6azu1 xenopus lae
99	32	71.1	273	2	Q8KX21_SYNP2	Q8kx21 synechococc
100	32	71.1	280	2	Q59FD5_HUMAN	Q59fd5 homo sapien
101	32	71.1	288	2	Q4U9P9_THEAN	Q4u9p9 theileria a
102	32	71.1	288	2	Q5RA15_PONPY	Q5ra15 pongo pygma
103	32	71.1	288	2	Q6DFR6_XENTR	Q6dfr6 xenopus tro
104	32	71.1	299	2	Q65KZ1_BACLD	Q65kz1 bacillus li

105	32	71.1	303	2	Q4KEX2_PSEF5	Q4kex2 pseudomonas	178	31	68.9	246	2	Q8CV72_STRR6	Q8cv72 streptococc
106	32	71.1	305	2	Q8CX43_HUMAN	Q86x43 homo sapien	179	31	68.9	246	2	Q7AJ02_LACJO	Q74j02 lactobacill
107	32	71.1	309	1	YESP_BACSU	Q3l519 bacillus su	180	31	68.9	247	2	Q9ZB13_LEUJA	Q92b13 leuconostoc
108	32	71.1	320	2	Q18428_CABEL	Q18428 caenorhabdi	181	31	68.9	250	2	Q7VJ96_HELHP	Q72v96 helicobacte
109	32	71.1	328	1	QPM6B_MOUSE	P35803 mus musculu	182	31	68.9	258	1	MYPR_ONCMY	P79826 oncorhynchu
110	32	71.1	328	1	Q8N956_HUMAN	Q8N956 homo sapien	183	31	68.9	263	2	Q8G807_BIFLO	Q8g807 bifidobacte
111	32	71.1	328	2	Q5RA06_PONPY	Q5ra06 pongo pygma	184	31	68.9	267	1	MYPB_YEREN	P33407 yerainia en
112	32	71.1	346	2	Q97Z17_SULSO	Q97z17 sulfolobus	185	31	68.9	268	2	Q8UUS8_BRARE	Q8uus8 brachydanio
113	32	71.1	353	2	Q8TNU4_METAC	Q8tnu4 methanosarc	186	31	68.9	268	2	Q5CZM4_BRARE	Q5czm4 brachydanio
114	32	71.1	356	2	Q7QFB0_ANOGA	Q7qfb0 anophelies g	187	31	68.9	273	2	Q5LYJ5_STRT1	Q5lyj5 streptococc
115	32	71.1	363	2	Q61TL3_CAEBR	Q61tl3 caenorhabdi	188	31	68.9	273	2	Q5M358_STRT2	Q5m358 streptococc
116	32	71.1	374	2	Q4HRU4_CAMUP	Q4hru4 campylobact	189	31	68.9	274	2	Q5ZZZ9_MYCHY	Q5zzz9 mycoplasma
117	32	71.1	396	2	Q7VLR6_HARDU	Q7vlr6 haemophilus	190	31	68.9	276	2	Q4J6J1_SULAC	Q4j6j1 sulfolobus
118	32	71.1	397	1	UXUA2_AGRF5	Q8ua46 agrobacteri	191	31	68.9	280	2	Q4PIP3_USTMA	Q4pip3 ustilago ma
119	32	71.1	397	2	Q4K6F1_PSEF5	Q4k6f1 pseudomonas	192	31	68.9	284	2	Q6GZ01_MYCPLA	Q6gz01 mycoplasma
120	32	71.1	413	2	Q9CDB8_MYCLE	Q9cdb8 mycobacteri	193	31	68.9	284	2	Q8NU03_CORGL	Q8nu03 corynebacte
121	32	71.1	425	2	Q8RGQ9_FUSNN	Q8rgq9 fusobacteri	194	31	68.9	289	2	Q7UUT0_BRARE	Q7uut0 brachydanio
122	32	71.1	458	2	Q5LM19_MAGRR	Q5lm19 magnaporthe	195	31	68.9	290	2	Q720D8_LISMF	Q720d8 listeria mo
123	32	71.1	472	2	Q4YPE4_PLABE	Q4ype4 plasmodium	196	31	68.9	290	2	Q92C69_LISIN	Q92c69 listeria in
124	32	71.1	474	2	Q5SWQ7_CRYNE	Q5swq7 cryptococcu	197	31	68.9	291	2	Q8X946_LWGPA	Q8x946 legionella
125	32	71.1	474	2	Q5KJ19_CRYNE	Q5kj19 cryptococcu	198	31	68.9	297	2	Q9Q8J3_MYCPU	Q9q8j3 mycoplasma
126	32	71.1	502	2	Q4L9N4_STAHL	Q4l9n4 staphylococ	199	31	68.9	298	2	Q45663_CABEL	Q45663 caenorhabdi
127	32	71.1	504	2	Q5YU93_NOCFA	Q5yu93 nocardia fa	200	31	68.9	304	2	Q830P2_ENTFA	Q830p2 enterococcu
128	32	71.1	508	2	Q7R4Z0_GIALA	Q7r4z0 giardia lam	201	31	68.9	308	2	Q8F562_LETPIN	Q8f562 leptospira
129	32	71.1	520	2	Q7SFQ2_NEUCR	Q7sfq2 neurospora	202	31	68.9	310	2	Q8D8V1_VIBVU	Q8d8v1 vibrio vuln
130	32	71.1	536	2	Q17813_CABEL	Q17813 caenorhabdi	203	31	68.9	310	2	Q7MLM3_VIBVY	Q7mlm3 vibrio vuln
131	32	71.1	554	2	Q7N107_PHOLL	Q7n107 photorhabdu	204	31	68.9	311	2	Q4SMD0_TETNG	Q4amd0 tetraodon n
132	32	71.1	554	2	Q7N714_PHOLL	Q7n714 photorhabdu	205	31	68.9	315	2	Q20116_CABEL	Q20116 caenorhabdi
133	32	71.1	554	2	Q7N7J9_PHOLL	Q7n7j9 photorhabdu	206	31	68.9	326	2	Q61I27_CABBR	Q61i27 caenorhabdi
134	32	71.1	557	2	Q6NWC8_BRARE	Q6nwc8 brachydanio	207	31	68.9	327	2	Q9KG11_BACHD	Q9kg11 bacillus ha
135	32	71.1	567	2	Q6CVP8_KIULA	Q6cvp8 kluveromyc	208	31	68.9	328	2	Q8BSF4_LACPL	Q8bsf4 lactobacill
136	32	71.1	614	2	Q81745_ARATH	Q81745 arabidopsis	209	31	68.9	332	2	Q7MYQ6_PHOLL	Q7myq6 photorhabdu
137	32	71.1	651	2	Q4KID1_STRPN	Q4kid1 streptococc	210	31	68.9	334	2	Q5ACZ1_CANAL	Q5acz1 candida alb
138	32	71.1	676	2	Q8JLE9_9POXV	Q8jle9 ectromelia	211	31	68.9	336	2	Q7XUS3_ORYSA	Q7xus3 oryza sativ
139	32	71.1	689	2	Q56W83_ARATH	Q56w83 arabidopsis	212	31	68.9	338	1	PKN1_BACSU	P37562 bacillus su
140	32	71.1	703	2	Q4WCY1_ASPFU	Q4wcyl aspergillus	213	31	68.9	339	2	Q6XBY2_ACTIBA	Q6xby2 acinetobact
141	32	71.1	726	1	RNR_MYCPN	P75529 mycoplasma	214	31	68.9	349	2	Q65125_ASF	Q65125 african swi
142	32	71.1	800	2	Q13878_SCHPO	Q13878 schizosacch	215	31	68.9	354	2	Q7MIX5_VIBVY	Q7mix5 vibrio vuln
143	32	71.1	855	2	Q98YJ9_ARATH	Q98yj9 arabidopsis	216	31	68.9	355	2	Q37423_9CARA	Q37423 carabus aur
144	32	71.1	859	2	Q58P62_ARATH	Q58p62 arabidopsis	217	31	68.9	355	2	Q85AL3_9CARA	Q85al3 carabus con
145	32	71.1	865	2	Q22774_ARATH	Q22774 arabidopsis	218	31	68.9	355	2	Q85H17_9CARA	Q85h17 carabus aur
146	32	71.1	867	2	Q8VYD4_ARATH	Q8vyd4 arabidopsis	219	31	68.9	355	2	Q85H18_9CARA	Q85h18 carabus aur
147	32	71.1	874	2	Q4UE05_THEAN	Q4ue05 theileria a	220	31	68.9	355	2	Q8ED41_SHEON	Q8ed41 shewanella
148	32	71.1	879	2	Q7DLK2_PEA	Q7dlk2 pisum sativ	221	31	68.9	357	2	Q9W4W6_DROME	Q9w4w6 drosophila
149	32	71.1	879	2	Q41010_PEA	Q41010 pisum sativ	222	31	68.9	357	2	QSLMT3_SILPO	Q5lmt9 silicibacte
150	32	71.1	887	2	Q4NKR1_PEA	Q4n516 theileria p	223	31	68.9	361	2	Q61908_CABEL	Q61908 caenorhabdi
151	32	71.1	1469	2	Q91KRI_PEA	Q91krl1 pisum sativ	224	31	68.9	361	2	Q61970_CABEL	Q61970 caenorhabdi
152	32	71.1	1503	2	Q81283_ARATH	Q81283 arabidopsis	225	31	68.9	368	2	Q76865_DROME	Q76865 drosophila
153	32	71.1	1540	2	Q29433_PIG	Q29433 sus scrofa	226	31	68.9	373	2	Q5YFH5_9VIRU	Q5yfh5 singapore g
154	32	71.1	2829	2	Q29021_PIG	Q29021 sus scrofa	227	31	68.9	373	2	Q5GAG5_9VIRU	Q5gag5 grouper iri
155	32	71.1	4133	2	Q63NJ3_BURPS	Q63nj3 burkholderi	228	31	68.9	375	2	Q5GAG5_9VIRU	Q5gag5 grouper iri
156	32	71.1	4580	2	Q4V2F5_BURMA	Q4v2f5 burkholderi	229	31	68.9	383	2	Q4FNP6_9RICK	Q4fnp6 candidatus
157	31	68.9	68	2	Q91M56_ARATH	Q91m56 arabidopsis	230	31	68.9	390	2	Q4HML6_CAMLA	Q4hml6 campylobact
158	31	68.9	85	2	Q7VBT7_PROMA	Q7vbt7 prochloroc	231	31	68.9	394	2	Q9Z5D4_RHOSH	Q9z5d4 rhodobacter
159	31	68.9	98	2	Q7VBD9_PROMA	Q7vbd9 prochloroc	232	31	68.9	413	2	Q5SKK1_THET8	Q5skk1 thermus the
160	31	68.9	108	2	Q87295_9BACT	Q87295 unidentified	233	31	68.9	415	2	Q7VH38_HELHP	Q7vh38 helicobacte
161	31	68.9	114	2	Q8DPN8_STRR6	Q8dpn8 streptococc	234	31	68.9	417	2	Q8HZ51_CANFA	Q8hz51 canis famli
162	31	68.9	119	2	Q5CT73_CRYPV	Q5ct73 cryptospori	235	31	68.9	420	1	PROA_PASMU	Q9cm98 pasteurella
163	31	68.9	119	2	Q5CLF3_CRYHO	Q5clf3 cryptospori	236	31	68.9	420	2	Q61635_MOUSE	Q61635 mus musculu
164	31	68.9	142	2	Q7XVA5_GRIJA	Q7xva5 griffithsia	237	31	68.9	420	2	Q6NYB8_RAT	Q6nyb8 rattus norv
165	31	68.9	163	2	Q5HV90_CAMJR	Q5hv90 campylobact	238	31	68.9	420	2	Q9NM59_MOUSE	Q9nm59 mus musculu
166	31	68.9	163	2	Q5FPL6_CAMJE	Q5fpl6 campylobact	239	31	68.9	423	2	Q5EA10_BOVIN	Q5ea10 bos taurus
167	31	68.9	171	2	Q72W04_LEPIC	Q72w04 leptospira	240	31	68.9	441	2	Q83EF9_COXBU	Q83ef9 coxiella bu
168	31	68.9	177	2	Q98U27_RANTE	Q98u27 rana tempor	241	31	68.9	452	2	Q8IYJ5_HUMAN	Q8iyj5 homo sapien
169	31	68.9	190	2	Q7RPUL_PLAYO	Q7rpul plasmodium	242	31	68.9	453	1	STE24_YEAST	P47154 saccharomyc
170	31	68.9	204	2	Q8FP90_LEPIN	Q8fp90 leptospira	243	31	68.9	454	2	Q60AU0_METCA	Q60au0 methylococc
171	31	68.9	226	2	Q97ND3_STRPN	Q97nd3 streptococc	244	31	68.9	456	2	Q9SL95_ARATH	Q9sl95 arabidopsis
172	31	68.9	229	2	Q97YX2_SULSO	Q97yx2 sulfolobus	245	31	68.9	471	2	Q6C3H0_YARLI	Q6c3h0 yarrowia li
173	31	68.9	238	2	Q6SI32_9BACT	Q6si32 uncultured	246	31	68.9	474	2	Q9HJ52_THEAC	Q9hj52 thermoplasm
174	31	68.9	241	2	Q6LUX6_PHOPR	Q6lux6 photobacter	247	31	68.9	476	2	Q97CU6_CUCSA	Q97cu6 thermoplasm
175	31	68.9	242	2	Q591Z9_9SMEG	Q591z9 cypselurus	248	31	68.9	478	2	Q9M5J2_CUCSA	Q9m5j2 cumicis sat
176	31	68.9	246	1	DMG_SQUAC	P36965 squalus aca	249	31	68.9	478	2	Q8W2N5_TOBAC	Q8w2n5 nicotiana t
177	31	68.9	246	2	Q5FK83_LACAC	Q5fk83 lactobacill	250	31	68.9	479	2	Q5DZH3_VIBF1	Q5dzh3 vibrio fisc

251	31	68.9	481	2	Q93XR3_CUCME	Q93XR3_cucumis mel	324	31	68.9	992	2	Q73GS7_WOLPM	Q73GS7_wolbachia p
252	31	68.9	483	2	Q7XB42_PRUDU	Q7XB42_prunus dulc	325	31	68.9	1032	2	Q512M8_CANFA	Q512M8_canis famil
253	31	68.9	489	2	Q8XZV1_RALSO	Q8XZV1_ralstonia s	326	31	68.9	1032	2	Q865B9_CANFA	Q865B9_canis famil
254	31	68.9	493	2	Q5WYR4_LEGPL	Q5WYR4_legionella	327	31	68.9	1050	2	Q4YXW6_PLABE	Q4YXW6_plasmodium
255	31	68.9	498	2	Q9LPR2_ATH	Q9LPR2_arabidopsis	328	31	68.9	1099	2	Q9JH70_9VRU	Q9JH70_turkey astr
256	31	68.9	503	2	Q6W294_RHISN	Q6W294_rhizobium s	329	31	68.9	1106	2	Q8ID15_PLAF7	Q8ID15_plasmodium
257	31	68.9	504	2	Q92NH3_RHIME	Q92NH3_rhizobium m	330	31	68.9	1224	2	Q7T024_BRARE	Q7T024_brachydanio
258	31	68.9	511	2	Q9FI39_ATH	Q9FI39_arabidopsis	331	31	68.9	1280	2	Q5THQ1_HUMAN	Q5THQ1_homo sapien
259	31	68.9	528	1	COX1_TRIRU	CO1555_trichophyto	332	31	68.9	1327	2	Q54ZF9_DICDI	Q54ZF9_dictyosteli
260	31	68.9	528	1	Q6FQ70_CANGA	Q6FQ70_candida gla	333	31	68.9	1337	2	Q75JY5_DICDI	Q75JY5_dictyosteli
261	31	68.9	529	1	YEJF_ECOLI	P33916_escherichia	334	31	68.9	1339	2	Q7RGE3_PLAVO	Q7RGE3_plasmodium
262	31	68.9	529	1	Q7AC69_ECO57	Q7AC69_escherichia	335	31	68.9	1393	2	Q75783_ASHGO	Q75783_ashbya goss
263	31	68.9	529	2	Q57MCO_SALCH	Q57MCO_salmonella	336	31	68.9	1397	2	Q6CNX5_KLUUA	Q6CNX5_kluyveromyc
264	31	68.9	529	2	Q8ZNU8_SALTY	Q8ZNU8_salmonella	337	31	68.9	1449	2	Q9VQZ1_DROME	Q9VQZ1_drosophila
265	31	68.9	529	2	Q8XE78_ECO57	Q8XE78_escherichia	338	31	68.9	1478	2	Q21237_RECAM	Q21237_reclinomona
266	31	68.9	529	2	Q8FFS4_ECOL6	Q8FFS4_escherichia	339	31	68.9	1502	2	Q8IKJ1_PLAF7	Q8IKJ1_plasmodium
267	31	68.9	529	2	Q5ZYV7_LEGPH	Q5ZYV7_legionella	340	31	68.9	1662	2	Q7PSM9_ANOFA	Q7PSM9_anopheles g
268	31	68.9	529	2	Q5X8G8_LEGPA	Q5X8G8_legionella	341	31	68.9	1740	2	Q8LJK9_PLAF7	Q8LJK9_plasmodium
269	31	68.9	529	2	Q5WZV3_LEGPL	Q5WZV3_legionella	342	31	68.9	1811	2	Q36184_9VRU	Q36184_plautia sta
270	31	68.9	529	2	Q5PE27_SALPA	Q5PE27_salmonella	343	31	68.9	1837	2	Q9VCZ9_DROME	Q9VCZ9_drosophila
271	31	68.9	529	2	Q8Z583_SALTI	Q8Z583_salmonella	344	31	68.9	2263	2	Q4P355_USTMA	Q4P355_ustilago ma
272	31	68.9	529	2	Q83KE1_SHIFL	Q83KE1_shigella fl	345	31	68.9	2577	2	Q19482_CABEL	Q19482_caenorhabdi
273	31	68.9	533	2	Q6MN71_BDERA	Q6MN71_bdellovibri	346	31	68.9	2592	2	Q61KA6_CABER	Q61KA6_caenorhabdi
274	31	68.9	543	2	Q4IGD2_GIBZE	Q4IGD2_gibberella	347	31	68.9	2596	2	Q6W3C6_CABEL	Q6W3C6_caenorhabdi
275	31	68.9	548	2	Q9MBP7_9CAUD	Q9MBP7_staphylococ	348	31	68.9	2621	2	Q9LMZ3_ATH	Q9LMZ3_arabidopsis
276	31	68.9	548	2	Q6YQ06_STAAU	Q6YQ06_staphylococ	349	31	68.9	2658	2	Q9SGE4_ATH	Q9SGE4_arabidopsis
277	31	68.9	548	2	Q6GI90_STAAH	Q6GI90_staphylococ	350	31	68.9	4638	2	Q8IK96_PLAF7	Q8IK96_plasmodium
278	31	68.9	548	2	Q6GIB8_STAAH	Q6GIB8_staphylococ	351	31	68.9	6973	2	Q7QXR7_GIALA	Q7QXR7_giardia lam
279	31	68.9	548	2	Q6GIX2_STAAH	Q6GIX2_staphylococ	352	30	5	2449	2	Q5OR46_ENTHI	Q5OR46_entamoeba h
280	31	68.9	548	2	Q6GIY7_STAAH	Q6GIY7_staphylococ	353	30	66.7	18	2	Q9ZY83_XYLV1	Q9ZY83_xylocopa vi
281	31	68.9	548	2	Q6GFB9_STAAH	Q6GFB9_staphylococ	354	30	66.7	53	2	Q6YVL2_ORYSA	Q6YVL2_oryza sativ
282	31	68.9	548	2	Q6GER7_STAAH	Q6GER7_staphylococ	355	30	66.7	61	2	Q4YB53_PLABE	Q4YB53_plasmodium
283	31	68.9	567	2	Q5ONJ8_ENTHI	Q5ONJ8_entamoeba h	356	30	66.7	79	2	Q44736_BORBU	Q44736_borrelia bu
284	31	68.9	582	2	Q8TC68_HUMAN	Q8TC68_homo sapien	357	30	66.7	86	2	Q8IP44_DROME	Q8IP44_drosophila
285	31	68.9	593	2	Q54GK2_DICDI	Q54GK2_dictyosteli	358	30	66.7	94	2	Q4K701_PSEF5	Q4K701_pseudomonas
286	31	68.9	598	2	Q6L297_PICTO	Q6L297_picophilus	359	30	66.7	102	2	Q59KS5_CANAL	Q59KS5_candida alb
287	31	68.9	598	2	Q87F05_XYLFT	Q87F05_xylella fas	360	30	66.7	104	2	Q97YM9_SULSO	Q97YM9_sulfolobus
288	31	68.9	598	2	Q9PGX6_XYLFA	Q9PGX6_xylella fas	361	30	66.7	109	2	Q5LCZ4_BACFN	Q5LCZ4_bacteroides
289	31	68.9	610	1	SYM_CORDI	Q6N1a5_corynebacte	362	30	66.7	115	2	Q96YV9_SULTO	Q96YV9_sulfolobus
290	31	68.9	610	1	SYM_CORGL	Q8NR4_corynebacte	363	30	66.7	116	2	Q5CBR6_THENE	Q5CBR6_thermotoga
291	31	68.9	612	2	Q4JUI8_CORJK	Q4JUI8_corynebacte	364	30	66.7	117	2	Q97TY5_SULSO	Q97TY5_sulfolobus
292	31	68.9	613	1	SYM_COREP	Q8FR00_corynebacte	365	30	66.7	129	2	Q97YF4_SULSO	Q97YF4_sulfolobus
293	31	68.9	621	1	NUOL_BUCBP	Q89AT6_buchnera ap	366	30	66.7	137	1	Y149A_MYCGE	Q9ZB80_mycoplasma
294	31	68.9	621	1	SYM_BIFLO	P59076_bifidobacte	367	30	66.7	138	2	Q5GSP5_WOLTR	Q5GSP5_wolbachia s
295	31	68.9	629	2	Q89NL2_BRAJA	Q89NL2_bifidobacte	368	30	66.7	143	2	Q5AIE9_CANAL	Q5AIE9_candida alb
296	31	68.9	640	2	Q4XNV6_PLACH	Q4XNV6_bradyrhizob	369	30	66.7	143	2	Q5A1K7_CANAL	Q5A1K7_candida alb
297	31	68.9	655	2	Q4NZC0_9DELT	Q4NZC0_plasmodium	370	30	66.7	149	2	Q4Q9A5_LETMA	Q4Q9A5_leishmania
298	31	68.9	655	2	Q6CR69_KLUUA	Q6CR69_aeromonas xob	371	30	66.7	149	2	Q97FY8_CLOAB	Q97FY8_clostridium
299	31	68.9	675	2	Q6CR69_KLUUA	Q6CR69_kluyveromyc	372	30	66.7	151	2	Q7R9G8_PLAYO	Q7R9G8_plasmodium
300	31	68.9	692	2	Q4H2P1_CTOIN	Q4H2P1_ciona intes	373	30	66.7	151	2	Q86LI2_LEIEN	Q86LI2_leishmania
301	31	68.9	692	2	Q6M4D4_CORGL	Q6M4D4_corynebacte	374	30	66.7	153	2	Q81BL7_BACCR	Q81BL7_bacillus ce
302	31	68.9	719	1	GSP_CRIPA	P90518_citridia f	375	30	66.7	159	1	DYL3_CHLRE	Q39584_chlamydomon
303	31	68.9	720	2	Q54SQ1_DICDI	Q54SQ1_dictyosteli	376	30	66.7	163	2	Q4HN32_CAMLA	Q4HN32_campylobact
304	31	68.9	729	2	Q8VAL5_WSSV	Q8VAL5_white spot	377	30	66.7	164	2	Q97VB4_SULSO	Q97VB4_sulfolobus
305	31	68.9	735	2	Q9SKA9_ATH	Q9SKA9_arabidopsis	378	30	66.7	164	2	P90291_9VRU	P90291_beet soil-b
306	31	68.9	749	2	Q7YV19_9TRYP	Q7YV19_trypanosoma	379	30	66.7	164	2	Q4LCH5_9VRU	Q4LCH5_beet soil-b
307	31	68.9	768	2	Q87G52_VIBPA	Q87G52_vibrio para	380	30	66.7	164	2	Q4LCH7_9VRU	Q4LCH7_beet soil-b
308	31	68.9	793	2	Q412R2_AZOV1	Q412R2_azotobacter	381	30	66.7	168	2	Q97WD3_SULSO	Q97WD3_sulfolobus
309	31	68.9	812	2	Q7D105_AGRF5	Q7D105_agrobacteri	382	30	66.7	170	1	LSPA_BORBU	Q51425_borrelia bu
310	31	68.9	816	2	Q58P71_ATH	Q58P71_arabidopsis	383	30	66.7	170	2	Q661F0_BORGA	Q661F0_borrelia ga
311	31	68.9	822	2	Q9ZUM0_ATH	Q9ZUM0_arabidopsis	384	30	66.7	173	2	Q91GS3_HHV8	Q91GS3_human herpe
312	31	68.9	856	2	Q5FLX5_LACAC	Q5FLX5_lactobacill	385	30	66.7	173	2	Q91GS4_HHV8	Q91GS4_human herpe
313	31	68.9	856	2	Q4SB07_TETNG	Q4SB07_tetradodon n	386	30	66.7	173	2	Q91GS5_HHV8	Q91GS5_human herpe
314	31	68.9	857	1	MUTS_LJCJO	P61668_lactobacill	387	30	66.7	173	2	Q91GS6_HHV8	Q91GS6_human herpe
315	31	68.9	882	2	Q5N0X9_SYNF6	Q5N0X9_synchococc	388	30	66.7	173	2	Q91GS7_HHV8	Q91GS7_human herpe
316	31	68.9	907	2	Q6FPA0_CANGA	Q6FPA0_candida gla	389	30	66.7	173	2	Q91GS8_HHV8	Q91GS8_human herpe
317	31	68.9	909	2	Q660X6_BORGA	Q660X6_borrelia ga	390	30	66.7	173	2	Q91GS9_HHV8	Q91GS9_human herpe
318	31	68.9	910	2	Q68FV1_9BACI	Q68FV1_bacillus sp	391	30	66.7	173	2	Q91GTO_HHV8	Q91GTO_human herpe
319	31	68.9	915	2	Q59221_CANAL	Q59221_candida alb	392	30	66.7	173	2	Q91GT1_HHV8	Q91GT1_human herpe
320	31	68.9	921	2	Q59283_CANAL	Q59283_candida alb	393	30	66.7	178	2	Q5NPL5_FRATT	Q5NPL5_francisella
321	31	68.9	943	2	Q7X805_ORYSA	Q7X805_oryza sativ	394	30	66.7	182	2	Q5JEY5_PYRKO	Q5JEY5_pyrococcus
322	31	68.9	951	2	Q9VQ36_DROME	Q9VQ36_drosophila	395	30	66.7	186	2	Q9ZQH1_ATH	Q9ZQH1_arabidopsis
323	31	68.9	967	2	Q81281_PLAF7	Q81281_plasmodium	396	30	66.7	186	2	Q7P0P5_CHRVO	Q7P0P5_chromobacte

397	30	66.7	189	2	Q9YMW9_NPVLID	Q9Ymw9	lymantria d	470	30	66.7	320	2	Q5B1A0_EMENI	Q5bia0	aspergillus
398	30	66.7	193	2	Q6YQ82_ONYPE	Q6yq82	onion yello	471	30	66.7	320	2	Q97EN0_CIOAB	Q97en0	clostridium
399	30	66.7	194	2	Q72MH3_LEPIC	Q72mh3	leptosira	472	30	66.7	321	2	Q84LK1_FICCA	Q84lk1	ficus caric
400	30	66.7	194	2	Q8E234_LEPIN	Q8ez34	leptosira	473	30	66.7	321	2	Q4MPV6_BACCE	Q4mpv6	bacillus ce
401	30	66.7	196	2	Q8E234_LEPIN	Q8ez34	leptosira	474	30	66.7	321	2	Q63GY3_BACCK	Q63gy3	bacillus ce
402	30	66.7	202	2	Q8XZ98_PYRAG	Q8xz98	pyrobaculum	475	30	66.7	321	2	Q6HPF6_BACHK	Q6hpf6	bacillus th
403	30	66.7	202	2	Q42Z88_PLABE	Q42z88	plasmodium	476	30	66.7	321	2	Q73EV6_BACCR	Q73ev6	bacillus ce
404	30	66.7	202	2	Q8D8L1_VIBVU	Q8d8l1	vibrio vuln	477	30	66.7	321	2	Q81IV1_BACCR	Q81iv1	bacillus ce
405	30	66.7	222	2	Q7WJPP_VIBVY	Q7wjpp	vibrio vuln	478	30	66.7	321	2	Q8R793_THETN	Q8r793	thermoanaer
406	30	66.7	224	2	Q6CMD5_KIOLA	Q6cmd5	kluyveromyc	479	30	66.7	321	2	Q97ML6_CIOAB	Q97ml6	clostridium
407	30	66.7	224	2	Q73RT1_TREDE	Q73rt1	treponema d	480	30	66.7	322	2	Q5L752_CHLAB	Q5l752	chlamydophi
408	30	66.7	225	1	PYRH_PYRHO	O50116	pyrococcus	481	30	66.7	322	2	Q824T2_CHLCV	Q824t2	chlamydophi
409	30	66.7	226	2	Q813R2_BACCR	O813r2	bacillus ce	482	30	66.7	322	2	Q4O920_HV8	Q4o920	human herpe
410	30	66.7	227	2	O5NGP0_FRATT	O5ngp0	francisella	483	30	66.7	323	2	Q73N84_TREDE	Q73n84	treponema d
411	30	66.7	230	2	Q18899_CABEL	Q18899	caenorhabdi	484	30	66.7	323	2	Q63D21_BACCK	Q63d21	bacillus ce
412	30	66.7	232	2	Q9YCB9_AERPE	Q9ycb9	aeropyrum p	485	30	66.7	323	2	Q5WAL7_BACSK	Q5wal7	bacillus cl
413	30	66.7	238	2	Q9K515_VIBCH	Q9k515	vibrio chol	486	30	66.7	323	2	Q97ED0_CIOAB	Q97ed0	clostridium
414	30	66.7	239	2	Q8CV66_OCBIH	Q8cv66	oceanobacil	487	30	66.7	323	2	Q661T2_BORGA	Q661t2	borrelia ga
415	30	66.7	241	2	Q83YD4_STRHY	Q83yd4	streptomyce	488	30	66.7	323	2	Q31310_BORBU	Q31310	borrelia bu
416	30	66.7	244	2	Q8TWM2_METAC	Q8tmw2	methanosarc	489	30	66.7	323	2	Q7XRX2_ORYSA	Q7xrx2	oryza sativ
417	30	66.7	244	2	Q87T96_VIBPA	Q87t96	vibrio para	490	30	66.7	324	2	Q9Z7M1_CHLPN	Q9z7m1	chlamydia p
418	30	66.7	250	2	Q84PD9_ORYSA	Q84pd9	oryza sativ	491	30	66.7	326	2	Q7X9F5_9FABA	Q7x9f5	galega orie
419	30	66.7	251	2	Q9X6P6_BACWE	Q9x6p6	bacillus me	492	30	66.7	326	2	Q9CP26_PASMU	Q9cp26	pasteurella
420	30	66.7	257	2	Q9HJ64_THEAC	Q9hj64	thermoplasma	493	30	66.7	327	2	Q7N9L8_PHOLL	Q7n9l8	photorhabdu
421	30	66.7	260	2	Q8BTA3_MOUSE	Q8bta3	mus musculu	494	30	66.7	327	1	DPFP_HAEIN	P45094	haemophilus
422	30	66.7	265	2	Q9ZM84_RHIME	Q9zm84	rhizobium m	495	30	66.7	327	2	Q4QLB5_HAEI8	Q4qlb5	haemophilus
423	30	66.7	266	2	Q515Z4_ENTHI	O515z4	entamoeba h	496	30	66.7	327	2	Q65ST9_MANSN	Q65st9	mannheimia
424	30	66.7	270	2	Q5FLD8_LACAC	O5fld8	lactobacill	497	30	66.7	328	2	Q535E9_MASGI	Q535e9	mastigopro
425	30	66.7	271	2	Q8EUV3_MYCPE	Q8euv3	mycoplasma	498	30	66.7	328	2	O5LVJ9_SILPO	O5lvj9	syllibobacte
426	30	66.7	273	2	Q7P1W5_CHRVO	Q7p1w5	chrysiobacte	499	30	66.7	328	2	Q67QE7_SYMTH	Q67qe7	syntrophobacte
427	30	66.7	273	2	Q71AC5_9NUCL	Q71ac5	manestra co	500	30	66.7	328	2	Q6HD25_BACHK	Q6hd25	bacillus th
428	30	66.7	273	2	O8JM66_9NUCL	Q8jm66	manestra co	501	30	66.7	328	2	O81L93_BACAN	O81l93	bacillus an
429	30	66.7	273	2	Q8QLE7_NPVNC	Q8qler	manestra co	502	30	66.7	329	1	APPP_BACSU	P42065	bacillus su
430	30	66.7	275	2	Q9ZRV6_RHIME	Q9zrv6	rhizobium m	503	30	66.7	329	2	Q8UK66_AGR5	Q8uk66	agrobacteri
431	30	66.7	276	2	Q6PFA7_ACTAD	Q6ffa7	acinetobact	504	30	66.7	333	2	Q4PBB8_USTMA	Q4pbz8	usstilago ma
432	30	66.7	276	2	Q8D8K1_VIBUO	Q8d8k1	rhizobium l	505	30	66.7	333	2	P90495_HV8	P37313	escherichia
433	30	66.7	276	2	Q98BU7_RHILU	Q98bu7	rhizobium l	506	30	66.7	334	1	DPFP_ECOLI	Q7vnm7	haemophilus
434	30	66.7	276	2	O84695_CHLTR	O84695	chlamydia t	507	30	66.7	334	2	Q92ML4_RHIME	Q92ml4	rhizobium m
435	30	66.7	278	2	Q7MLM5_VIBVY	Q7mlw5	vibrio vuln	508	30	66.7	334	2	Q8FCG4_ECOL6	Q8fcg4	escherichia
436	30	66.7	278	2	Q4HK64_CAMLA	Q4hk64	campylobact	509	30	66.7	334	2	Q8XJ48_ECO57	Q8xj48	escherichia
437	30	66.7	279	2	Q8DDW9_VIBVU	Q8ddw9	vibrio vuln	510	30	66.7	334	2	Q83J45_SHIFL	Q83j45	shigella fl
438	30	66.7	281	2	Q8KR51_ESCFE	Q8kr51	escherichia	511	30	66.7	334	2	Q4SY27_TBNG	Q4sy27	tetradodon n
439	30	66.7	282	2	O57BT9_BRUAB	O57bt9	brucella ab	512	30	66.7	334	2	O61F05_HUMAN	Q61f05	homo sapien
440	30	66.7	282	2	O8FZAB_BRUSU	O8fzab	brucella su	513	30	66.7	335	2	Q82A23_YERPE	Q82a23	yersinia pe
441	30	66.7	282	2	O81IK6_BRUME	O81ik6	brucella su	514	30	66.7	335	2	Q82A23_YERPE	Q82a23	yersinia pe
442	30	66.7	290	2	Q8KSS2_ENTFC	Q8kss2	enterococcu	515	30	66.7	336	2	Q61VG9_BACAN	Q61vg9	bacillus an
443	30	66.7	290	2	Q9PLN8_CHLMU	Q9pln8	chlamydia m	516	30	66.7	336	2	Q6CYW5_ERWCT	Q6cyw5	erwinia car
444	30	66.7	291	2	O5ZG66_LEGPH	O5zgz6	legionella	517	30	66.7	337	2	O57IJ9_SALCH	O57ij9	salmonella
445	30	66.7	306	2	Q6AP18_DESPS	Q6ap18	desulfotale	518	30	66.7	337	2	Q6ARZ5_DESPS	Q6arz5	desulfotale
446	30	66.7	306	2	Q7MPV7_VIBVY	Q7mpv7	vibrio vuln	519	30	66.7	337	2	Q72FP8_DESVH	Q72fp8	desulfovibr
447	30	66.7	307	2	Q6F239_MESFL	Q6f239	mesoplasma	520	30	66.7	337	2	Q8ZLB2_SALTY	Q8zlb2	salmonella
448	30	66.7	309	2	Q5NZ51_AZOSE	O5nz51	azococcus sp	521	30	66.7	337	2	Q8Z296_SALTY	Q8z296	salmonella
449	30	66.7	310	1	OR2A4_HUMAN	O95047	homo sapien	522	30	66.7	337	2	Q5PLL2_SALPA	Q5pll2	salmonella
450	30	66.7	310	1	OR2A4_HUMAN	O96445	homo sapien	523	30	66.7	340	2	Q65LD1_BACLD	Q65ld1	bacillus li
451	30	66.7	310	2	O61FP4_HUMAN	Q61fp4	homo sapien	524	30	66.7	344	2	O8YBN5_BRUME	Q8ybn5	brucella me
452	30	66.7	310	2	O5CBP5_THENE	O5cbp5	thermotoga	525	30	66.7	346	2	O8CZL6_YERPE	Q8czl6	yersinia pe
453	30	66.7	310	2	Q5FT64_GLUOX	O5ft64	gluconobact	526	30	66.7	348	2	Q5ABE6_CANAL	Q5abe6	candida alb
454	30	66.7	312	1	OR8K3_HUMAN	O8nh51	homo sapien	527	30	66.7	349	1	PTER_MOUSE	Q60dw5	homo sapien
455	30	66.7	312	2	Q61FC4_HUMAN	Q61fc4	homo sapien	528	30	66.7	349	1	PTER_MOUSE	Q60dw5	homo sapien
456	30	66.7	314	2	Q9MD53_9TRYP	Q9md53	phytomonas	529	30	66.7	349	1	PTER_MOUSE	Q60dw5	homo sapien
457	30	66.7	314	2	O92XV5_RHIME	Q92xv5	rhizobium m	530	30	66.7	349	1	PTER_MOUSE	Q60dw5	homo sapien
458	30	66.7	315	2	Q4UCD8_THEAN	Q4ucd8	thaileria a	531	30	66.7	349	2	O6AYV7_RAT	Q6ayv7	rattus norv
459	30	66.7	316	2	Q54GU6_DICTDI	Q54gu6	dictyosteli	532	30	66.7	349	2	Q7SZS3_XENLA	Q7szs3	xenopus lae
460	30	66.7	316	2	Q9FX02_ARATH	Q9fx02	arabidopsis	533	30	66.7	349	2	Q4RWX9_TETNG	Q4rwx9	tetradodon n
461	30	66.7	316	2	Q5WXM8_LEGPL	O5wxm8	legionella	534	30	66.7	350	2	Q8WVG4_HUMAN	Q8wvg4	homo sapien
462	30	66.7	317	2	O577J4_BRUAB	O577j4	brucella ab	535	30	66.7	353	1	Y4TS_RHIN	Q34937	leishmania
463	30	66.7	317	2	O8FWP2_BRUSU	O8fwp2	brucella su	536	30	66.7	355	2	Q74QU6_YERPE	Q74qu6	yersinia pe
464	30	66.7	318	2	Q7WTK9_BACCE	Q7wtk9	bacillus ce	537	30	66.7	358	2	O664D1_YERPS	Q664d1	yersinia ps
465	30	66.7	318	2	Q4MU16_BACCE	Q4mu16	bacillus ce	538	30	66.7	358	2	O664D1_YERPS	Q664d1	yersinia ps
466	30	66.7	318	2	Q6HKG1_BACHK	Q6hkg1	bacillus th	539	30	66.7	361	2	Q7XIK9_ORYSA	Q7xik9	oryza sativ
467	30	66.7	318	2	Q73AC3_BACCK	Q73ac3	bacillus ce	540	30	66.7	361	2	Q5WBR3_BACSK	Q5wbr3	bacillus cl
468	30	66.7	318	2	O81S83_BACAN	Q81s83	bacillus an	541	30	66.7	363	2	Q6PA30_XENLA	Q6pa30	xenopus lae
469	30	66.7	320	1	O2AK2_HUMAN	Q8ng84	homo sapien	542	30	66.7	364	1	SERC_BACSK	Q5wh79	bacillus cl

543	30	66.7	365	2	Q4MKT1_BACCE	Q4mkt1 bacillus ce	616	30	66.7	485	2	Q6FRX4_CANGA	Q6frx4 candida gla
544	30	66.7	365	2	Q733R7_BACCL	Q733r7 bacillus ce	617	30	66.7	485	2	Q4FMA5_GRICK	Q4fma5 candidatus
545	30	66.7	365	2	Q81AJ1_BACCR	Q81aj1 bacillus ce	618	30	66.7	492	1	GERXA_BACAN	Q9zfb4 bacillus an
546	30	66.7	365	2	Q81YB8_BACAN	Q81yb8 bacillus an	619	30	66.7	492	1	Q4MUS4_BACE	Q4mue4 bacillus ce
547	30	66.7	365	2	Q6HFM1_BACHK	Q6hfm1 bacillus th	620	30	66.7	496	1	GSHRC_ORYSA	P48642 oryza sativ
548	30	66.7	365	2	Q637P8_BACCC	Q637p8 bacillus ce	621	30	66.7	496	2	Q6K3E8_ORYSA	Q6k3e8 oryza sativ
549	30	66.7	367	2	Q7RSH0_PLAYO	Q7rsh0 plasmodium	622	30	66.7	496	2	Q6UQ06_TRIMO	Q6uq06 triticum mo
550	30	66.7	370	2	Q97U32_SULSO	Q97u32 sulfolobus	623	30	66.7	497	2	Q4Y4Z2_PLACH	Q4y4z2 plasmodium
551	30	66.7	374	2	Q4Z4Z8_PLABE	Q4z4z8 plasmodium	624	30	66.7	498	2	Q968W4_PLAF7	Q968w4 plasmodium
552	30	66.7	381	2	Q4QWZ1_OLEEU	Q4qwz1 olea europ	625	30	66.7	498	2	Q815A0_PLAF7	Q815a0 plasmodium
553	30	66.7	382	2	Q8GJE3_CAMJIS	Q8gje3 campylobact	626	30	66.7	502	2	Q7RBD6_PLAYO	Q7rbd6 plasmodium
554	30	66.7	384	2	Q4ZJ66_ENTFA	Q4zj66 enterococcu	627	30	66.7	502	1	ALAT_SCHPO	Q10334 schizosacch
555	30	66.7	384	2	Q836N1_ENTFA	Q836n1 enterococcu	628	30	66.7	505	2	Q54DM9_DICDI	Q54dm9 dictyostell
556	30	66.7	384	2	Q9WYX0_THEMEA	Q9wyx0 thermotoga	629	30	66.7	511	2	Q5HSK7_CAWJR	Q5hsk7 campylobact
557	30	66.7	385	1	CYB_NEUCR	P00162 neurospora	630	30	66.7	516	1	ROA_EUGGR	R30397 euglena gra
558	30	66.7	385	2	Q9ZT27_TREDE	Q9zt27 treponema d	631	30	66.7	516	2	Q82S11_NITEU	Q82s11 nitrosomona
559	30	66.7	385	2	Q73NT5_TREDE	Q73nt5 treponema d	632	30	66.7	516	2	Q6LI35_PHOPR	Q6li35 photobacter
560	30	66.7	387	2	Q9CJ77_LACLA	Q9cj77 lactococcus	633	30	66.7	517	2	Q4XYX7_PLACH	Q4xyx7 plasmodium
561	30	66.7	393	2	Q8GR72_ENTFA	Q8gr72 enterococcu	634	30	66.7	518	2	Q878W0_STRP3	Q878w0 streptococc
562	30	66.7	395	2	Q9FIH4_ARATH	Q9fih4 arabidopsis	635	30	66.7	518	2	Q5XBL1_STRP6	Q5xb11 streptococc
563	30	66.7	395	2	Q57CX2_BRUAB	Q57cx2 brucella ab	636	30	66.7	518	2	Q99289_STRPY	Q99289 streptococc
564	30	66.7	395	2	Q8G0D1_BRUSU	Q8g0d1 brucella su	637	30	66.7	518	2	Q8P0H7_STRP8	Q8p0h7 streptococc
565	30	66.7	395	2	Q8YH11_BRUME	Q8yh11 brucella me	638	30	66.7	519	2	Q514G5_ENTHI	Q514g5 entamoeba h
566	30	66.7	395	2	Q5LIY6_BACFN	Q5liy6 bacteroides	639	30	66.7	519	2	Q5FHP1_EHRRG	Q5fhp1 ehrlichia r
567	30	66.7	397	2	Q6BS70_DEBHA	Q6bs70 debaryomyce	640	30	66.7	519	2	Q5HBG7_EHRRW	Q5hbg7 ehrlichia r
568	30	66.7	399	2	Q6EPP2_ORYSA	Q6epf2 oryza sativ	641	30	66.7	523	2	Q5LVL0_SILPO	Q5lvh0 silicibacte
569	30	66.7	400	2	Q4IRJ5_GIBZE	Q4irj5 gibberella	642	30	66.7	524	2	Q4KAQ8_PSRF5	Q4kaq8 pseudomonas
570	30	66.7	402	2	Q650A0_BACFR	Q650a0 bacteroides	643	30	66.7	525	2	Q4WBY0_ASPFU	Q4wbv0 aspergillus
571	30	66.7	404	2	Q5CBD4_9THEM	Q5cbd4 thermotoga	644	30	66.7	525	2	Q4ZSD3_PSRSY	Q4zsd3 pseudomonas
572	30	66.7	404	2	Q5CBG0_9THEM	Q5cbg0 thermotoga	645	30	66.7	525	2	Q880W8_PSRSM	Q880w8 pseudomonas
573	30	66.7	407	2	Q5ORP0_ENTHI	Q5orp0 entamoeba h	646	30	66.7	527	2	Q500F7_PSRSM	Q500f7 pseudomonas
574	30	66.7	410	2	Q566C9_RAT	Q566c9 rattus norv	647	30	66.7	527	2	Q88AW9_PSRSM	Q88aw9 pseudomonas
575	30	66.7	413	2	Q9X0L5_THEMEA	Q9x0l5 thermotoga	648	30	66.7	530	1	PPCK_LRPIC	Q72vt0 leptospira
576	30	66.7	413	2	Q9Q285_MOUSE	Q9q285 mus musculu	649	30	66.7	530	1	PPCK_LRPIN	Q8f9e4 leptospira
577	30	66.7	413	2	Q9Z1M3_MOUSE	Q9z1m3 mus musculu	650	30	66.7	532	2	Q8TD32_HUMAN	Q8td32 homo sapien
578	30	66.7	414	2	Q54JL1_DICDI	Q54jl1 dictyostell	651	30	66.7	532	2	Q5LWP9_SILPO	Q5lwp9 silicibacte
579	30	66.7	416	2	Q8K2V4_MOUSE	Q8k2v4 mus musculu	652	30	66.7	533	2	Q8MLQ7_DROME	Q8mlq7 dirosophila
580	30	66.7	417	2	Q8VDW7_MOUSE	Q8vdw7 mus musculu	653	30	66.7	533	2	Q92V53_RHIME	Q92v53 rhizobium m
581	30	66.7	417	2	Q5FVQ6_RAT	Q5fvq6 rattus norv	654	30	66.7	534	2	Q88FE7_STRPK	Q88fe7 pseudomonas
582	30	66.7	417	2	Q4V797_RAT	Q4v797 rattus norv	655	30	66.7	536	2	Q4ZVL9_PSRSY	Q4zvl9 pseudomonas
583	30	66.7	418	2	Q9KYZ8_STRCO	Q9kyz8 streptomyc	656	30	66.7	536	2	Q4KBH3_PSRF5	Q4kbh3 pseudomonas
584	30	66.7	424	2	Q8ZAZ2_LACPL	Q8zaz2 lactobacill	657	30	66.7	536	2	Q912T7_PSEAB	Q912t7 pseudomonas
585	30	66.7	435	2	Q6HSP7_BACAN	Q6hsp7 bacillus an	658	30	66.7	536	2	Q912S4_PSEAB	Q912s4 pseudomonas
586	30	66.7	439	2	Q633U1_BACCC	Q633u1 bacillus ce	659	30	66.7	536	2	Q87YS2_PSRSM	Q87ys2 pseudomonas
587	30	66.7	441	2	Q9XKY5_9TRYP	Q9xky5 phytonoma	660	30	66.7	537	2	Q4VA79_XENTR	Q4va79 xenopus tro
588	30	66.7	442	2	Q83DL1_COXBU	Q83dl1 coxiella bu	661	30	66.7	537	2	Q5K8F2_CRYNE	Q5k8f2 cryptococcu
589	30	66.7	448	2	Q6VQZ6_PSEPA	Q6vqz6 pseudomonas	662	30	66.7	538	2	Q81AT9_PLAP7	Q81at9 plasmodium
590	30	66.7	451	2	Q4XYH7_PLACH	Q4xyh7 plasmodium	663	30	66.7	539	2	Q985N3_RHILO	Q985n3 rhizobium l
591	30	66.7	451	2	Q4LNM4_9BURK	Q4lnw4 burkholderi	664	30	66.7	539	2	Q9KKX3_VIBCH	Q9kkx3 vibrio chol
592	30	66.7	452	2	Q6C6E8_YARLI	Q6c6e8 yarrowia li	665	30	66.7	541	2	Q521A4_XENLA	Q521a4 xenopus lae
593	30	66.7	452	2	Q5LTT4_SILPO	Q5ltt4 silicibacte	666	30	66.7	541	2	Q6P7H8_XENLA	Q6p7h8 xenopus lae
594	30	66.7	453	2	Q62BQ5_BURWA	Q62bq5 burkholderi	667	30	66.7	542	2	Q8D5V9_VIBVU	Q8d5v9 vibrio vuln
595	30	66.7	453	2	Q63Y91_BURPS	Q63y91 burkholderi	668	30	66.7	542	2	Q7MCX8_VIBVY	Q7mcx8 vibrio vuln
596	30	66.7	459	1	GSHR_ANASP	P48638 anabaena sp	669	30	66.7	543	2	Q55MCI_CRYNE	Q55mci cryptococcu
597	30	66.7	460	2	Q9W1J2_DROME	Q9wj12 dirosophila	670	30	66.7	543	2	Q87G22_VIBPA	Q87g22 vibrio para
598	30	66.7	461	2	Q7UR82_RHOPH	Q7ur82 rhodopirell	671	30	66.7	544	2	Q7WJX8_BORBR	Q7wjx8 bordetella
599	30	66.7	461	2	Q8DIH9_SYNEL	Q8dih9 synecococc	672	30	66.7	544	2	Q7WAS0_BORPA	Q7was0 bordetella
600	30	66.7	463	2	Q6L1L4_PICTO	Q6l1l4 picophilus	673	30	66.7	544	2	Q7VVQ3_BORPE	Q7vvq3 bordetella
601	30	66.7	463	2	Q92PC0_RHIME	Q92pc0 rhizobium m	674	30	66.7	545	2	Q41WX6_AZOV1	Q41wx6 azobacter
602	30	66.7	463	2	Q98WM1_RHILO	Q98wm1 rhizobium l	675	30	66.7	546	2	Q97CH7_THERVO	Q97ch7 thermoplasm
603	30	66.7	464	2	Q57DB7_BRUAB	Q57db7 brucella ab	676	30	66.7	547	2	Q4WZ10_ASPFU	Q4wz10 aspergillus
604	30	66.7	464	2	Q8G0S5_BRUSU	Q8g0s5 brucella su	677	30	66.7	547	2	Q8NMX7_CORGL	Q8nmx7 corynebacte
605	30	66.7	464	2	Q8URZ2_AGRF5	Q8ur22 agrobacteri	678	30	66.7	551	2	Q987J1_RHILO	Q987j1 rhizobium l
606	30	66.7	467	2	Q4YXB6_PLABE	Q4yxb6 plasmodium	679	30	66.7	551	2	Q8UAG2_AGRF5	Q8uag2 agrobacteri
607	30	66.7	467	2	Q8KES3_MSTEX	Q8kes3 methylobact	680	30	66.7	551	2	Q5N0W8_SYNP6	Q5n0w8 synecococc
608	30	66.7	468	2	Q5BNF3_EMENI	Q5bnf3 aspergillus	681	30	66.7	555	1	GLPD_BACSU	P18158 bacillus su
609	30	66.7	471	2	Q73U43_SULSO	Q73u43 sulfolobus	682	30	66.7	555	2	Q8U6G1_AGRF5	Q8u6g1 agrobacteri
610	30	66.7	471	2	Q73LM7_TREDE	Q73lm7 treponema d	683	30	66.7	556	2	Q7D2L0_AGRF5	Q7d2l0 agrobacteri
611	30	66.7	476	2	Q9HIG0_THEAC	Q9hig0 thermoplasm	684	30	66.7	557	2	Q6G5M3_BARHE	Q6g5m3 bartonella
612	30	66.7	476	2	Q9HM23_THEAC	Q9hm23 thermoplasm	685	30	66.7	560	2	Q83DX2_COXBU	Q83dx2 coxiella bu
613	30	66.7	480	2	Q6N1Z9_RHOPA	Q6n1z9 rhodopseudo	686	30	66.7	561	2	Q8FN17_COREP	Q8fn17 corynebacte
614	30	66.7	480	2	Q6NFZ2_CORDI	Q6nfz2 corynebacte	687	30	66.7	561	2	Q5YZ00_NOCLD	Q5yz00 nocardia fa
615	30	66.7	483	2	Q8YH32_BRUME	Q8yh32 brucella me	688	30	66.7	562	2	Q65JP2_BACLD	Q65jp2 bacillus li

689	30	66.7	562	2	Q6AFU2_LEIXX	Q6afu2	leifsonia x	762	30	66.7	908	2	Q8TG57_YEAST	Q8tg57	saccharomyc
690	30	66.7	563	2	Q62V47_BACLD	Q62v47	bacillus li	763	30	66.7	915	2	Q6P179_HUMAN	Q6p179	homo sapien
691	30	66.7	564	2	Q4NI77_9MICC	Q4ni77	arthrobacte	764	30	66.7	923	1	PHO87_YEAST	PHO87	saccharomyc
692	30	66.7	565	2	Q5RFK8_PONPY	Q5rfk8	pongo pygma	765	30	66.7	931	2	P87544_9VIRU	P87544	beet soill-b
693	30	66.7	566	2	Q6DB29_ERWCT	Q6db29	erwinia car	766	30	66.7	950	2	Q7MW12_PORGI	Q7mw12	porphyromon
694	30	66.7	567	2	Q5CTF0_CRYPV	Q5ctf0	cryptospori	767	30	66.7	960	2	Q7Z5K1_HUMAN	Q7z5k1	homo sapien
695	30	66.7	568	2	Q7NUL2_CHRVO	Q7nul2	chromobacte	768	30	66.7	960	2	Q9HBX2_HUMAN	Q9hbx2	homo sapien
696	30	66.7	569	2	Q28891_ARCFU	Q28891	archaeoglob	769	30	66.7	960	2	Q5RFP3_PONPY	Q5rfp3	pongo pygma
697	30	66.7	569	2	Q61T29_PHLSP	Q61t29	philaenus s	770	30	66.7	977	2	Q6CX54_KLULA	Q6cx54	kluyveromyc
698	30	66.7	569	2	Q6NMW5_EDEBA	Q6nmw5	bdellovibri	771	30	66.7	990	1	ANPM_MANSE	ANPM	manduca sex
699	30	66.7	569	2	Q7NWK5_CHROMO	Q7nwk5	chromobacte	772	30	66.7	995	2	Q9U7N8_MANDU	Q9u7n8	manduca sex
700	30	66.7	572	2	Q5CM19_CRYHO	Q5cm19	cryptospori	773	30	66.7	1007	2	Q6KZ39_PICTO	Q6kz39	picrophilus
701	30	66.7	573	2	Q9ADX9_9RHIZ	Q9adx9	agrobacteri	774	30	66.7	1043	2	Q5L7P9_BACFR	Q5l7p9	bacteroides
702	30	66.7	575	2	Q6D8G9_ERWCT	Q6d8g9	erwinia car	775	30	66.7	1061	2	Q64MW9_BACFR	Q64mw9	bacteroides
703	30	66.7	583	2	Q82878_STRMU	Q82878	streptococc	776	30	66.7	1068	2	Q42391_CHICK	Q42391	gallus gall
704	30	66.7	583	2	Q840W3_STRMU	Q840w3	streptococc	777	30	66.7	1083	2	Q39483_9RETR	Q39483	avian sarco
705	30	66.7	583	2	Q840W9_STRMU	Q840w9	streptococc	778	30	66.7	1090	2	Q9HJU1_THEAC	Q9hj11	thermoplasm
706	30	66.7	583	2	Q8DUS1_STRMU	Q8dus1	streptococc	779	30	66.7	1143	2	Q4SP84_THEAC	Q4sp84	tetraploasm
707	30	66.7	593	2	Q8DKD3_SYNEL	Q8dkd3	synechococc	780	30	66.7	1155	2	Q6RJU3_HUMAN	Q6rju3	homo sapien
708	30	66.7	593	2	Q62582_ORYSA	Q62582	oryza sativ	781	30	66.7	1165	2	Q6RJU1_HUMAN	Q6rju1	homo sapien
709	30	66.7	599	2	Q6FDM4_ACIAD	Q6fdm4	acinetobact	782	30	66.7	1168	2	Q6RJU2_HUMAN	Q6rju2	homo sapien
710	30	66.7	600	2	Q4YW73_PLABE	Q4yw73	plasmodium	783	30	66.7	1191	2	Q6RJU5_HUMAN	Q6rju5	homo sapien
711	30	66.7	605	2	Q7QUZ8_GIALA	Q7quz8	giardia lam	784	30	66.7	1194	2	Q9P2F6_HUMAN	Q9p2f6	homo sapien
712	30	66.7	608	2	Q93RE9_9BACT	Q93re9	pseudogluco	785	30	66.7	1217	2	Q4I7S6_GIBZE	Q4i7s6	gibberella
713	30	66.7	611	1	YCR3_YEAST	P25351	saccharomyc	786	30	66.7	1218	2	Q6RYF4_HORVD	Q6ryf4	hordeum vul
714	30	66.7	617	2	Q9ZUV9_ARATH	Q9zuv9	arabidopsis	787	30	66.7	1285	2	Q5IS11_9REOV	Q5is11	avian ortho
715	30	66.7	627	2	Q8YVZC_ANASP	Q8ymz6	anabaena sp	788	30	66.7	1285	2	Q5IS12_9REOV	Q5is12	avian ortho
716	30	66.7	632	2	Q83428_TREPA	Q83428	treponema p	789	30	66.7	1285	2	Q5IS13_9REOV	Q5is13	avian ortho
717	30	66.7	633	2	Q6BVX3_DEBHA	Q6bv33	debaromyce	790	30	66.7	1285	2	Q5IS14_9REOV	Q5is14	avian ortho
718	30	66.7	634	2	Q4K4S9_PSEFP5	Q4k4s9	pseudomonas	791	30	66.7	1285	2	Q5IS15_9REOV	Q5is15	avian ortho
719	30	66.7	650	2	P73220_SYNY3	P73220	synechocyst	792	30	66.7	1285	2	Q5IS16_9REOV	Q5is16	avian ortho
720	30	66.7	652	2	Q6ARM7_DESPS	Q6arm7	desulfotale	793	30	66.7	1285	2	Q5IS17_9REOV	Q5is17	avian ortho
721	30	66.7	680	2	Q515Q0_ENTHI	Q515q0	entamoeba h	794	30	66.7	1285	2	Q5IS18_9REOV	Q5is18	avian ortho
722	30	66.7	684	2	Q61N24_CABER	Q61n24	caenorhabdi	795	30	66.7	1285	2	Q5IS19_9REOV	Q5is19	avian ortho
723	30	66.7	684	2	Q6A634_PROAC	Q6a634	propionibac	796	30	66.7	1285	2	Q8JU11_9REOV	Q8juv1	avian reovi
724	30	66.7	688	2	Q7Q0Z3_ANOGA	Q7q0z3	anopheles g	797	30	66.7	1346	2	Q7QEF8_ANOGA	Q7qef8	anopheles h
725	30	66.7	688	2	Q7Q573_GIALA	Q7q573	giardia lam	798	30	66.7	1408	2	Q51BS0_ENTHI	Q51bs0	entamoeba h
726	30	66.7	695	2	Q9G8R8_NABGR	Q9g8r8	naegleria g	799	30	66.7	1441	1	CPSP1_MOUSE	CPsp1	mus musculu
727	30	66.7	707	2	Q9LIH5_STRCO	Q9lih5	streptomyce	800	30	66.7	1443	1	CPSP1_HUMAN	CPsp1	homo sapien
728	30	66.7	721	2	Q52B74_MAGGR	Q52b74	magnaporthe	801	30	66.7	1444	1	CPSP1_BOVIN	CPsp1	bos taurus
729	30	66.7	725	2	Q6JHU8_CHICK	Q6jhu8	gallus gall	802	30	66.7	1511	2	Q4UFS2_THEAP	Q4ufs2	theileria a
730	30	66.7	738	2	Q4YVC1_PLABE	Q4yvc1	plasmodium	803	30	66.7	1519	2	Q4N3P8_THEPA	Q4n3p8	theileria p
731	30	66.7	741	1	Y335_MYCPN	P75443	mycoplasma	804	30	66.7	1526	2	Q8IK87_PLAF7	Q8ik87	plasmodium
732	30	66.7	752	2	Q5WU59_LEGPL	Q5wu59	legionella	805	30	66.7	1643	2	Q4KD35_PSEFP5	Q4kd35	pseudomonas
733	30	66.7	752	2	Q5X3D6_LEGPA	Q5x3d6	legionella	806	30	66.7	1704	2	Q51EB3_ENTHI	Q51ef3	entamoeba h
734	30	66.7	752	2	Q5TK00_LEGPH	Q5tk00	legionella	807	30	66.7	1752	2	Q4Z6E8_PLABE	Q4z6e8	plasmodium
735	30	66.7	773	2	Q98K35_RHIL0	Q98k35	rhizobium l	808	30	66.7	1851	2	Q4Z3B8_PLABE	Q4z3b8	plasmodium
736	30	66.7	777	2	Q7RRD7_PLAYO	Q7rrd7	plasmodium	809	30	66.7	1877	2	Q6CFU4_YARLI	Q6cfu4	yarrowia li
737	30	66.7	785	2	Q8ZTY7_PYRAE	Q8zty7	pyrobaculum	810	30	66.7	1946	2	Q4S290_TETNG	Q4s290	tetradion n
738	30	66.7	793	2	Q6BMR2_DEBHA	Q6bmr2	debaromyce	811	30	66.7	2330	1	EGFL4_MOUSE	EGfl4	mus musculu
739	30	66.7	798	2	Q76CT8_PAROL	Q76ct8	paralichthy	812	30	66.7	2386	1	EGFL4_HUMAN	EGfl4	homo sapien
740	30	66.7	810	2	Q58P72_ARATH	Q58p72	arabidopsis	813	30	66.7	3774	2	Q7R3R9_GIALA	Q7r3r9	giardia lam
741	30	66.7	817	2	Q9FYC1_ARATH	Q9fyc1	arabidopsis	814	30	66.7	3971	2	Q9R9J1_BACSU	Q9r9j1	bacillus su
742	30	66.7	818	2	Q67ZY0_ARATH	Q67zy0	arabidopsis	815	30	66.7	4053	2	Q5CZ43_CABEL	Q5cz43	caenorhabdi
743	30	66.7	818	2	Q8GX92_ARATH	Q8gx92	arabidopsis	816	30	66.7	4061	2	Q6A4L2_CABEL	Q6a4l2	caenorhabdi
744	30	66.7	818	2	Q5HXC5_CAMJR	Q5hxc6	campylobact	817	30	66.7	4064	2	Q18667_CABEL	Q18667	caenorhabdi
745	30	66.7	818	2	Q76CU0_PAROL	Q76cu0	paralichthy	818	30	66.7	4562	2	Q7RT51_PLAYO	Q7rt51	plasmodium
746	30	66.7	822	1	NRF6_CABEL	Q92225	caenorhabdi	819	30	66.7	5146	2	Q9VXR3_DROME	Q9vvr3	drosophila
747	30	66.7	831	2	Q7VNB0_HABDU	Q7vnb0	haemophilus	820	29.5	65.6	883	2	Q4K8P7_PSEFP5	Q4k8p7	pseudomonas
748	30	66.7	835	2	Q6CEF9_YARLI	Q6cef9	yarrowia li	821	29	64.4	34	2	Q4Z013_PLABE	Q4z013	plasmodium
749	30	66.7	843	1	AMPN_LACLC	P37897	lactococcus	822	29	64.4	38	2	Q4XHX2_PLACH	Q4xhx2	plasmodium
750	30	66.7	846	1	AMPN1_LACLA	Q9ciq1	lactococcus	823	29	64.4	45	2	Q5BRG0_SCHJA	Q5brg0	schistosoma
751	30	66.7	867	1	MUTS_OCEIH	Q8CX96	oceanobacil	824	29	64.4	48	2	Q48270_HELPY	Q48270	helicobacte
752	30	66.7	873	2	Q9UTC4_SCHPO	Q9utc4	schizosacch	825	29	64.4	48	2	Q9UW33_NEIMA	Q9uw33	neisseria m
753	30	66.7	873	2	Q7RC76_PLAYO	Q7rc76	plasmodium	826	29	64.4	55	2	Q6BLQ7_DEBHA	Q6blq7	debaromyce
754	30	66.7	874	1	EGFL4_RAT	Q9gy00	rattus norv	827	29	64.4	65	2	Q6HJX0_CABHK	Q6hjx0	bacillus th
755	30	66.7	876	2	Q50UH1_ENTHI	Q50uh1	entamoeba h	828	29	64.4	65	2	Q63CG4_BACAZ	Q63cg4	bacillus ce
756	30	66.7	880	2	Q7YRA9_BOVIN	Q7yra9	bos taurus	829	29	64.4	65	2	Q81RP5_BACAN	Q81rp5	bacillus an
757	30	66.7	891	2	Q6LID3_PICTO	Q6lid3	picrophilus	830	29	64.4	66	2	Q96YX7_SULTO	Q96yx7	sulfolobus
758	30	66.7	904	1	PMS1_YEAST	P14242	saccharomyc	831	29	64.4	73	2	Q6KZY0_PICTO	Q6kzy0	picrophilus
759	30	66.7	908	2	Q8TG48_YEAST	Q8tg48	saccharomyc	832	29	64.4	79	2	Q4YYA3_PLABE	Q4yya3	plasmodium
760	30	66.7	908	2	Q8TG50_YEAST	Q8tg50	saccharomyc	833	29	64.4	86	2	Q4XZQ9_PLACH	Q4xzq9	plasmodium
761	30	66.7	908	2	Q8TG54_YEAST	Q8tg54	saccharomyc	834	29	64.4	87	2	Q98675_9BETA	Q98675	simian cyto



835	29	64.4	92	2	Q31389	CARAU	Q31389	carassius a	908	29	64.4	233	2	Q8A699	BACTN	Q8A699	bacteroides
836	29	64.4	93	2	Q8ZHX3	YERPE	Q8ZHX3	yersinia pe	909	29	64.4	233	2	Q8CV70	OCEIH	Q8CV70	oceanobacila
837	29	64.4	93	2	Q666B4	YERPS	Q666e4	yersinia ps	910	29	64.4	234	2	Q8WFN3	CANGA	Q8WFN3	candida gla
838	29	64.4	96	2	Q4YG44	PLABE	Q4YG44	plasmodium	911	29	64.4	238	2	Q6SNB3	TRAAU	Q6SNB3	trachypithe
839	29	64.4	96	2	Q9FL73	ARATH	Q9FL73	arabidopsis	912	29	64.4	243	2	Q6LR89	ARATH	Q6LR89	arabidopsis
840	29	64.4	98	2	Q97LW5	CLOAB	Q97LW5	clostridium	913	29	64.4	243	2	Q5NDY1	LACSN	Q5NDY1	lactobacilli
841	29	64.4	103	2	Q32718	TOBAC	Q32718	nicotiana t	914	29	64.4	244	2	Q5BS68	SCHJA	Q5BS68	schistosoma
842	29	64.4	103	2	Q87672	ABERY	Q87672	aeromonas h	915	29	64.4	248	2	Q61SV0	CAEBR	Q61SV0	caenorhabdi
843	29	64.4	104	2	Q9C9P5	ARATH	Q9C9P5	arabidopsis	916	29	64.4	250	2	Q8TN15	MORSA	Q8TN15	methanosarc
844	29	64.4	104	2	Q7UP41	RHOBA	Q7UP41	rhodopiell	917	29	64.4	254	2	Q8TN15	METAC	Q8TN15	metanosaarc
845	29	64.4	105	2	Q4Y9R8	PLABE	Q4Y9R8	plasmodium	918	29	64.4	254	2	Q4T2C6	TETNG	Q4T2C6	tetraodon n
846	29	64.4	105	2	Q9PXK6	BLIV	Q9PXK6	bovine leuk	919	29	64.4	255	2	Q70NW3	9BILA	Q70NW3	strongyloid
847	29	64.4	106	2	Q59QW6	CANAL	Q59QW6	candida alb	920	29	64.4	255	2	Q7Q2G0	ANOGA	Q7Q2G0	anopheles g
848	29	64.4	108	1	YD88	SCHPO	Q10413	schizosacch	921	29	64.4	256	2	Q51TL8	MAGGR	Q51TL8	magnaporth
849	29	64.4	115	2	Q4XZ14	PLACH	Q4XZ14	plasmodium	922	29	64.4	257	2	Q54K90	DICDI	Q54K90	dictyosteli
850	29	64.4	122	2	Q9CM14	PASMU	Q9CM14	paeteurella	923	29	64.4	257	2	Q51485	BORBU	Q51485	borrelia bu
851	29	64.4	123	2	Q74RH3	YERPE	Q74RH3	yersinia pe	924	29	64.4	258	1	ETXD	STAAU	ETXD	staphylococ
852	29	64.4	128	2	Q84M05	ORYSA	Q84M05	oryza sativ	925	29	64.4	260	2	Q7VM54	HAEDU	Q7VM54	haemophilus
853	29	64.4	128	2	Q88T19	PLAPE	Q98T19	platichtys	926	29	64.4	261	2	Q90GB7	RHIL0	Q90GB7	rhizobium l
854	29	64.4	136	1	RS9	PROMP	Q7UZW9	prochloroco	927	29	64.4	262	2	Q930P5	RHIME	Q930P5	rhizobium m
855	29	64.4	137	2	Q4YG29	PLABE	Q4YG29	plasmodium	928	29	64.4	263	2	Q7RGH4	PLAYC	Q7RGH4	plasmodium
856	29	64.4	143	2	Q8KJW7	PROVU	Q8KJW7	proteus vul	929	29	64.4	263	2	Q9AB49	CAUCR	Q9AB49	caulobacter
857	29	64.4	148	2	Q8XYR2	RALSO	Q8XYR2	ralstonia s	930	29	64.4	264	2	Q9S511	LOWBP	Q9S511	loofah witc
858	29	64.4	152	2	Q4N994	THEPA	Q4N994	theileria p	931	29	64.4	265	2	Q8EUM9	MYCPE	Q8EUM9	mycoplasma
859	29	64.4	152	2	Q6R2F9	STAAU	Q6R2F9	staphylococ	932	29	64.4	268	2	Q85217	STAAU	Q85217	staphylococ
860	29	64.4	153	2	Q8ZT14	PYRAE	Q8ZT14	pyrobaculum	933	29	64.4	268	2	Q76LS7	STAAU	Q76LS7	staphylococ
861	29	64.4	153	2	Q6YR18	ONYPE	Q6YR18	onion yello	934	29	64.4	268	2	Q8XH55	CLOPE	Q8XH55	clostridum
862	29	64.4	154	2	Q4JCH9	SULAC	Q4JCH9	sulfolobus	935	29	64.4	268	2	Q25073	HELPU	Q25073	helicobacte
863	29	64.4	154	2	Q5CND8	CRYHO	Q5CND8	cryptospori	936	29	64.4	268	2	Q9ZMD4	HELPU	Q9ZMD4	helicobacte
864	29	64.4	157	2	Q34R91	9HYME	Q94R91	syncoscapter	937	29	64.4	269	1	SURP4	FUGRU	SURP4	fugu rubrip
865	29	64.4	157	2	Q7U5T6	RHOBA	Q7U5T6	rhodopiell	938	29	64.4	269	1	SURP4	HUMAN	SURP4	homo sapien
866	29	64.4	157	2	Q5NM50	ZYMMO	Q5NM50	zymomonas m	939	29	64.4	269	1	SURP4	MOUSE	SURP4	mus musculu
867	29	64.4	160	2	Q6W6W1	CANFA	Q6W6W1	canis famil	940	29	64.4	269	2	Q5R705	PONPY	Q5R705	pongo pygma
868	29	64.4	162	2	Q91IB4	9VIRU	Q91IB4	potato mop-	941	29	64.4	269	2	Q545Q2	MOUSE	Q545Q2	mus musculu
869	29	64.4	163	2	Q8QRC2	9VIRU	Q8QRC2	potato mop-	942	29	64.4	269	2	Q8V9M7	9VIRU	Q8V9M7	sulfolobus
870	29	64.4	168	2	Q75H68	ORISA	Q75H68	oryza sativ	943	29	64.4	269	2	Q800K9	CHICK	Q800K9	gallus gall
871	29	64.4	169	2	Q772M4	9VIRU	Q772M4	potato mop-	944	29	64.4	269	2	Q6AZP7	XENLA	Q6AZP7	xenopus lae
872	29	64.4	169	2	Q8QRC3	9VIRU	Q8QRC3	potato mop-	945	29	64.4	269	2	Q6DGJ8	BRARE	Q6DGJ8	brachydanio
873	29	64.4	172	2	Q8QRC3	9VIRU	Q8QRC3	potato mop-	946	29	64.4	269	2	Q6NTY0	XENLA	Q6NTY0	xenopus lae
874	29	64.4	176	2	Q85283	9VIRU	Q85283	potato mop-	947	29	64.4	269	2	Q6NTY0	XENLA	Q6NTY0	xenopus lae
875	29	64.4	176	2	Q31W99	9VIRU	Q31W99	potato mop-	948	29	64.4	269	2	Q6P344	XENTR	Q6P344	xenopus tro
876	29	64.4	181	2	Q4Y286	PLABE	Q4Y286	plasmodium	949	29	64.4	269	2	Q7SZQ7	BRARE	Q7SZQ7	brachydanio
877	29	64.4	187	2	Q9EMZ9	AMEPV	Q9EMZ9	ameaecta moo	950	29	64.4	269	2	Q642N6	XENTR	Q642N6	xenopus tro
878	29	64.4	189	2	Q87V81	9PESM	Q87V81	pseudomonas	951	29	64.4	270	1	SURF4	DROME	SURF4	drosophila
879	29	64.4	190	2	Q9G882	9RUKA	Q9G882	malawimonas	952	29	64.4	271	2	Q8SYW4	DROME	Q8SYW4	drosophila
880	29	64.4	195	2	Q97UV8	SULSO	Q97UV8	sulfolobus	953	29	64.4	271	2	Q9ZGM9	STAAU	Q9ZGM9	staphylococ
881	29	64.4	197	2	Q9CHZ0	LACLA	Q9CHZ0	lactococcus	954	29	64.4	271	2	Q93RG9	STAAU	Q93RG9	staphylococ
882	29	64.4	198	2	Q5SSR0	CRINE	Q5SSR0	cryptococcu	955	29	64.4	271	2	Q8NUX3	STAAU	Q8NUX3	staphylococ
883	29	64.4	198	2	Q5KH47	CRINE	Q5KH47	cryptococcu	956	29	64.4	271	2	Q8CQC7	STABP	Q8CQC7	staphylococ
884	29	64.4	198	2	Q98674	9BETA	Q98674	simian cyto	957	29	64.4	271	2	Q7A3N3	STAAU	Q7A3N3	staphylococ
885	29	64.4	199	2	Q4YGD4	PLABE	Q4YGD4	plasmodium	958	29	64.4	271	2	Q6GDX1	STAAU	Q6GDX1	staphylococ
886	29	64.4	201	2	Q4HK99	CAMLA	Q4HK99	campylobact	959	29	64.4	271	2	Q6G6K6	STAAU	Q6G6K6	staphylococ
887	29	64.4	206	2	Q8FRJ6	SCHJA	Q8FRJ6	schistosoma	960	29	64.4	271	2	Q5HKH6	STAAU	Q5HKH6	staphylococ
888	29	64.4	208	1	RK99	ARATH	Q9XJ27	arabidopsis	961	29	64.4	271	2	Q5HDB7	STAAU	Q5HDB7	staphylococ
889	29	64.4	208	1	Q9BLI2	BOMMO	Q9BLI2	bombyx mori	962	29	64.4	272	2	Q6LJ08	PHOPR	Q6LJ08	photobacter
890	29	64.4	208	2	Q681V1	ARATH	Q681V1	arabidopsi	963	29	64.4	273	2	Q86G65	DEPVA	Q86G65	dermatocent
891	29	64.4	208	2	Q681W6	ARATH	Q681W6	arabidopsis	964	29	64.4	274	2	Q9BHE9	LEIMA	Q9BHE9	leishmania
892	29	64.4	208	2	Q4HTJ5	CAMUP	Q4HTJ5	campylobact	965	29	64.4	274	2	Q6YJ66	9BILA	Q6YJ66	longistetriat
893	29	64.4	210	1	Y743	CAEBL	Q11071	caenorhabdi	966	29	64.4	274	2	Q6XJ70	9BILA	Q6XJ70	longistetriat
894	29	64.4	212	1	FUPA	PICTO	Q6KZQ5	picrophilus	967	29	64.4	274	2	Q6MFP29	PARUM	Q6MFP29	parachlamyid
895	29	64.4	216	2	Q6FLG6	CANGA	Q6FLG6	candida gla	968	29	64.4	275	2	Q55K98	CRYNQ	Q55K98	cryptococcu
896	29	64.4	216	2	Q4WF76	ASPFU	Q4WF76	aspergillus	969	29	64.4	278	2	Q7W4W7	BORDTELLA	Q7W4W7	bordetella
897	29	64.4	216	2	Q4HL23	CAMLA	Q4HL23	campylobact	970	29	64.4	278	2	Q7WK23	BORBA	Q7WK23	bordetella
898	29	64.4	216	2	Q53099	RHOSH	Q53099	rhodobacter	971	29	64.4	278	2	Q8XUN0	RALSO	Q8XUN0	ralstonia s
899	29	64.4	219	2	Q613W5	CAEBR	Q613W5	caenorhabdi	972	29	64.4	278	2	Q98BT3	RHIL0	Q98BT3	rhizobium l
900	29	64.4	219	2	Q5HMZ9	STAEQ	Q5HMZ9	staphylococ	973	29	64.4	279	2	Q8EJH7	SHEON	Q8EJH7	shewanella
901	29	64.4	219	2	Q8CRR8	STABP	Q8CRR8	staphylococ	974	29	64.4	280	2	Q4JLE1	LACRE	Q4JLE1	lactobacilli
902	29	64.4	223	1	YCX1	MESVI	Q9MUQ5	mesostigma	975	29	64.4	280	2	Q4LHX1	9BURK	Q4LHX1	burkholderi
903	29	64.4	227	2	Q6YVX8	ORYSA	Q6YVX8	oryza sativ	976	29	64.4	281	2	Q8UH85	AGRT5	Q8UH85	agrobacteri
904	29	64.4	230	2	Q8TN19	METAC	Q8TN19	methanosarc	977	29	64.4	282	2	Q576V4	BRUAB	Q576V4	bruceella ab
905	29	64.4	232	2	Q5QBP9	MESCR	Q5QBP9	mesembryant	978	29	64.4	282	2	Q7NP25	GLOVI	Q7NP25	gloeobacter
906	29	64.4	233	2	Q4J736	SULFAC	Q4J736	sulfolobus	979	29	64.4	282	2	Q8FV43	BRUSU	Q8FV43	bruceella su
907	29	64.4	233	2	Q4I515	GIBZEE	Q4I515	gibberella	980	29	64.4	282	2	Q8YD89	BRUME	Q8YD89	bruceella me

981 29 64.4 283 2 Q50SL5\_ENTHI  
 982 29 64.4 283 2 O11438\_9VIRU  
 983 29 64.4 283 2 O36303\_9VIRU  
 984 29 64.4 283 2 Q08349\_9VIRU  
 985 29 64.4 283 2 Q66603\_9VIRU  
 986 29 64.4 284 2 Q7TBL5\_9VIRU  
 987 29 64.4 284 2 CLN8\_HUMAN  
 988 29 64.4 286 2 Q41QR4\_GIBZE  
 989 29 64.4 287 2 Q81IH8\_DROER  
 990 29 64.4 288 1 CLN8\_MOUSE  
 991 29 64.4 288 1 CLN8\_RAT  
 992 29 64.4 288 2 Q8BNW2\_MOUSE  
 993 29 64.4 288 2 Q542J5\_MOUSE  
 994 29 64.4 296 2 Q4LI42\_BURKH  
 995 29 64.4 298 2 Q60S94\_CABER  
 996 29 64.4 298 2 Q63QD8\_BURPS  
 997 29 64.4 298 2 Q62G49\_BURMA  
 998 29 64.4 299 1 T2R50\_MACMU  
 999 29 64.4 299 1 T2R50\_PAPHA  
 1000 29 64.4 301 2 Q7X520\_CAMCO

## ALIGNMENTS

RESULT 1  
 QPQPS7\_UREPA PRELIMINARY; PRT; 247 AA.  
 AC Q9PQS7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Protein phosphatase.  
 GN Name=ptci; OrderedLocusNames=UV215;  
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=134821;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 700970;  
 RX MEDLINE=20500219; PubMed=11048724; DOI=10.1038/35037619;  
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,  
 RA Cassell G.H.;  
 RT "The complete sequence of the mucosal pathogen Ureaplasma  
 RT urealyticum.";  
 RL Nature 407:757-762(2000).  
 DR EMBL; AB002120; AAF30623.1; -; Genomic DNA.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR InterPro; IPR001932; PP2C-like.  
 DR Pfam; PF00481; PP2C; 1.  
 DR SMART; SM00332; PP2CC; 1.  
 DR SMART; SM00331; PP2C\_SIG; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 247 AA; 28322 MW; A81EFB16AF275C80 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 9.2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0;

Qy 1 FLSYDLFV 8  
 |||||  
 Db 176 FLSYDLFV 183

RESULT 2  
 Q7BHL0\_9FUSO PRELIMINARY; PRT; 69 AA.  
 AC Q7BHL0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE OppF (Fragment).  
 GN Name=oppF;

OS Fusobacterium necrophorum.  
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
 OC Fusobacterium.  
 OX NCBI\_TaxID=859;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=A25;  
 RX MEDLINE=21391803; PubMed=11500416;  
 RX DOI=10.1128/JAI.69.9.5447-5455.2001;  
 RA Narayanan S.K., Nagaraja T.G., Chengappa M.M., Stewart G.C.;  
 RT "Cloning, sequencing, and expression of the leukotoxin gene from  
 RT Fusobacterium necrophorum.";  
 RL Infect. Immun. 69:5447-5455(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=A25;  
 RX Oelke A.M., Nagaraja T.G., Wilkerson M.J., Stewart G.C.;  
 RT "The leukotoxin operon of Fusobacterium necrophorum.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=A25;  
 RA Stewart G.C., Narayanan S., Oelke A.M., Nagaraja T.G., Chengappa M.M.;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF312861; AAS45303.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 69 AA; 8271 MW; 82443BD96429965 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 69;  
 Best Local Similarity 77.8%; Pred. No. 10;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLSYDLFV 9  
 |:::|  
 Db 16 FISHDLFV 24

RESULT 3  
 Q50J25\_CABER PRELIMINARY; PRT; 534 AA.  
 ID Q60J25;  
 AC Q60J25;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein CBG24720.  
 GN Name=CBG24720;  
 OS Caenorhabditis briggsae.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6238;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RG The C.briggsae Sequencing Consortium;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 DR EMBL; CAAC01000351; CAE56881.1; -; Genomic DNA.  
 DR GO; GO:0016758; P:transferase activity, transferring hexosyl . . .; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002213; UDP\_glucos\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Glycosyltransferase; Hypothetical protein; Transferase.  
 SQ SEQUENCE 534 AA; 61065 MW; 997230390014F032 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 534;  
 Best Local Similarity 77.8%; Pred. No. 79;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 FLSYDLFV 9  
 |:::|

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Db      492 FLSYDIFV 500

RESULT 4
ID Q99T82 STAMP PRELIMINARY; PRT; 259 AA.
AC Q99T82;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated transposase.
GN OrderedLocusNames=SAV1787;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hirumatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB57949.1; -; Genomic_DNA.
DR FIR; C89964; C89964.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0004803; P:transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR002559; Transposase_11.
DR Pfam; PF01609; Transposase_11; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 259 AA; 30921 MW; 73B1B908A649E4AC CRC64;

Query Match 82.2%; Score 37; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLF 7
|||
Db 12 FLSYDLF 18

RESULT 5
ID Q4XPX6 FLACH PRELIMINARY; PRT; 31 AA.
AC Q4XPX6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC107882.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
[1]
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berlman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D.E., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

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DR EMBL; CAAJ01004080; CAH81036.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 31 AA; 3980 MW; AD54A82D59901EBE CRC64;

Query Match 80.0%; Score 36; DB 2; Length 31;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
|||
Db 19 FLSYDIFVI 27

RESULT 6
ID Q9XOX9 THEMATA PRELIMINARY; PRT; 191 AA.
AC Q9XOX9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TM1252;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001780; AAD36327.1; -; Genomic_DNA.
DR FIR; F72277; F72277.
DR TIGR; TW1252; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 191 AA; 21566 MW; 82A6ABCD45D08498 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 191;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
|||
Db 44 FLSDFDFVI 52

RESULT 7
ID Q9D9A8 MOUSE PRELIMINARY; PRT; 101 AA.
AC Q9D9A8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:1700113101 product:hypothetical protein, full insert
DE sequence.
GN Name=2900055D14R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;

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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (KISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK007197; BAB24895.1; -; mRNA.  
DR Ensembl; ENSMUSG00000024666; Mus musculus.  
DR MGI; MGI:1920232; 2900055DI4R1X.  
DR GO; GO:0005085; P:guanyl-nucleotide exchange factor activity; IEA.  
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.  
DR InterPro; IPR000651; RasGef N.  
DR PROSITE; PS50212; RASGEF\_NTER; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 101 AA; 11635 MW; E9277CDA50D73D30 CRC64;  
Query Match 77.8%; Score 35; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
RESULT 8  
Q5JPE1 HUMAN PRELIMINARY; PRT; 161 AA.  
AC Q5JPE1;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein DKFP667J203.  
GS Name=DKFP667J203;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph node;  
RG The German cDNA Consortium;  
RA Ansoerge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL832879; CAI46174.1; -; -.  
KW Hypothetical protein.  
SQ SEQUENCE 161 AA; 18992 MW; FED9DF88C354C87D CRC64;  
Query Match 77.8%; Score 35; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
RESULT 9  
Q9NP10 HUMAN PRELIMINARY; PRT; 162 AA.  
AC Q9NP10;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE HSPC198 (Hypothetical protein HSPC196).  
GN Name=HSPC196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Umbilical cord blood;  
RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,

RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
 RT Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Bladder;  
 RC MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Bladder;  
 RC NTH MGC Project;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF151032; AAF36118.1; -; mRNA.  
 DR EMBL; BC005201; AAH05201.1; -; mRNA.  
 DR EMBL; AF151030; AAF36116.1; -; mRNA.  
 DR Ensembl; ENSG00000149483; Homo sapiens.  
 KW Hypothetical protein.  
 SQ SEQUENCE 162 AA; 1262 MW; 31D76DD5C953333D CRC64;  
 Query Match 77.8%; Score 35; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LSYDLFV 8 PRT; 162 AA.  
 DB 18 LSYDLFV 24  
 RESULT 10  
 Q9D6G5\_MOUSE PRELIMINARY; PRT; 162 AA.  
 AC Q9D6G5;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched  
 DE library, clone:2900055D14 product:hypothetical protein, full insert  
 DE sequence (Mus musculus adult pancreas islet cells cDNA, RIKEN full-  
 DE length enriched library, clone:C820001003 product:hypothetical  
 DE protein, full insert sequence) (RIKEN cDNA 2900055D14).  
 GN Name=2900055D14Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Hippocampus, and Pancreas;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX

RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RN Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Hippocampus, and Pancreas;  
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Hippocampus, and Pancreas;  
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Vagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.L.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Hippocampus, and Pancreas;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Hippocampus, and Pancreas;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RX



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RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivy A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002);
DR EMBL: ALJ29359, CAD52036.1; -; Genomic_DNA.
DR InterPro: IPR006496; DUF_PFAU7.
DR TIGRPFAMS: TIGR01609; PF_unchar_267; 1.
KW Hypothetical protein.
SQ SEQUENCE 192 AA; 23573 MW; DCFAA5B8802CC7A3 CRC64;

Query Match 77.8%; Score 35; DB 2; Length 192;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
Db |||||::
37 FLSYDMLII 45

RESULT 13
Q84AF2_BACST
ID Q84AF2_BACST PRELIMINARY; PRT; 203 AA.
AC Q84AF2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BstYI.
GN Name-bstYIR;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Y406;
RA Xu S.-Y., Samuelson J., Pelletier J., Sibley M., Wilson G.G.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY197779; AA048714.1; -; Genomic_DNA.
DR PDB: 1SD0; X-ray; A=1-203.
SQ SEQUENCE 203 AA; 23193 MW; C6F5C22A35DB04EF CRC64;

Query Match 77.8%; Score 35; DB 2; Length 203;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 8
Db |||||::
136 FVAYDLFV 143

RESULT 14
Q59WS4_CANAL
ID Q59WS4_CANAL PRELIMINARY; PRT; 506 AA.
AC Q59WS4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Potential vacuolar protein sorting kinase Vps15p.
DR ORFNames=CA019.129, CA019.7775;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;

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RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scher S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tsung K.-W.,
RA Jones T., Scher S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AACQ01000112; EAK94965.1; -; Genomic_DNA.
DR EMBL: AACQ01000106; EAK95266.1; -; Genomic_DNA.
KW Kinase.
SQ SEQUENCE 506 AA; 57762 MW; 8564C55136C0040E CRC64;

Query Match 77.8%; Score 35; DB 2; Length 506;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
Db |||||::
124 FLSYDLSII 132

RESULT 15
Q4UN00_RICFE
ID Q4UN00_RICFE PRELIMINARY; PRT; 673 AA.
AC Q4UN00;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Cytochrome c-type biogenesis protein CcmP.
GN Name-ccmP; OrderedlocusNames=RF_0207;
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxID=42862;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=URRWKcal2;
RX PubMed=15984913; DOI=10.1371/journal.pbio.0030248;
RA Ogata H., Rensato P., Audic S., Robert C., Blanc G., Fournier P.-E.,
RA Parinello H., Claverie J.-M., Raoult D.;
RT "The genome sequence of Rickettsia felis identifies the first putative
RT conjugative plasmid in an obligate intracellular parasite.";
RL PLoS Biol. 3:E248-E248(2005).
DR EMBL: CP000053; AAY61058.1; -; Genomic_DNA.
DR InterPro: IPR003567; Cyt c biog.
DR InterPro: IPR002541; Cyt c asm.
DR Pfam: PF01578; Cytochrom_C_asm; 1.
DR PRINTS: PR01410; CCIOGENESIS.
KW Complete proteome.
SQ SEQUENCE 673 AA; 76214 MW; E54FF99B66BDC31 CRC64;

Query Match 77.8%; Score 35; DB 2; Length 673;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
Db |||||::
622 YLSYDLFV 630

RESULT 16
Q4N4P9_THEPA
ID Q4N4P9_THEPA PRELIMINARY; PRT; 1066 AA.
AC Q4N4P9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

```

DE Hypothetical protein.  
GN ORFNames=FP02\_0591;  
OS Theileria parva.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae; Theileria.  
OX NCBI\_TaxID=5875;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Muguga;  
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M., Hall N., Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B., Silva J.C., Uterback T.R., Feldblyum T.V., Perce M., Allen J., Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;  
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms lymphocytes.";  
RL Science 309:134-137(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Muguga;  
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R., Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C., Uterback T., Feldblyum T., Perce M., Allen J., Taracha E.L., Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBSJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is preliminary data.  
CC EMBL; AAGK01000002; EAN32874.1; -; Genomic\_DNA.  
DR EMBL; AAGK01000002; EAN32874.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 1066 AA; 122010 MW; 165PEFA06D1C09FE CRC64;  
  
Query Match 77.8%; Score 35; DB 2; Length 1066;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SYDLFWV 9  
DB 348 SYDLFWV 354  
  
RESULT 17  
ID Q88216\_PSESM PRELIMINARY; PRT; 35 AA.  
AC Q88216;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Lipoprotein, putative.  
GN OrderedLocNames=PSPT02641;  
OS Pseudomonas syringae (pv. tomato).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=323;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=DC3000;  
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;  
RA Buehl C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.P., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidlsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,

RA Bender C.L., White O., Fraser C.M., Collmer A.;  
RT "The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomato DC3000.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).  
DR EMBL; AE016853; AAO56144.1; -; Genomic\_DNA.  
DR TIGR; PSPT02641; -;  
KW Complete proteome; Lipoprotein.  
SQ SEQUENCE 35 AA; 3854 MW; E209450422A75C09 CRC64;  
  
Query Match 75.6%; Score 34; DB 2; Length 35;  
Best Local Similarity 66.7%; Pred. NO. 33;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 FLSYDLFWV 9  
DB 9 FLSYGLYVI 17  
  
RESULT 18  
ID Q8ZDH9\_YERPE PRELIMINARY; PRT; 95 AA.  
AC Q8ZDH9; Q74VZ3; Q7CJW2;  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
DE Hypothetical protein YPO2589 (Hypothetical protein yll159).  
GN OrderedLocNames=Yll126, YPO2589, Yll159;  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CO-92 / Biovar Orientalis;  
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;  
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Pringle M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
RL Nature 413:523-527(2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=KIM5 / Biovar Mediaevalis;  
RX MEDLINE=22137863; PubMed=12142430;  
RX DOI=10.1128/JB.184.16.4601-4611.2002;  
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.;  
RT "Genome sequence of Yersinia pestis KIM.";  
RL J. Bacteriol. 184:4601-4611(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=91001;  
RX PubMed=15368893;  
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D., Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z., Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R.;  
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate avirulent to humans.";  
RL DNA Res. 11:179-197(2004).  
DR EMBL; AJ414152; CAC91389.1; -; Genomic\_DNA.  
DR EMBL; AE033739; AAM84736.1; -; Genomic\_DNA.  
DR EMBL; AE017131; AAS61372.1; -; Genomic\_DNA.  
DR FIR; AI0315; AI0315.  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.



```

DR GO; GO:0017000; P:antibiotic biosynthesis; IEA.
DR InterPro; IPR007138; ABM.
DR Pfam; PF03992; ABM; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 95 AA; 11144 MW; 13192FF15A3A9429 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 95;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8
Db |||||:
36 LSYDLFI 42

RESULT 19
Q6DG3 YERP5
ID Q6DG3 YERP5 PRELIMINARY; PRT; 95 AA.
AC Q6DG3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=XPB1083;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I;
RX PubMed=1535858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Laximer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georges A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RA "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH20232.1; -; Genomic_DNA.
DR GO; GO:0005737; Cytoplasm; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0017000; P:antibiotic biosynthesis; IEA.
DR InterPro; IPR007138; ABM.
DR Pfam; PF03992; ABM; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 95 AA; 11144 MW; 13192FF15A3A9429 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 95;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8
Db |||||:
36 LSYDLFI 42

RESULT 20
Q6AC3 LEIXX
ID Q6AC3 LEIXX PRELIMINARY; PRT; 182 AA.
AC Q6AC3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Orotate phosphoribosyltransferase.
GN Name=pyrE; OrderedLocusNames=Lxx23400;
OS Leifsonia xyli (subsp. xyli).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Query Match 75.6%; Score 34; DB 2; Length 184;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.P., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyli subsp. xyli.";
RL Mol. Plant Microbe Interact. 17:827-836(2004).
CC -!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate + diphosphate = orotate
CC + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -!- COFACTOR: Magnesium (By similarity)
CC -!- PATHWAY: Pyrimidine biosynthesis; fifth step.
CC -!- SUBUNIT: Homodimer (By similarity).
DR EMBL; AB016822; AA78990.1; -; Genomic DNA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004588; F:orotate phosphoribosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0003116; F:nucleoside metabolism; IEA.
DR GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.
DR InterPro; IPR004467; Or_pshpho trans.
DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF0156; Priboyltran; 1.
DR TIGRPFAM; TIGR00336; pyrE; 1.
KW Complete proteome; Glycosyltransferase; Magnesium;
KW Pyrimidine biosynthesis; Transferase.
SQ SEQUENCE 182 AA; 19091 MW; 2A56B021E814C108 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 182;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSYDLFV 9
Db |||||:
89 LSYDAFV 96

RESULT 21
Q6L299 PICTO
ID Q6L299 PICTO PRELIMINARY; PRT; 184 AA.
AC Q6L299;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PTO0318;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AB017261; AA42903.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 184 AA; 21010 MW; 2332E9F3E1A636 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 184;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 FLSYDLFV 8  
|:|||||:  
Db 104 FVYDLFI 111

## RESULT 22

ID Q4UG8\_THEAN PRELIMINARY; PRT; 340 AA.  
AC Q4UG8;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=TA19505;  
OS Theileria annulata.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;  
OC Theileria.  
OX NCBI\_TaxID=5874;  
RN [1]\_TaxID=5874;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Ankara isolate clone C9;  
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,  
RA Hall N., Barrell B.G.;  
RT "The chromosome 1 sequence of Theileria annulata."  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR940347; CAI73821.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 340 AA; 39031 MW; 839B2D67FD8A855D CRC64;

Query Match 75.6%; Score 34; DB 2; Length 340;  
Best Local Similarity 55.6%; Pred. No. 3.2e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
|:|||||:  
Db 94 FINYDVYV 102

## RESULT 23

ID Q4V194\_BACCZ PRELIMINARY; PRT; 363 AA.  
AC Q4V194;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Probable low temperature requirement protein A.  
GN Name=ltrA; ORFNames=pE33L466\_0370;  
OS Bacillus cereus (strain ZK).  
OG Plasmid pE33L466.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=288681;  
RN [1]\_TaxID=288681;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=E33L;  
RG Joint Genome Institute Microbial Sequencing, Finishing and Annotation  
RG Team;  
RT "Complete genome sequence of Bacillus cereus E33L."  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=E33L;  
RG Joint Genome Institute Microbial Sequencing, Finishing and Annotation  
RG Team;  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CP000040; AAY60513.1; -; Genomic\_DNA.  
KW Plasmid.  
SQ SEQUENCE 363 AA; 42679 MW; DBC69977546D9687 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 363;  
Best Local Similarity 66.7%; Pred. No. 3.4e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
|:|||||:  
Db 332 FLIFDLFV 340

## RESULT 24

ID Q9ZPF4\_ARATH PRELIMINARY; PRT; 382 AA.  
AC Q9ZPF4;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE T3H13.9 protein.  
GN Name=T3H13.9;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Washu;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Drone K., Nguyen C.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF128396; AAD17374.1; -; Genomic\_DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005215; P:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001114; MFS.  
DR InterPro; IPR011701; MFS.  
DR Pfam; PF07690; MFS.1.  
DR PROSITE; PS50850; MFS; 1.  
SQ SEQUENCE 382 AA; 41929 MW; 979C03576443F8D7 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 382;  
Best Local Similarity 85.7%; Pred. No. 3.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFV 9  
|:|||||:  
Db 18 SYDLFVI 24

## RESULT 25

ID UXUA\_BACTN STANDARD; PRT; 389 AA.  
AC Q8A7U2;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Mannanase dehydratase (EC 4.2.1.8) (D-mannanase hydrolase).  
GN Name=uxuA; OrderedLocusNames=BT1432;  
OS Bacteroides thetaiotaomicron.  
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=VPI-5482 / ATCC 29148;  
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
RA Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."  
RL Science 299:2074-2076(2003).  
CC -!- CATALYTIC ACTIVITY: D-mannanase = 2-dehydro-3-deoxy-D-gluconate +  
H(2)O.

```

CC -!- PATHWAY: Hexuronate conversion to KDG.
CC -!- SIMILARITY: Belongs to the mannionate dehydratase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AEO16931; AAC76539.1; -; Genomic_DNA.
CC HAMAP; MF 00106; -; 1.
CC InterPro; IPR004628; Man_dehyd.
CC Pfam; PF03786; Uxua; 1.
CC TIGRFAMs; TIGR00695; uxua; 1.
CC Complete proteome; Lyase.
CC SEQUENCE 389 AA; 44460 MW; 49AF971B14104B8E CRC64;
CC -----
Query Match 75.6%; Score 34; DB 1; Length 389;
Best Local Similarity 55.8%; Pred. No. 3.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 1 FLSYDLFVV 9
DB 136 FLAPDLFIL 144
CC -----
RESULT 26
UXUA RHIL0 STANDARD; PRT; 394 AA.
AC Q987X5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Mannionate dehydratase (EC 4.2.1.8) (D-mannionate hydrolase).
GN Name-uxua; OrderedLocNames=ml-6866;
GN Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OC NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimoto S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338 (2000).
CC -!- CATALYTIC ACTIVITY: D-mannionate = 2-dehydro-3-deoxy-D-gluconate +
CC H(2)O.
CC -----
CC -!- PATHWAY: Hexuronate conversion to KDG.
CC -!- SIMILARITY: Belongs to the mannionate dehydratase family.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BAA00012; BAB53075.1; -; Genomic_DNA.
CC HAMAP; MF 00106; -; 1.
CC InterPro; IPR004628; Man_dehyd.
CC Pfam; PF03786; Uxua; 1.
CC TIGRFAMs; TIGR00695; uxua; 1.
CC Complete proteome; Lyase.
CC SEQUENCE 394 AA; 44543 MW; EBE0BC1E8FFC4003 CRC64;
CC -----
Query Match 75.6%; Score 34; DB 1; Length 394;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 FLSYDLFVV 9
DB 133 FAAYDLFVL 141
CC -----
RESULT 27
Q7VHG1 HELHP PRELIMINARY; PRT; 409 AA.
ID Q7VHG1;
AC Q7VHG1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ubiquinol cytochrome c oxidoreductase.
DE OrderedLocNames=HH1006;
GN Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OC NCBI_TaxID=32025;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus".
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC EMBL; AB017147; AAP77603.1; -; Genomic DNA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0048872; F:metal ion binding; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro; IPR005798; Cytb_b6_C.
CC InterPro; IPR005797; Cytb_b6_N.
CC Pfam; PF00032; Cytochrom_B_C; 1.
CC Pfam; PF00033; Cytochrom_B_N; 1.
CC PROSITE; PS51003; CYTB_CTER; 1.
CC PROSITE; PS51002; CYTB_NTER; 1.
CC Complete proteome; Electron transport; Heme; Iron; Metal-binding;
CC Respiratory chain; Transmembrane; Transport.
CC SEQUENCE 409 AA; 47066 MW; DEC091B8DC05C49 CRC64;
CC -----
Query Match 75.6%; Score 34; DB 2; Length 409;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 1 FLSYDLFVV 9
DB 252 FLKDLFVV 260
CC -----
RESULT 28
Q7MTQ1 WOLSU PRELIMINARY; PRT; 411 AA.
ID Q7MTQ1;
AC Q7MTQ1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE UBIQUINOL CYTOCHROME C OXIDOREDUCTASE, CYTOCHROME B SUBUNIT
DE (PBCH).
GN Name=CYTB; OrderedLocNames=WS2153;

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OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSMZ 1740;
RX MEDLINE=2282897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Ianz C., Klimek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC EMBL; BX571162; CAE11147.1; -; Genomic DNA.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0046872; F:metal ion binding; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro; IPR005798; Cytb_b6_C.
CC Pfam; PF00032; Cytochrom_B_C; 1.
CC Pfam; PF00033; Cytochrom_B_N; 1.
CC PROSITE; PS51003; CYTB_CTER; 1.
CC PROSITE; PS51002; CYTB_NTER; 1.
CC Complete proteome; Electron transport; Heme; Iron; Metal-binding;
KW Respiratory chain; Transmembrane; Transport.
SQ SEQUENCE 411 AA; 47252 MW; A5170467BEED61CF CRC64;

Query Match 75.6%; Score 34; DB 2; Length 411;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
DB 253 FLSKIDFVV 261

RESULT 29
O26064_HELPY
ID O26064_HELPY PRELIMINARY; PRT; 412 AA.
AC O26064;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ubiquinol cytochrome c oxidoreductase, cytochrome b subunit
DE (FbCh)
GN OrderedLocusNames=HP1539;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kervlaave A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;

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RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC EMBL; AE000652; AAD08579.1; -; Genomic DNA.
CC PIR; C64712; C64712.
CC TIGR; HP1539; -.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
CC GO; GO:0046872; F:metal ion binding; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0006118; P:electron transport; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro; IPR005798; Cytb_b6_C.
CC InterPro; IPR005797; Cytb_b6_N.
CC Pfam; PF00032; Cytochrom_B_C; 1.
CC Pfam; PF00033; Cytochrom_B_N; 1.
CC PROSITE; PS51003; CYTB_CTER; 1.
CC PROSITE; PS51002; CYTB_NTER; 1.
CC Complete proteome; Electron transport; Heme; Iron; Metal-binding;
KW Respiratory chain; Transmembrane; Transport.
SQ SEQUENCE 412 AA; 47511 MW; 954646D95A1F925A CRC64;

Query Match 75.6%; Score 34; DB 2; Length 412;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
DB 253 FLSKIDFVV 261

RESULT 30
Q9ZJ55_HELPY
ID Q9ZJ55_HELPY PRELIMINARY; PRT; 412 AA.
AC Q9ZJ55;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ubiquinol cytochrome c oxidoreductase, cytochrome b subunit.
DE Name=petB; OrderedLocusNames=JHP1460;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nichelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC EMBL; AE001568; AAD07045.1; -; Genomic DNA.
CC PIR; D71803; D71803.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0005746; C:mitochondrial electron transport chain; IEA.

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DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR005798; Cytb_b6_C.
DR InterPro: IPR005797; Cytb_b6_N.
DR Pfam: PF00032; Cytochrom_B_C_1.
DR Pfam: PF00033; Cytochrom_B_N_1.
DR PROSITE: PS1003; CYTB_CTER; 1.
DR PROSITE: PS1002; CYTB_NTER; 1.
KW Complete proteome; Electron transport; Heme; Iron; Metal-binding;
KW Respiratory chain; Transmembrane; Transport.
SQ SEQUENCE 412 AA; 47632 MW; 363F3CDB3638B0BD CRC64;

Query Match 75.6%; Score 34; DB 2; Length 412;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
Db 253 FLSKDFW 261

RESULT 31
Q9X019_THEMEA
ID Q9X019_THEMEA PRELIMINARY; PRT; 452 AA.
AC Q9X019;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase, putative.
GN OrderedLocusNames=TM1105;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Uterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-325 (1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AB001769; AAD36181.1; -; Genomic DNA.
DR PIR; C72295; C72295.
DR TIGR; TW1105; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; Oxidored_q1; 1.
KW Complete proteome; NAD; Oxidoreductase; Transmembrane.
SQ SEQUENCE 452 AA; 50539 MW; 19BEFCD6664F4E95 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 452;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLF 7
Db 102 FVSYDLF 108

RESULT 32
Q9ZWT3_ARATH
ID Q9ZWT3_ARATH PRELIMINARY; PRT; 516 AA.

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AC Q9ZWT3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Inorganic phosphate transporter.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99087485; PubMed=9872450;
RA Okumura S., Mitsukawa N., Shirano Y., Shibata D.;
RT "Phosphate transporter gene family of Arabidopsis thaliana.";
RL DNA Res. 5:261-269 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63 (2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AB005746; BAA34390.1; -; Genomic DNA.
DR EMBL; AB025638; BAA97413.1; -; Genomic DNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006817; P:phosphate transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR007114; MFS.
DR InterPro: IPR004738; P:phosphatase.
DR InterPro: IPR005828; Sub_transporter.
DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF00083; Sugar_tr; 1.
DR TIGRPFAM; TIGR00887; 2A0109; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 516 AA; 56246 MW; 97B2BEFEA894A145 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 516;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFV 9
Db 37 SYDLFVI 43

RESULT 33
Q8Y105_RALSO
ID Q8Y105_RALSO PRELIMINARY; PRT; 590 AA.
AC Q8Y105;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PROBABLE ACTIVATION/SECRETION PROTEIN.
GN OrderedLocusNames=RSC0888; ORFNames=RS04850;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

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RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RA Weisenbach J., Boucher C.A.;  
 RL "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";  
 RT Nature 415:497-502(2002).  
 DR EMBL; AL646061; CAD14590.1; -; Genomic\_DNA.  
 DR InterPro; IPR005565; H1YB.  
 DR Pfam; PF03865; Sh1B; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 590 AA; 64535 MW; DCOD1907965D5A0D CRC64;  
 Query Match 75.6%; Score 34; DB 2; Length 590;  
 Best Local Similarity 85.7%; Pred. No. 5.5e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
 |||||  
 Db 559 LSYDLFI 565

RESULT 34  
 Q7NIU9 GLOVI  
 ID Q7NIU9\_GLOVI PRELIMINARY; PRT; 618 AA.  
 AC Q7NIU9;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE NADH dehydrogenase subunit 5.  
 GN Name=ndhF; OrderedLocustNames=gll2083;  
 OS Gloeobacter violaceus.  
 OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter.  
 NCBI\_TaxID=33072;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=PCC 7421;  
 RX MEDLINE=22977040; PubMed=14621292;  
 RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,  
 RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,  
 RA Kohara M., Matsuno M., Matsuno A., Nakazaki N., Shimpō S.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RA "Complete genome structure of Gloeobacter violaceus PCC 7421, a  
 RT cyanobacterium that lacks thylakoids";  
 RL DNA RES. 10:137-145(2003).  
 CC -!- FUNCTION: NDH-1 shuttles electrons from NAD(P)H, via FMN and iron-  
 CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The  
 CC immediate electron acceptor for the enzyme in this species is  
 CC believed to be plastoquinone. Couples the redox reaction to proton  
 CC translocation (for every two electrons transferred, four hydrogen  
 CC ions are translocated across the cytoplasmic membrane), and thus  
 CC conserves the redox energy in a proton gradient (By similarity).  
 CC -!- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) +  
 CC plastoquinol.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC EMBL; BA000045; EAC90024.1; -; Genomic DNA.  
 DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.  
 DR GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.  
 DR InterPro; IPR003916; NADH\_oxred5.  
 DR InterPro; IPR010217; NdhF3\_CO2.  
 DR InterPro; IPR001750; Oxidored\_q1.  
 DR PANTHER; PTHR19377:SF7; NdhF3\_CO2; 1.  
 DR Pfam; PF00361; Oxidored\_q1; 1.  
 DR PRINTS; PR01434; NADHDHGNASE5.  
 DR TIGRfam; TIGR01960; ndhF3\_CO2; 1.  
 KW Complete proteome; NAD; NADP; Oxidoreductase; Plastoquinone;  
 KW Transmembrane.  
 SQ SEQUENCE 618 AA; 66634 MW; D1EBFAB93BEFAD02 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 618;  
 Best Local Similarity 62.5%; Pred. No. 5.7e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
 |||||

Db 534 FLAYDLYI 541  
 RESULT 35  
 Q4NOP8 THEPA  
 ID Q4NOP8\_THEPA PRELIMINARY; PRT; 659 AA.  
 AC Q4NOP8;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE CysteinyI-tRNA synthetase, putative (EC 6.1.1.16).  
 GN ORFNames=TP03\_0065;  
 OS Theileria parva.  
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;  
 OC Theileria.  
 NCBI\_TaxID=5875;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Muguga;  
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,  
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,  
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,  
 RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,  
 RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,  
 RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,  
 RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,  
 RA Venter J.C., Fraser C.M., Nene V.;  
 RA "Genome sequence of Theileria parva, a bovine pathogen that transforms  
 RT lymphocytes.";  
 RL Science 309:134-137(2005).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Muguga;  
 RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,  
 RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,  
 RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,  
 RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,  
 RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,  
 RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,  
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,  
 RA Fraser C.M., Nene V.;  
 RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC preliminary data.  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AAGK0100005; EAN30801.1; -; Genomic\_DNA.  
 DR Aminoacyl-tRNA synthetase; Ligase.  
 KW SEQUENCE 659 AA; 76376 MW; ED1782DF14157A93 CRC64;  
 SQ SEQUENCE 659 AA; 76376 MW; ED1782DF14157A93 CRC64;  
 Query Match 75.6%; Score 34; DB 2; Length 659;  
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
 :|||  
 Db 124 VLYNDLFFV 132

RESULT 36  
 KBTB6 HUMAN  
 ID KBTB6\_HUMAN STANDARD; PRT; 674 AA.  
 AC Q86V97; Q8N8L0; Q8NDM5; Q96MP6;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Kelch repeat and BTB domain containing protein 6.  
 GN Name=KBTBD6;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain;  
RX PubMed=14702039; DOI=10.1038/ngl1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakatani A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosori T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi K., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T.,  
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togai S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsuno K., Ichihara T., Shiohata N., Sano S.,  
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45 (2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain, and Prostate;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zengberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prance C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 21-674.  
RC TISSUE=Brain;  
RG The German cDNA consortium;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Contains 1 BTB (POZ) domain.  
CC -!- SIMILARITY: Contains 6 Kelch repeats.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; AK056633; BAB71238.1; -; mRNA.

DR EMBL; AK096608; BAC04826.1; ALT\_INIT; mRNA.  
DR EMBL; BC000560; AAH00560.1; -; mRNA.  
DR EMBL; BC051349; AAH51349.1; -; mRNA.  
DR EMBL; AL833839; CAD38699.1; -; mRNA.  
DR Ensembl; ENSG00000165572; Homo sapiens.  
DR HGNC; HGNC:25340; KRTBD6.  
DR InterPro; IPR011705; BACK.  
DR InterPro; IPR000210; BTB\_POZ.  
DR InterPro; IPR006652; Kelch\_rep.  
DR Pfam; PF07707; BACK; 1.  
DR Pfam; PF00651; BTB; 1.  
DR Pfam; PF01344; Kelch\_1; 1.  
DR PROSITE; PS0097; BTB; 1.  
KW Kelch repeat; Repeat.  
FT DOMAIN 63 138 BTB.  
FT REPEAT 386 435 Kelch 1.  
FT REPEAT 436 484 Kelch 2.  
FT REPEAT 486 523 Kelch 3.  
FT REPEAT 524 564 Kelch 4.  
FT REPEAT 567 616 Kelch 5.  
FT REPEAT 642 673 Kelch 6.  
FT CONFLICT 61 61 L -> Q (in Ref. 1; BAB71238).  
SQ SEQUENCE 674 AA; 76138 MW; 5ED49AAEC6350CB5 CRC64;  
Query Match 75.6%; Score 34; DB 1; Length 674;  
Best Local Similarity 66.7%; Pred. No. 6.3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLSYDLFVV 9  
DB 474 FLSFDLMVI 482  
RESULT 37  
QST6Y8 HUMAN  
ID QST6Y8 HUMAN PRELIMINARY; PRT; 674 AA.  
AC QST6Y8;  
DT 01-FEB-2005 (TREMBLrel. 29, Created)  
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)  
DE OTTHUMP00000018312.  
GN ORFNames=RP11-74J13.5-001;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Pearce A.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL354696; CA11611.1; -; Genomic DNA.  
DR GO; GO:0005515; F:protein binding; IEA.  
SQ SEQUENCE 674 AA; 76137 MW; 5ED49AAEC6350CB5 CRC64;  
Query Match 75.6%; Score 34; DB 2; Length 674;  
Best Local Similarity 66.7%; Pred. No. 6.3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLSYDLFVV 9  
DB 474 FLSFDLMVI 482  
RESULT 38  
Q4UCZ7 THEAN  
ID Q4UCZ7 THEAN PRELIMINARY; PRT; 694 AA.  
AC Q4UCZ7;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Cysteinyln-TRNA synthetase, putative (BC 6.1.1.16).  
GN ORFNames=TA03175;

```

OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
CN NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 3 genome sequence of Theileria annulata.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; CR940352; CAI75304.1; -; Genomic_DNA.
KW Aminoacyl-tRNA synthetase; Ligase.
SQ SEQUENCE 694 AA; 80840 MW; 449B7DD1C053AD9F CRC64;

Query Match 75.6%; Score 34; DB 2; Length 694;
Best Local Similarity 56.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFFV 9
DB 124 YLYNDLFFV 132

RESULT 39
Q91L83 WSSV
ID Q91L83_WSSV PRELIMINARY; PRT; 729 AA.
AC Q91L83;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF169.
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WSSV-TH;
EX MEDLINE=21342572; PubMed=11448154; DOI=10.1006/viro.2001.1002;
RA van Hulten M.C., Witteveldt J., Peters S., Kloosterboer N.,
RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.;
RT "The white spot syndrome virus DNA genome sequence.";
RL Virology 286:7-22(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WSSV-TH;
RX PubMed=15845251; DOI=10.1016/j.virusres.2005.01.002;
RA Marks H., van Duijse J.J., Zuidema D., van Hulten M.C., Vlak J.M.;
RT "Fitness and virulence of an ancestral White Spot Syndrome Virus isolate from shrimp.";
RL Virus Res. 110:9-20(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WSSV-TH;
RA Marks H., van Duijse J.J.A., Zuidema D., van Hulten M.C.W., Vlak J.M.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF369029; AAK77838.1; -; Genomic_DNA.
SQ SEQUENCE 729 AA; 85128 MW; 918166B756F02B3A CRC64;

Query Match 75.6%; Score 34; DB 2; Length 729;
Best Local Similarity 55.6%; Pred. No. 6.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFFV 9
DB 705 FLSYDTYVI 713

RESULT 40
ATG11 YARLI
ID ATG11_YARLI STANDARD; PRT; 924 AA.
AC Q6CFR0;
DT 13-SEP-2005 (Rel. 48, Created)

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DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Autophagy-related protein 11.
CN Name=ATG11; OrderedLocNames=YALI0B04598g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CLIB 122 / E 150;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrien P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Bianchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrons A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -!- FUNCTION: Involved in cytoplasm to vacuole transport (Cvt) and
CC peroxophagy (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-associated. Vacuolar and
CC perivacuolar punctate structures. Concentrated in a region of the
CC vacuolar membrane that contacts the peroxisome during the
CC engulfment process (By similarity).
CC -!- SIMILARITY: Belongs to the AFG11 family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; CR382128; CAG82729.1; -; Genomic DNA.
KW Autophagy; Coiled coil; Complete proteome; Membrane;
KW Protein transport; Transport; Vacuole.
FT COILED 552 682 Potential.
SQ SEQUENCE 924 AA; 104021 MW; C1E0853B5CB5AA03 CRC64;

Query Match 75.6%; Score 34; DB 1; Length 924;
Best Local Similarity 75.0%; Pred. No. 8.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
DB 786 FLDYDLYV 793

RESULT 41
Q4UEU7 THEAN
ID Q4UEU7_THEAN PRELIMINARY; PRT; 1111 AA.
AC Q4UEU7
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TA14030;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 2 sequence of Theileria annulata.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR940348; CAI74392.1; -; Genomic_DNA.
SQ SEQUENCE 1111 AA; 127939 MW; DBE881D0864A7001 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 1111;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9
DB 354 SYDLFVI 360
|||||:

RESULT 42
Q8IDC3_P1AF7 PRELIMINARY; PRT; 1559 AA.
AC Q8IDC3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Phat60.
GN Names=Phat60; Synonyms=MA113P1.286, PF13_0311, Phat61;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3D7;
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL844509; CAD52702.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1559 AA; 187166 MW; E7F2B3BB60E83B17 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 1559;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
DB 1080 FLSYSLFI 1087
|||||:

RESULT 43
Q55GM7_DICDI PRELIMINARY; PRT; 1807 AA.
AC Q55GM7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80189398;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugeng R., Berriman M., Song J., Olsen R., Szafarski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

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RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wandroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lousegod H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaolsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAF10100009; EAL73254.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1807 AA; 203825 MW; 1B9093AFC40AFC57 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 1807;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
DB 928 FVDYDLFTV 936
|: |||||

RESULT 44
Q51BD7_ENTHI PRELIMINARY; PRT; 2422 AA.
AC Q51BD7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=27.t00010;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=1579342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoest U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sacheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RL Nature 433:865-868(2005).
RT "The genome of the protist parasite Entamoeba histolytica.";
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAFB01000113; EAL50163.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 2422 AA; 282258 MW; B01CB610FAP55D17 CRC64;

Query Match 74.4%; Score 33.5; DB 2; Length 2422;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 FLSY---DLFVV 9
DB 1725 FLSYKXHDLFVV 1736
||||| |||||

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RESULT 45
NU3M_ARTSA
ID NU3M_ARTSA STANDARD; PRT; 70 AA.
AC P19043;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3) (NADH
dehydrogenase subunit 3) (Fragments).
GN Name=ND3;
OS Artemia salina (Brine shrimp).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae; Artemia.
OX NCBI_TaxID=85549;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88289417; PubMed=3135541;
RA Batuecas B., Garesse R., Calleja M., Valverde J.R., Marco R.;
RT "Genome organization of Artemia mitochondrial DNA.";
RL Nucleic Acids Res. 16:6515-6529(1988).
CC -|- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -|- SIMILARITY: Belongs to the complex I subunit 3 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
DR EMBL; X07664; CAA30511.1; -; Genomic DNA.
DR EMBL; X07665; CAA30512.1; -; Genomic DNA.
DR InterPro; IPR000440; Oxidored_g4.
DR PANTHER; PTHR11058; Oxidored_g4; 1.
DR Pfam; PF00507; Oxidored_g4; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_CONS 31 32
FT NON_TER 1 1
FT NON_TER 70 70
SQ SEQUENCE 70 AA; 8443 MW; C2D7A01B98AF62D0 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 70;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
Db 33 FLSYPLFI 40
|||||:|:|

RESULT 46
Q4Q8H5_LEIMA
ID Q4Q8H5_LEIMA PRELIMINARY; PRT; 189 AA.
AC Q4Q8H5;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF28.0920;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DDJ databases.
DR EMBL; CT005266; CAJ05216.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 189 AA; 22427 MW; 05E16B1E0DD1380E CRC64;
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Query Match 73.3%; Score 33; DB 2; Length 189;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
Db 41 FQSYDMFV 48
|||||:|:|

RESULT 47
Q45405_BACSU
ID Q45405_BACSU PRELIMINARY; PRT; 203 AA.
AC Q45405;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE SpAG.
GN Name=spaG;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC6633;
RX MEDLINE=93175869; PubMed=8439156;
RA Klein C., Kaletta C., Entian K.-D.;
RT "Biosynthesis of the lantibiotic subtilin is regulated by a histidine
kinase/response regulator system.";
RL Appl. Environ. Microbiol. 59:296-303(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC6633;
RA Klein C.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U09819; AAB91595.1; -; Genomic DNA.
DR PIR; I40517; I40517.
SQ SEQUENCE 203 AA; 22324 MW; F5045CAE34DCA347 CRC64;

Query Match 73.3%; Score 33; DB 2; Length 203;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFVV 9
Db 78 LSYDIFIM 85
|||||:|:|

RESULT 48
Q5UR23_MIMIV
ID Q5UR23_MIMIV PRELIMINARY; PRT; 262 AA.
AC Q5UR23;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MIMI_L361;
OS Mimivirus.
OC Viruses; dsDNA viruses, no RNA stage; Mimivirus.
OX NCBI_TaxID=212035;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX MEDLINE=22550848; PubMed=12663918; DOI=10.1126/science.1081867;
RA La Scola B., Audic S., Robert C., Jungang L., de Lamballerie X.,
RA Drancourt M., Birtles R., Claverie J.M., Raoult D.;
RT "A giant virus in amoebae.";
RL Science 299:2033-2033(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX PubMed=15486256; DOI=10.1126/science.1101485;
RA Raoult D., Audic S., Robert C., Abergel C., Renesto P., Ogata H.,
RA La Scola B., Susan M., Claverie J.M.;
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RT "The 1.2-Mb Genome Sequence of Mimivirus.";
RL Science 306:1344-1350(2004).
DR EMBL; AY653733; AAV50630.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 30953 MW; 151C1E2C6243A861 CRC64;

Query Match 73.3%; Score 33; DB 2; Length 262;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
|:|||||
Db 209 FTYTDLFV 216

RESULT 49
Q9CEL4 LACIA
ID Q9CEL4_LACIA PRELIMINARY; PRT; 305 AA.
AC Q9CEL4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Oxidoreductase.
GN Name=ysjB; OrderedLocusNames=LL1823;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=ILI403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr-1697R;
RA Bolotin A., Wincker P., Manger S., Jailion O., Malarne K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006412; AAK05921.1; -; Genomic_DNA.
DR PIR; G86852;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000683; GFO/IDH/MOCA_N.
DR Pfam; PF01408; GFO_IDH_MOCA; 1.
KW Complete proteome.
SQ SEQUENCE 305 AA; 34663 MW; 29E857F0D936FC0B CRC64;

Query Match 73.3%; Score 33; DB 2; Length 305;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
|||:|
Db 155 FLMYDIFI 162

RESULT 50
Q4Z603 PLABE
ID Q4Z603_PLABE PRELIMINARY; PRT; 310 AA.
AC Q4Z603;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB000481.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
[1]
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:25:44 ; Search time 25.2 Seconds  
(without alignments)  
29.527 Million cell updates/sec

Title: US-09-870-216C-9  
Perfect score: 45  
Sequence: 1 FLSYDLPV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	77.8	65	2	US-08-905-223-453
2	35	77.8	85	2	US-09-513-999C-5304
3	35	77.8	162	2	US-09-663-600A-126
4	35	77.8	162	2	US-09-663-600A-220
5	35	77.8	163	2	US-09-149-476-462
6	35	77.8	203	2	US-09-766-055A-4
7	35	77.8	231	2	US-09-270-767-38981
8	35	77.8	231	2	US-09-270-767-54198
9	35	77.8	382	2	US-09-248-796A-18423
10	34	75.6	108	2	US-09-270-767-45072
11	34	75.6	195	2	US-09-270-767-35680
12	34	75.6	195	2	US-09-270-767-50897
13	34	75.6	363	2	US-09-328-352-5693
14	33	73.3	103	2	US-09-543-681A-4764
15	33	73.3	370	1	US-08-837-593-7
16	33	73.3	593	2	US-09-248-796A-19856
17	31	68.9	132	2	US-09-270-767-36909
18	31	68.9	132	2	US-09-270-767-52126
19	31	68.9	158	2	US-09-583-110-3871
20	31	68.9	160	2	US-09-438-185A-79
21	31	68.9	170	2	US-09-107-433-3765
22	31	68.9	195	2	US-09-270-767-38485
23	31	68.9	195	2	US-09-270-767-53702
24	31	68.9	246	2	US-09-583-110-4242
25	31	68.9	249	2	US-09-107-433-4836
26	31	68.9	284	2	US-09-603-208A-188
27	31	68.9	335	2	US-09-248-796A-17099

28	31	68.9	344	2	US-09-107-532A-5546	Sequence 5546, Ap
29	31	68.9	346	2	US-09-248-796A-15456	Sequence 15456, A
30	31	68.9	349	2	US-09-328-352-7078	Sequence 7078, Ap
31	31	68.9	400	2	US-09-107-532A-6266	Sequence 6266, Ap
32	31	68.9	437	2	US-09-540-236-2207	Sequence 2207, Ap
33	31	68.9	451	2	US-09-184-964-3	Sequence 3, Appli
34	31	68.9	453	2	US-09-538-092-472	Sequence 472, App
35	31	68.9	472	2	US-09-486-192-3	Sequence 3, Appli
36	31	68.9	472	2	US-10-328-459A-3	Sequence 3, Appli
37	31	68.9	481	2	US-09-537-357-7	Sequence 7, Appli
38	31	68.9	487	2	US-09-537-357-15	Sequence 15, Appl
39	31	68.9	621	2	US-09-605-703B-1624	Sequence 1624, Ap
40	30	66.7	75	2	US-09-134-000C-5626	Sequence 5626, Ap
41	30	66.7	123	2	US-09-248-796A-24081	Sequence 24081, A
42	30	66.7	126	2	US-09-889-463A-6	Sequence 6, Appli
43	30	66.7	130	2	US-09-198-452A-528	Sequence 528, App
44	30	66.7	156	2	US-09-270-767-43152	Sequence 43152, A
45	30	66.7	215	2	US-09-248-796A-28019	Sequence 28019, A
46	30	66.7	324	2	US-09-198-452A-724	Sequence 724, App
47	30	66.7	328	2	US-09-438-185A-685	Sequence 685, App
48	30	66.7	333	2	US-09-230-637-30	Sequence 30, Appl
49	30	66.7	343	2	US-09-489-039A-10892	Sequence 10892, A
50	30	66.7	346	2	US-09-543-681A-6716	Sequence 6716, Ap
51	30	66.7	349	1	US-08-343-027A-12	Sequence 12, Appl
52	30	66.7	380	2	US-09-949-016-7909	Sequence 7909, Ap
53	30	66.7	402	2	US-09-107-532A-5454	Sequence 5454, Ap
54	30	66.7	420	2	US-09-252-991A-29911	Sequence 29911, A
55	30	66.7	440	2	US-09-328-352-7336	Sequence 7336, Ap
56	30	66.7	502	2	US-09-328-352-6968	Sequence 6968, Ap
57	30	66.7	555	2	US-09-252-991A-30276	Sequence 30276, A
58	30	66.7	565	2	US-09-252-991A-25040	Sequence 25040, A
59	30	66.7	580	2	US-09-328-352-7656	Sequence 7656, Ap
60	30	66.7	611	2	US-09-538-092-75	Sequence 75, Appl
61	30	66.7	748	2	US-09-543-681A-6676	Sequence 6676, Ap
62	30	66.7	960	2	US-09-345-650-1	Sequence 1, Appli
63	30	66.7	990	2	US-09-657-931A-11	Sequence 11, Appl
64	30	66.7	995	2	US-09-657-931A-1	Sequence 1, Appli
65	29	64.4	10	2	US-09-339-922A-52	Sequence 52, Appl
66	29	64.4	10	2	US-09-016-061-52	Sequence 52, Appl
67	29	64.4	48	1	US-08-849-480A-8	Sequence 8, Appli
68	29	64.4	66	2	US-09-248-796A-21750	Sequence 21750, A
69	29	64.4	73	2	US-09-248-796A-27344	Sequence 27344, A
70	29	64.4	74	2	US-09-252-991A-31965	Sequence 31965, A
71	29	64.4	123	2	US-09-674-741-16	Sequence 16, Appl
72	29	64.4	123	2	US-09-248-796A-27106	Sequence 27106, A
73	29	64.4	123	2	US-10-379-010-16	Sequence 16, Appl
74	29	64.4	154	2	US-09-954-987B-16	Sequence 16, Appl
75	29	64.4	156	2	US-09-673-395A-2868	Sequence 2868, App
76	29	64.4	177	2	US-09-270-767-38440	Sequence 38440, A
77	29	64.4	177	2	US-09-270-767-53657	Sequence 53657, A
78	29	64.4	181	2	US-09-134-000C-3561	Sequence 3561, Ap
79	29	64.4	219	2	US-09-543-681A-5930	Sequence 5930, Ap
80	29	64.4	222	2	US-09-134-001C-4748	Sequence 4748, Ap
81	29	64.4	228	2	US-08-896-933-25	Sequence 25, Appl
82	29	64.4	228	2	US-09-314-235-25	Sequence 25, Appl
83	29	64.4	228	2	US-09-708-008B-25	Sequence 25, Appl
84	29	64.4	245	2	US-09-248-796A-17929	Sequence 17929, A
85	29	64.4	273	2	US-09-134-001C-3474	Sequence 3474, Ap
86	29	64.4	286	2	US-09-949-016-6939	Sequence 6939, Ap
87	29	64.4	287	2	US-09-270-767-37165	Sequence 37165, A
88	29	64.4	287	2	US-09-270-767-52382	Sequence 52382, A
89	29	64.4	289	2	US-09-949-016-11194	Sequence 11194, A
90	29	64.4	303	2	US-09-674-741-8	Sequence 8, Appli
91	29	64.4	303	2	US-10-379-010-8	Sequence 8, Appli
92	29	64.4	306	2	US-09-107-532A-6274	Sequence 6274, Ap
93	29	64.4	310	2	US-10-151-832-3	Sequence 3, Appli
94	29	64.4	314	2	US-09-107-532A-7287	Sequence 7287, Ap
95	29	64.4	321	2	US-09-134-000C-4439	Sequence 4439, Ap
96	29	64.4	330	2	US-09-489-039A-7373	Sequence 7373, Ap
97	29	64.4	363	2	US-09-270-767-44161	Sequence 44161, A
98	29	64.4	387	1	US-08-484-575A-7	Sequence 7, Appli
99	29	64.4	387	2	US-08-477-459-7	Sequence 7, Appli
100	29	64.4	387	2	US-08-479-869-7	Sequence 7, Appli

101	29	64.4	387	2	US-08-486-414-7	Sequence 7, Appli	174	29	64.4	1239	1	US-08-026-138E-3	Sequence 3, Appli
102	29	64.4	387	4	PCT-US94-01826A-7	Sequence 7, Appli	175	29	64.4	1239	1	US-08-231-193A-52	Sequence 52, Appl
103	29	64.4	387	4	PCT-US94-02252A-7	Sequence 7, Appli	176	29	64.4	1239	1	US-08-480-273A-52	Sequence 52, Appl
104	29	64.4	427	2	US-09-328-352-5205	Sequence 5205, Ap	177	29	64.4	1239	2	US-08-480-474-52	Sequence 52, Appl
105	29	64.4	438	2	US-09-583-110-3288	Sequence 3288, Ap	178	29	64.4	1239	2	US-08-940-086A-52	Sequence 52, Appl
106	29	64.4	485	2	US-09-540-236-2761	Sequence 2761, Ap	179	29	64.4	1239	2	US-08-940-035A-52	Sequence 52, Appl
107	29	64.4	547	2	US-09-489-039A-8381	Sequence 8381, Ap	180	29	64.4	1239	2	US-08-935-105A-52	Sequence 52, Appl
108	29	64.4	568	2	US-09-489-039A-7990	Sequence 7990, Ap	181	29	64.4	1239	2	US-09-648-797-52	Sequence 52, Appl
109	29	64.4	568	2	US-09-437-568A-4	Sequence 4, Appli	182	29	64.4	1239	2	US-09-386-123-52	Sequence 52, Appl
110	29	64.4	568	2	US-10-418-036-6	Sequence 6, Appli	183	29	64.4	1239	2	US-10-038-937-52	Sequence 52, Appl
111	29	64.4	595	2	US-08-264-578-8	Sequence 8, Appli	184	29	64.4	1239	2	US-10-007-747-52	Sequence 52, Appl
112	29	64.4	660	2	US-09-583-110-4478	Sequence 4478, Ap	185	29	64.4	1239	2	US-09-945-901-52	Sequence 46, Appl
113	29	64.4	664	2	US-09-107-433-3490	Sequence 3490, Ap	186	29	64.4	1244	1	US-08-231-193A-46	Sequence 46, Appl
114	29	64.4	774	1	US-08-231-193A-42	Sequence 42, Appl	187	29	64.4	1244	2	US-08-486-273A-46	Sequence 46, Appl
115	29	64.4	774	2	US-08-486-273A-42	Sequence 42, Appl	188	29	64.4	1244	2	US-08-480-474-46	Sequence 46, Appl
116	29	64.4	774	2	US-08-480-474-42	Sequence 42, Appl	189	29	64.4	1244	2	US-08-940-086A-46	Sequence 46, Appl
117	29	64.4	774	2	US-08-940-086A-42	Sequence 42, Appl	190	29	64.4	1244	2	US-08-940-035A-46	Sequence 46, Appl
118	29	64.4	774	2	US-08-940-035A-42	Sequence 42, Appl	191	29	64.4	1244	2	US-08-935-105A-46	Sequence 46, Appl
119	29	64.4	774	2	US-08-935-105A-42	Sequence 42, Appl	192	29	64.4	1244	2	US-09-648-797-46	Sequence 46, Appl
120	29	64.4	774	2	US-09-648-797-42	Sequence 42, Appl	193	29	64.4	1244	2	US-09-386-123-46	Sequence 46, Appl
121	29	64.4	774	2	US-09-386-123-42	Sequence 42, Appl	194	29	64.4	1244	2	US-10-038-937-46	Sequence 46, Appl
122	29	64.4	774	2	US-10-038-937-42	Sequence 42, Appl	195	29	64.4	1244	2	US-10-007-747-46	Sequence 46, Appl
123	29	64.4	774	2	US-10-007-747-42	Sequence 42, Appl	196	29	64.4	1244	2	US-09-945-901-46	Sequence 46, Appl
124	29	64.4	774	2	US-09-945-901-42	Sequence 42, Appl	197	29	64.4	1336	1	US-08-026-138E-4	Sequence 4, Appli
125	29	64.4	836	2	US-09-491-356C-21	Sequence 21, Appl	198	29	64.4	1336	1	US-08-231-193A-58	Sequence 58, Appl
126	29	64.4	1032	2	US-09-954-987B-3	Sequence 3, Appli	199	29	64.4	1336	2	US-08-486-273A-58	Sequence 58, Appl
127	29	64.4	1032	2	US-09-954-987B-6	Sequence 6, Appli	200	29	64.4	1336	2	US-08-940-086A-58	Sequence 58, Appl
128	29	64.4	1171	2	US-09-949-016-9738	Sequence 9738, Ap	201	29	64.4	1336	2	US-08-940-035A-58	Sequence 58, Appl
129	29	64.4	1190	2	US-09-107-532A-7146	Sequence 7146, Ap	202	29	64.4	1336	2	US-08-935-105A-58	Sequence 58, Appl
130	29	64.4	1214	1	US-08-231-193A-54	Sequence 54, Appl	203	29	64.4	1336	2	US-09-648-797-58	Sequence 58, Appl
131	29	64.4	1214	2	US-08-486-273A-54	Sequence 54, Appl	204	29	64.4	1336	2	US-09-386-123-58	Sequence 58, Appl
132	29	64.4	1214	2	US-08-480-474-54	Sequence 54, Appl	205	29	64.4	1336	2	US-10-038-937-58	Sequence 58, Appl
133	29	64.4	1214	2	US-08-940-086A-54	Sequence 54, Appl	206	29	64.4	1336	2	US-10-007-747-58	Sequence 58, Appl
134	29	64.4	1214	2	US-08-940-035A-54	Sequence 54, Appl	207	29	64.4	1336	2	US-09-945-901-58	Sequence 58, Appl
135	29	64.4	1214	2	US-08-935-105A-54	Sequence 54, Appl	208	29	64.4	1345	2	US-09-949-016-11209	Sequence 11209, A
136	29	64.4	1214	2	US-09-648-797-54	Sequence 54, Appl	209	29	64.4	1509	2	US-09-410-551B-23	Sequence 23, Appl
137	29	64.4	1214	2	US-09-386-123-54	Sequence 54, Appl	210	29	64.4	1509	2	US-09-940-316B-23	Sequence 23, Appl
138	29	64.4	1214	2	US-10-038-937-54	Sequence 54, Appl	211	29	64.4	1517	2	US-09-410-551B-19	Sequence 19, Appl
139	29	64.4	1214	2	US-10-007-747-54	Sequence 54, Appl	212	29	64.4	1517	2	US-09-940-316B-19	Sequence 19, Appl
140	29	64.4	1214	2	US-09-945-901-54	Sequence 54, Appl	213	29	64.4	1588	2	US-09-410-551B-29	Sequence 29, Appl
141	29	64.4	1219	1	US-08-231-193A-50	Sequence 50, Appl	214	29	64.4	1588	2	US-09-940-316B-29	Sequence 29, Appl
142	29	64.4	1219	1	US-08-486-273A-50	Sequence 50, Appl	215	29	64.4	1605	2	US-09-410-551B-33	Sequence 33, Appl
143	29	64.4	1219	2	US-08-480-474-50	Sequence 50, Appl	216	29	64.4	1605	2	US-09-940-316B-33	Sequence 33, Appl
144	29	64.4	1219	2	US-08-940-086A-50	Sequence 50, Appl	217	29	64.4	1724	2	US-08-857-076-12	Sequence 12, Appl
145	29	64.4	1219	2	US-08-940-035A-50	Sequence 50, Appl	218	29	64.4	1724	2	US-09-205-658-12	Sequence 12, Appl
146	29	64.4	1219	2	US-08-935-105A-50	Sequence 50, Appl	219	29	64.4	1820	2	US-07-998-289B-8	Sequence 8, Appli
147	29	64.4	1219	2	US-09-648-797-50	Sequence 50, Appl	220	29	64.4	2100	1	US-08-808-793-23	Sequence 23, Appl
148	29	64.4	1219	2	US-09-386-123-50	Sequence 50, Appl	221	29	64.4	2100	2	US-08-772-512A-19	Sequence 19, Appl
149	29	64.4	1219	2	US-10-038-937-50	Sequence 50, Appl	222	29	64.4	2100	2	US-09-428-371-19	Sequence 19, Appl
150	29	64.4	1219	2	US-10-007-747-50	Sequence 50, Appl	223	29	64.4	2104	1	US-08-808-793-4	Sequence 4, Appli
151	29	64.4	1219	2	US-09-945-901-50	Sequence 50, Appl	224	29	64.4	2104	2	US-08-772-512A-4	Sequence 4, Appli
152	29	64.4	1231	1	US-08-231-193A-48	Sequence 48, Appl	225	29	64.4	2104	2	US-09-428-371-4	Sequence 4, Appli
153	29	64.4	1231	1	US-08-486-273A-48	Sequence 48, Appl	226	29	64.4	2105	1	US-08-808-793-3	Sequence 3, Appli
154	29	64.4	1231	2	US-08-480-474-48	Sequence 48, Appl	227	29	64.4	2105	2	US-08-772-512A-3	Sequence 3, Appli
155	29	64.4	1231	2	US-08-940-086A-48	Sequence 48, Appl	228	29	64.4	2105	2	US-09-428-371-3	Sequence 7, Appli
156	29	64.4	1231	2	US-08-940-035A-48	Sequence 48, Appl	229	28	62.2	28	2	US-08-379-580-7	Sequence 73, Appl
157	29	64.4	1231	2	US-08-935-105A-48	Sequence 48, Appl	230	28	62.2	39	2	US-08-630-915A-73	Sequence 73, Appl
158	29	64.4	1231	2	US-09-648-797-48	Sequence 48, Appl	231	28	62.2	39	2	US-09-879-957-73	Sequence 73, Appl
159	29	64.4	1231	2	US-09-386-123-48	Sequence 48, Appl	232	28	62.2	45	2	US-09-270-767-57856	Sequence 57856, A
160	29	64.4	1231	2	US-10-038-937-48	Sequence 48, Appl	233	28	62.2	52	1	US-08-459-568-55	Sequence 55, Appl
161	29	64.4	1231	2	US-10-007-747-48	Sequence 48, Appl	234	28	62.2	52	1	US-08-399-411-55	Sequence 55, Appl
162	29	64.4	1231	2	US-09-945-901-48	Sequence 48, Appl	235	28	62.2	52	2	US-08-516-859A-55	Sequence 55, Appl
163	29	64.4	1236	1	US-08-231-193A-6	Sequence 6, Appli	236	28	62.2	52	2	US-09-586-472-55	Sequence 55, Appl
164	29	64.4	1236	1	US-08-486-273A-6	Sequence 6, Appli	237	28	62.2	52	2	US-09-528-706-55	Sequence 55, Appl
165	29	64.4	1236	2	US-08-480-474-6	Sequence 6, Appli	238	28	62.2	53	2	US-08-379-580-9	Sequence 9, Appli
166	29	64.4	1236	2	US-08-940-086A-6	Sequence 6, Appli	239	28	62.2	56	1	US-08-167-035-30	Sequence 30, Appl
167	29	64.4	1236	2	US-08-940-035A-6	Sequence 6, Appli	240	28	62.2	56	1	US-08-208-887A-30	Sequence 30, Appl
168	29	64.4	1236	2	US-08-935-105A-6	Sequence 6, Appli	241	28	62.2	56	2	US-08-539-005-30	Sequence 30, Appl
169	29	64.4	1236	2	US-09-648-797-6	Sequence 6, Appli	242	28	62.2	56	2	US-09-280-598-32	Sequence 32, Appl
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171	29	64.4	1236	2	US-10-038-937-6	Sequence 6, Appli	244	28	62.2	67	2	US-09-205-258-808	Sequence 808, App
172	29	64.4	1236	2	US-10-007-747-6	Sequence 6, Appli	245	28	62.2	67	2	US-10-004-860-808	Sequence 2, Appli
173	29	64.4	1236	2	US-09-945-901-6	Sequence 6, Appli	246	28	62.2	78	2	US-08-379-580-2	

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249	28	62.2	83	2	US-09-270-767-58915	Sequence 58915, A	322	28	62.2	329	2	US-09-107-532A-4431	Sequence 4431, Ap
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251	28	62.2	97	2	US-09-248-796A-21686	Sequence 21686, A	324	28	62.2	336	1	US-07-704-288C-3	Sequence 3, Appli
252	28	62.2	103	2	US-09-134-001C-2861	Sequence 2861, A	325	28	62.2	336	1	US-08-093-372-2	Sequence 2, Appli
253	28	62.2	107	2	US-08-858-207A-461	Sequence 461, App	326	28	62.2	336	1	US-08-379-259-3	Sequence 3, Appli
254	28	62.2	119	2	US-09-134-000C-4289	Sequence 4289, Ap	327	28	62.2	358	2	US-09-270-767-11449	Sequence 41449, A
255	28	62.2	115	2	US-09-248-796A-21686	Sequence 21686, A	328	28	62.2	367	2	US-09-583-110-3544	Sequence 3544, Ap
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258	28	62.2	145	2	US-09-270-767-39242	Sequence 39242, A	331	28	62.2	382	2	US-09-540-236-3736	Sequence 3736, Ap
259	28	62.2	145	2	US-09-270-767-54559	Sequence 54559, A	332	28	62.2	388	2	US-10-104-047-2353	Sequence 2353, Ap
260	28	62.2	147	2	US-09-583-110-2856	Sequence 2856, Ap	333	28	62.2	389	2	US-09-134-000C-3706	Sequence 3706, Ap
261	28	62.2	167	2	US-09-248-796A-24968	Sequence 24968, A	334	28	62.2	396	2	US-09-902-540-15559	Sequence 15559, A
262	28	62.2	167	2	US-09-710-279-1176	Sequence 1176, Ap	335	28	62.2	397	2	US-09-710-279-1244	Sequence 1244, Ap
263	28	62.2	178	2	US-09-107-532A-7297	Sequence 7297, Ap	336	28	62.2	400	2	US-10-300-819B-2	Sequence 2, Appli
264	28	62.2	181	2	US-09-328-352-6761	Sequence 6761, Ap	337	28	62.2	404	2	US-09-491-577-80	Sequence 80, Appli
265	28	62.2	191	2	US-09-540-236-3680	Sequence 3680, Ap	338	28	62.2	407	2	US-09-769-787-14	Sequence 14, Appli
266	28	62.2	201	2	US-09-248-796A-16101	Sequence 16101, A	339	28	62.2	412	2	US-09-489-039A-8180	Sequence 8180, Ap
267	28	62.2	202	2	US-08-896-933-24	Sequence 9852, Ap	340	28	62.2	431	2	US-09-252-991A-23720	Sequence 23720, A
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271	28	62.2	224	1	US-08-924-759-22	Sequence 22, Appli	344	28	62.2	446	2	US-09-382-218A-19	Sequence 19, Appli
272	28	62.2	234	2	US-09-248-796A-16101	Sequence 22, Appli	345	28	62.2	453	2	US-09-583-110-3842	Sequence 3842, Ap
273	28	62.2	224	2	US-09-489-039A-9852	Sequence 9852, Ap	346	28	62.2	459	2	US-09-134-001C-5466	Sequence 5466, Ap
274	28	62.2	226	2	US-08-896-933-24	Sequence 24, Appli	347	28	62.2	461	2	US-09-107-433-3722	Sequence 3722, Ap
275	28	62.2	226	2	US-09-314-235-24	Sequence 24, Appli	348	28	62.2	470	2	US-09-270-767-57120	Sequence 57120, A
276	28	62.2	233	2	US-09-708-008B-24	Sequence 24, Appli	349	28	62.2	474	2	US-09-134-001C-4657	Sequence 4657, Ap
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279	28	62.2	239	2	US-09-216-295-6	Sequence 6, Appli	352	28	62.2	506	2	US-09-328-352-6467	Sequence 4, Appli
280	28	62.2	239	2	US-09-632-570-6	Sequence 36, Appli	353	28	62.2	518	2	US-08-379-580-4	Sequence 4, Appli
281	28	62.2	239	2	US-09-332-575-36	Sequence 36, Appli	354	28	62.2	527	2	US-09-248-796A-14631	Sequence 14631, A
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284	28	62.2	255	2	US-09-667-373-2	Sequence 2, Appli	357	28	62.2	570	2	US-09-999-248A-13	Sequence 13, Appli
285	28	62.2	255	2	US-10-305-413-2	Sequence 2, Appli	358	28	62.2	570	2	US-09-437-568A-38	Sequence 38, Appli
286	28	62.2	257	2	US-08-486-099-112	Sequence 112, App	359	28	62.2	570	2	US-10-418-036-2	Sequence 2, Appli
287	28	62.2	257	2	US-08-360-107A-122	Sequence 122, App	360	28	62.2	577	2	US-09-248-796A-20164	Sequence 20164, A
288	28	62.2	257	2	US-08-484-223B-112	Sequence 112, App	361	28	62.2	583	2	US-09-248-796A-20244	Sequence 20244, A
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290	28	62.2	257	2	US-08-475-668A-112	Sequence 112, App	363	28	62.2	609	2	US-09-107-532A-5110	Sequence 5110, Ap
291	28	62.2	257	2	US-08-485-551A-112	Sequence 112, App	364	28	62.2	625	2	US-09-252-991A-26336	Sequence 26336, A
292	28	62.2	257	2	US-08-471-913A-112	Sequence 112, App	365	28	62.2	625	2	US-09-489-039A-12750	Sequence 12750, A
293	28	62.2	257	2	US-08-485-264A-112	Sequence 112, App	366	28	62.2	648	2	US-08-800-291B-8	Sequence 8, Appli
294	28	62.2	257	2	US-08-474-349A-112	Sequence 112, App	367	28	62.2	670	2	US-09-248-796A-17669	Sequence 17669, A
295	28	62.2	257	2	US-08-470-896-112	Sequence 112, App	368	28	62.2	750	2	US-09-902-540-11016	Sequence 11016, A
296	28	62.2	257	2	US-08-485-546A-112	Sequence 112, App	369	28	62.2	790	2	US-09-487-558B-228	Sequence 228, App
297	28	62.2	257	2	US-08-487-266A-112	Sequence 112, App	370	28	62.2	863	2	US-09-619-353-14	Sequence 14, Appli
298	28	62.2	257	2	US-08-484-741-112	Sequence 112, App	371	28	62.2	870	1	US-08-190-687B-25	Sequence 25, Appli
299	28	62.2	263	2	US-09-252-991A-27515	Sequence 27515, A	372	28	62.2	870	4	PCT-US94-00198-5	Sequence 5, Appli
300	28	62.2	264	2	US-09-270-767-33073	Sequence 33073, A	373	28	62.2	874	2	US-09-369-364A-15	Sequence 15, Appli
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302	28	62.2	266	2	US-08-612-025-10	Sequence 10, Appli	375	28	62.2	883	2	US-09-667-373-4	Sequence 4, Appli
303	28	62.2	266	2	US-07-791-931-10	Sequence 10, Appli	376	28	62.2	885	2	US-10-305-413-4	Sequence 4, Appli
304	28	62.2	266	2	US-09-138-873A-10	Sequence 10, Appli	377	28	62.2	895	2	US-09-489-039A-13127	Sequence 13127, A
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307	28	62.2	282	2	US-09-270-767-50952	Sequence 50952, A	380	28	62.2	997	2	US-09-369-364A-7	Sequence 7, Appli
308	28	62.2	282	2	US-09-248-796A-22260	Sequence 22260, A	381	28	62.2	1047	1	US-08-190-687B-8	Sequence 8, Appli
309	28	62.2	284	2	US-09-443-067-6	Sequence 6, Appli	382	28	62.2	1297	2	US-09-540-245A-17	Sequence 17, Appli
310	28	62.2	301	2	US-09-443-067-8	Sequence 8, Appli	383	28	62.2	1297	2	US-10-289-776-17	Sequence 17, Appli
311	28	62.2	301	2	US-09-540-236-2519	Sequence 2519, Ap	384	28	62.2	1358	1	US-08-404-665-4	Sequence 4, Appli
312	28	62.2	311	1	US-08-794-216-1	Sequence 1, Appli	385	28	62.2	1358	1	US-08-404-671-4	Sequence 4, Appli
313	28	62.2	312	2	US-09-107-532A-5438	Sequence 5438, Ap	386	28	62.2	1358	1	US-08-404-781-4	Sequence 4, Appli
314	28	62.2	315	2	US-09-248-796A-20438	Sequence 20438, A	387	28	62.2	1358	2	US-09-949-002-353	Sequence 353, App
315	28	62.2	318	2	US-09-134-001C-4689	Sequence 4689, Ap	388	28	62.2	1379	2	US-09-270-767-41876	Sequence 41876, A
316	28	62.2	318	2	US-09-710-279-3118	Sequence 3118, Ap	389	28	62.2	1385	2	US-09-949-002-431	Sequence 431, App
317	28	62.2	320	2	US-09-520-781-81	Sequence 81, Appli	390	28	62.2	1627	2	US-09-540-236-3533	Sequence 3533, Ap
318	28	62.2	320	2	US-09-957-187-81	Sequence 81, Appli	391	28	62.2	1882	2	US-09-369-364A-13	Sequence 13, Appli
319	28	62.2	322	2	US-09-991-053-81	Sequence 81, Appli	392	28	62.2	2004	1	US-08-375-709-15	Sequence 15, Appli
					Sequence 4064, Ap								

393	28	62.2	2004	1	US-08-752-929-15	Sequence 15, Appl	466	27	60.0	254	1	US-08-047-413-9	Sequence 9, Appl
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395	28	62.2	2004	2	US-09-231-899-9	Sequence 9, Appl	468	27	60.0	254	2	US-08-801-563-9	Sequence 9, Appl
396	28	62.2	3289	1	US-08-477-451-2	Sequence 2, Appl	469	27	60.0	255	2	US-08-311-731A-141	Sequence 141, Appl
397	27	60.0	10	2	US-09-341-982-35	Sequence 35, Appl	470	27	60.0	256	2	US-09-534-229C-1	Sequence 1, Appl
398	27	60.0	11	2	US-09-341-982-56	Sequence 56, Appl	471	27	60.0	259	2	US-09-522-714-18	Sequence 18, Appl
399	27	60.0	30	2	US-09-890-821-11	Sequence 11, Appl	472	27	60.0	260	2	US-09-328-352-7647	Sequence 7647, Ap
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404	27	60.0	62	2	US-09-248-796A-27176	Sequence 27176, A	477	27	60.0	278	2	US-09-107-532A-5114	Sequence 5114, Ap
405	27	60.0	64	2	US-09-270-767-39098	Sequence 39098, A	478	27	60.0	281	2	US-09-949-016-8447	Sequence 8447, Ap
406	27	60.0	64	2	US-09-270-767-54315	Sequence 54315, A	479	27	60.0	282	2	US-08-911-853-37	Sequence 37, Appl
407	27	60.0	65	2	US-09-268-364-6	Sequence 6, Appl	480	27	60.0	282	2	US-09-479-409-37	Sequence 37, Appl
408	27	60.0	66	2	US-09-134-000C-5777	Sequence 5777, Ap	481	27	60.0	282	2	US-09-479-453-37	Sequence 37, Appl
409	27	60.0	69	2	US-09-270-767-62365	Sequence 62365, A	482	27	60.0	282	2	US-09-543-681A-8275	Sequence 8275, Ap
410	27	60.0	76	1	US-08-117-952-757	Sequence 757, App	483	27	60.0	284	2	US-09-328-352-6033	Sequence 6033, Ap
411	27	60.0	76	1	US-09-107-532A-6844	Sequence 6844, Ap	484	27	60.0	290	2	US-09-248-796A-19488	Sequence 19488, A
412	27	60.0	83	2	US-09-134-001C-4548	Sequence 4548, Ap	485	27	60.0	292	2	US-09-543-681A-5549	Sequence 5549, Ap
413	27	60.0	98	2	US-09-248-796A-25502	Sequence 25502, A	486	27	60.0	296	2	US-09-710-279-1674	Sequence 1674, Ap
414	27	60.0	105	2	US-09-270-767-60054	Sequence 60054, A	487	27	60.0	301	2	US-09-134-001C-2220	Sequence 2220, Ap
415	27	60.0	105	2	US-09-270-767-62342	Sequence 62342, A	488	27	60.0	304	2	US-09-248-796A-21762	Sequence 21762, A
416	27	60.0	108	2	US-09-830-230A-182	Sequence 182, App	489	27	60.0	308	2	US-09-583-110-2950	Sequence 2950, Ap
417	27	60.0	118	2	US-09-732-210-1209	Sequence 1209, Ap	490	27	60.0	308	2	US-09-583-110-2953	Sequence 2953, Ap
418	27	60.0	123	2	US-09-489-039A-12668	Sequence 12668, A	491	27	60.0	313	2	US-09-107-433-3357	Sequence 3357, Ap
419	27	60.0	128	2	US-09-270-767-44607	Sequence 44607, A	492	27	60.0	315	1	US-08-910-927B-3	Sequence 3, Appl
420	27	60.0	128	2	US-09-270-767-46724	Sequence 46724, A	493	27	60.0	315	2	US-09-270-270-3	Sequence 3, Appl
421	27	60.0	129	2	US-09-830-230A-181	Sequence 181, App	494	27	60.0	315	2	US-10-164-595-12	Sequence 12, Appl
422	27	60.0	131	2	US-09-710-279-52	Sequence 52, Appl	495	27	60.0	315	2	US-10-164-595-61	Sequence 61, Appl
423	27	60.0	131	2	US-09-710-279-738	Sequence 738, App	496	27	60.0	318	1	US-07-704-288C-9	Sequence 9, Appl
424	27	60.0	138	2	US-09-270-767-46763	Sequence 46763, A	497	27	60.0	318	1	US-08-379-259-9	Sequence 9, Appl
425	27	60.0	143	2	US-09-270-767-45159	Sequence 45159, A	498	27	60.0	325	2	US-09-540-236-2444	Sequence 2444, Ap
426	27	60.0	147	2	US-09-134-001C-4542	Sequence 4542, Ap	499	27	60.0	328	2	US-07-791-931-7	Sequence 7, Appl
427	27	60.0	147	2	US-09-270-767-35818	Sequence 35818, A	500	27	60.0	331	2	US-09-107-433-2623	Sequence 2623, Ap
428	27	60.0	147	2	US-09-270-767-51035	Sequence 51035, A	501	27	60.0	332	2	US-09-437-568A-23	Sequence 23, Appl
429	27	60.0	149	1	US-08-612-840A-8	Sequence 8, Appl	502	27	60.0	338	2	US-09-841-786-7	Sequence 7, Appl
430	27	60.0	149	2	US-09-969-763-3	Sequence 3, Appl	503	27	60.0	338	2	US-10-324-316-18	Sequence 18, Appl
431	27	60.0	150	2	US-09-270-767-39067	Sequence 39067, A	504	27	60.0	340	2	US-09-489-039A-10379	Sequence 10379, A
432	27	60.0	150	2	US-09-270-767-54284	Sequence 54284, A	505	27	60.0	341	2	US-09-328-352-7178	Sequence 7178, Ap
433	27	60.0	163	2	US-09-328-352-7212	Sequence 7212, Ap	506	27	60.0	341	2	US-09-543-681A-4755	Sequence 4755, Ap
434	27	60.0	168	2	US-09-583-110-2842	Sequence 2842, Ap	507	27	60.0	345	2	US-09-543-681A-4410	Sequence 4410, Ap
435	27	60.0	169	2	US-09-270-767-35239	Sequence 35239, A	508	27	60.0	345	2	US-10-155-947-4	Sequence 4, Appl
436	27	60.0	169	2	US-09-270-767-50456	Sequence 50456, A	509	27	60.0	348	2	US-09-198-452A-922	Sequence 922, App
437	27	60.0	179	2	US-09-270-767-35148	Sequence 35148, A	510	27	60.0	348	2	US-09-438-185A-856	Sequence 856, App
438	27	60.0	179	2	US-09-270-767-50365	Sequence 50365, A	511	27	60.0	348	2	US-09-692-570-20	Sequence 20, Appl
439	27	60.0	181	2	US-09-134-000C-4266	Sequence 4266, Ap	512	27	60.0	351	2	US-09-270-767-39825	Sequence 39825, A
440	27	60.0	192	1	US-08-408-120-22	Sequence 22, Appl	513	27	60.0	351	2	US-09-270-767-55042	Sequence 55042, A
441	27	60.0	194	2	US-09-248-796A-20920	Sequence 20920, A	515	27	60.0	357	2	US-09-491-577-86	Sequence 86, Appl
442	27	60.0	196	2	US-09-270-767-36727	Sequence 36727, A	515	27	60.0	357	2	US-09-692-570-9	Sequence 9, Appl
443	27	60.0	204	2	US-09-248-796A-23484	Sequence 23484, A	516	27	60.0	358	2	US-09-692-570-19	Sequence 19, Appl
444	27	60.0	211	2	US-10-090-365-36	Sequence 36, Appl	517	27	60.0	363	2	US-09-692-570-17	Sequence 17, Appl
445	27	60.0	211	2	US-09-728-911-36	Sequence 36, Appl	518	27	60.0	366	2	US-09-270-767-44498	Sequence 44498, A
446	27	60.0	223	2	US-09-134-000C-4761	Sequence 4761, Ap	519	27	60.0	366	2	US-09-328-352-6796	Sequence 6796, Ap
447	27	60.0	223	2	US-09-107-433-3592	Sequence 3592, Ap	520	27	60.0	367	2	US-09-134-000C-6173	Sequence 6173, Ap
448	27	60.0	226	2	US-09-270-767-40552	Sequence 40552, A	521	27	60.0	374	2	US-09-692-570-18	Sequence 18, Appl
449	27	60.0	234	2	US-09-134-000C-8200	Sequence 8200, Ap	522	27	60.0	375	2	US-09-134-000C-4981	Sequence 4981, Ap
450	27	60.0	236	2	US-09-270-767-41232	Sequence 41232, A	523	27	60.0	378	2	US-09-107-532A-4742	Sequence 4742, Ap
451	27	60.0	236	2	US-09-270-767-56448	Sequence 56448, A	524	27	60.0	381	2	US-09-107-433-3123	Sequence 3123, Ap
452	27	60.0	239	2	US-09-532-856-10	Sequence 10, Appl	525	27	60.0	382	2	US-09-543-681A-4239	Sequence 4239, Ap
453	27	60.0	239	2	US-09-524-100C-10	Sequence 10, Appl	526	27	60.0	388	2	US-09-222-938A-37	Sequence 37, Appl
454	27	60.0	239	2	US-10-212-507-10	Sequence 10, Appl	527	27	60.0	388	2	US-09-949-016-7122	Sequence 7122, Ap
455	27	60.0	241	2	US-09-890-821-1	Sequence 1, Appl	528	27	60.0	393	2	US-09-692-570-16	Sequence 16, Appl
456	27	60.0	241	2	US-09-248-796A-17889	Sequence 17889, A	529	27	60.0	397	2	US-09-583-110-2946	Sequence 2946, Ap
457	27	60.0	244	2	US-09-949-016-7557	Sequence 7557, Ap	530	27	60.0	400	2	US-09-583-110-5080	Sequence 5080, Ap
458	27	60.0	247	2	US-09-134-000C-6348	Sequence 6348, Ap	531	27	60.0	404	2	US-09-107-433-3747	Sequence 3747, Ap
459	27	60.0	250	1	US-08-162-475A-4	Sequence 4, Appl	532	27	60.0	424	1	US-08-484-993B-18	Sequence 18, Appl
460	27	60.0	252	2	US-09-522-714-20	Sequence 20, Appl	533	27	60.0	424	1	US-08-484-158B-18	Sequence 18, Appl
461	27	60.0	253	1	US-08-162-475A-2	Sequence 2, Appl	534	27	60.0	424	1	US-08-484-596A-18	Sequence 18, Appl
462	27	60.0	253	1	US-08-162-475A-5	Sequence 5, Appl	535	27	60.0	424	1	US-08-480-150A-18	Sequence 18, Appl
463	27	60.0	253	2	US-07-791-931-9	Sequence 9, Appl	536	27	60.0	424	2	US-08-458-731-18	Sequence 18, Appl
464	27	60.0	253	2	US-10-030-808-4	Sequence 4, Appl	537	27	60.0	424	2	US-08-149-223A-18	Sequence 18, Appl
465	27	60.0	253	2	US-10-300-819B-18	Sequence 18, Appl	538	27	60.0	424	2	US-09-710-279-2756	Sequence 2756, Ap



539	27	60.0	438	2	US-09-134-001C-3634	Sequence 3634, Ap	612	27	60.0	633	2	US-09-328-352-6163	Sequence 6163, Ap
540	27	60.0	439	2	US-09-902-540-11372	Sequence 11372, A	613	27	60.0	641	2	US-09-370-767-41391	Sequence 41391, A
541	27	60.0	441	2	US-09-252-991A-21723	Sequence 21723, A	614	27	60.0	641	2	US-09-370-767-56507	Sequence 56507, A
542	27	60.0	443	2	US-09-134-001C-3767	Sequence 3767, Ap	615	27	60.0	649	2	US-09-418-963-2	Sequence 2, Appli
543	27	60.0	443	2	US-09-489-039A-9088	Sequence 9088, Ap	616	27	60.0	655	2	US-10-152-886-89	Sequence 89, Appli
544	27	60.0	455	2	US-09-270-767-46056	Sequence 46056, A	617	27	60.0	662	2	US-09-534-228B-2	Sequence 2, Appli
545	27	60.0	467	2	US-09-134-000C-5767	Sequence 5767, Ap	618	27	60.0	667	2	US-09-902-540-10448	Sequence 10448, A
546	27	60.0	474	2	US-09-248-796A-16212	Sequence 16212, A	619	27	60.0	680	2	US-09-248-796A-15089	Sequence 15089, A
547	27	60.0	486	2	US-09-825-561A-73	Sequence 73, Appl	620	27	60.0	693	2	US-09-252-991A-19167	Sequence 19167, A
548	27	60.0	488	2	US-09-540-236-3327	Sequence 3327, Ap	621	27	60.0	717	2	US-09-107-532A-6277	Sequence 6277, Ap
549	27	60.0	489	2	US-09-310-463-14	Sequence 14, Appl	622	27	60.0	780	2	US-09-252-991A-32892	Sequence 32892, A
550	27	60.0	489	2	US-08-842-248A-14	Sequence 14, Appl	623	27	60.0	789	2	US-09-489-039A-9210	Sequence 9210, Ap
551	27	60.0	489	2	US-09-949-016-6765	Sequence 6765, Ap	624	27	60.0	795	2	US-09-031-563-23	Sequence 23, Appl
552	27	60.0	499	2	US-09-437-568A-42	Sequence 42, Appl	625	27	60.0	795	2	US-09-392-277-23	Sequence 23, Appl
553	27	60.0	508	1	US-07-891-942G-10	Sequence 10, Appl	626	27	60.0	795	2	US-09-258-000-23	Sequence 23, Appl
554	27	60.0	516	2	US-09-949-002-526	Sequence 526, App	627	27	60.0	816	2	US-09-999-833A-375	Sequence 375, App
555	27	60.0	518	2	US-09-252-991A-31586	Sequence 31586, A	628	27	60.0	816	2	US-10-020-445A-375	Sequence 375, App
556	27	60.0	519	2	US-09-270-767-41281	Sequence 41281, A	629	27	60.0	823	2	US-09-491-356C-23	Sequence 23, Appl
557	27	60.0	519	2	US-09-270-767-56497	Sequence 56497, A	630	27	60.0	823	2	US-09-949-016-6888	Sequence 6888, Ap
558	27	60.0	526	2	US-09-071-035-84	Sequence 84, Appl	631	27	60.0	843	2	US-09-491-356C-20	Sequence 20, Appl
559	27	60.0	526	2	US-10-206-576-84	Sequence 84, Appl	632	27	60.0	848	2	US-09-491-356C-22	Sequence 22, Appl
560	27	60.0	527	2	US-09-538-092-60	Sequence 60, Appl	633	27	60.0	852	2	US-09-897-427A-6	Sequence 6, Appli
561	27	60.0	529	1	US-07-891-942G-8	Sequence 8, Appli	634	27	60.0	857	2	US-08-887-534A-47	Sequence 47, Appl
562	27	60.0	529	1	US-08-370-909-19	Sequence 19, Appl	635	27	60.0	857	2	US-09-527-431-47	Sequence 47, Appl
563	27	60.0	529	1	US-08-504-048-8	Sequence 8, Appli	636	27	60.0	857	2	US-09-446-861-47	Sequence 47, Appl
564	27	60.0	529	2	US-09-341-982-1	Sequence 1, Appli	637	27	60.0	873	2	US-09-489-039A-11755	Sequence 11755, A
565	27	60.0	529	2	US-09-404-641-85	Sequence 85, Appl	638	27	60.0	886	2	US-09-328-352-6985	Sequence 6985, Ap
566	27	60.0	529	2	US-09-732-234-6	Sequence 6, Appli	639	27	60.0	891	2	US-09-134-001C-4913	Sequence 4913, Ap
567	27	60.0	529	2	US-09-784-859-6	Sequence 6, Appli	640	27	60.0	918	2	US-09-809-920-2	Sequence 2, Appli
568	27	60.0	529	2	US-09-169-717B-39	Sequence 39, Appl	641	27	60.0	933	2	US-09-949-016-8386	Sequence 8386, Ap
569	27	60.0	529	2	US-10-011-436-4	Sequence 4, Appli	642	27	60.0	953	2	US-09-949-016-8387	Sequence 8387, Ap
570	27	60.0	529	2	US-10-414-186-85	Sequence 85, Appl	643	27	60.0	985	2	US-09-543-681A-6501	Sequence 6501, Ap
571	27	60.0	529	2	US-09-825-561A-12	Sequence 12, Appl	644	27	60.0	1006	2	US-09-710-279-154	Sequence 154, App
572	27	60.0	529	2	US-10-243-072-85	Sequence 85, Appl	645	27	60.0	1025	2	US-09-248-796A-20573	Sequence 20573, A
573	27	60.0	529	2	US-08-533-895A-39	Sequence 39, Appl	646	27	60.0	1045	1	US-07-596-467-6	Sequence 6, Appli
574	27	60.0	535	2	US-09-248-796A-18860	Sequence 18860, A	647	27	60.0	1045	1	US-07-334-374-6	Sequence 6, Appli
575	27	60.0	536	2	US-09-328-352-4689	Sequence 4689, Ap	648	27	60.0	1045	1	US-07-783-861C-6	Sequence 6, Appli
576	27	60.0	537	2	US-08-540-922D-12	Sequence 12, Appl	649	27	60.0	1068	2	US-08-390-874C-11	Sequence 11, Appl
577	27	60.0	544	2	US-09-248-796A-18968	Sequence 18968, A	650	27	60.0	1068	2	US-09-265-772-11	Sequence 11, Appl
578	27	60.0	546	2	US-09-071-035-82	Sequence 82, Appl	651	27	60.0	1068	1	US-09-538-092-1111	Sequence 111, Ap
579	27	60.0	546	2	US-10-206-576-82	Sequence 82, Appl	652	27	60.0	1069	1	US-08-162-081B-37	Sequence 37, Appl
580	27	60.0	549	2	US-09-489-039A-8814	Sequence 8814, Ap	653	27	60.0	1069	1	US-08-780-872-37	Sequence 37, Appl
581	27	60.0	552	2	US-09-949-016-11728	Sequence 11728, A	654	27	60.0	1069	2	US-09-085-957-37	Sequence 37, Appl
582	27	60.0	553	2	US-09-491-356C-24	Sequence 24, Appl	655	27	60.0	1076	2	US-09-134-001C-4037	Sequence 4037, Ap
583	27	60.0	557	1	US-08-424-788-6	Sequence 6, Appli	656	27	60.0	1080	1	US-08-162-081B-36	Sequence 36, Appl
584	27	60.0	560	1	US-07-891-942G-5	Sequence 5, Appli	657	27	60.0	1080	2	US-08-780-872-36	Sequence 36, Appl
585	27	60.0	563	2	US-09-437-568A-21	Sequence 21, Appl	658	27	60.0	1080	2	US-09-085-957-36	Sequence 36, Appl
586	27	60.0	564	2	US-09-437-568A-2	Sequence 2, Appli	659	27	60.0	1248	2	US-08-726-214-16	Sequence 16, Appl
587	27	60.0	564	2	US-09-999-248A-14	Sequence 14, Appl	660	27	60.0	1780	2	US-09-949-016-6899	Sequence 6899, Ap
588	27	60.0	572	1	US-08-605-703B-2210	Sequence 2210, Ap	661	27	60.0	1786	2	US-09-949-016-7880	Sequence 7880, Ap
589	27	60.0	578	1	US-08-424-788-5	Sequence 5, Appli	662	27	60.0	1901	2	US-09-738-946-12	Sequence 12, Appl
590	27	60.0	578	1	US-08-110-683-2	Sequence 2, Appli	663	27	60.0	3084	2	US-09-562-702A-12	Sequence 12, Appl
591	27	60.0	578	1	US-08-683-743-2	Sequence 2, Appli	664	27	60.0	3106	2	US-09-562-702A-10	Sequence 10, Appl
592	27	60.0	578	1	US-08-477-166-2	Sequence 2, Appli	665	27	60.0	3335	1	US-08-523-170B-2	Sequence 2, Appli
593	27	60.0	578	1	US-08-472-097-2	Sequence 2, Appli	666	27	60.0	3335	2	US-08-954-441-2	Sequence 2, Appli
594	27	60.0	578	2	US-09-439-672-2	Sequence 2, Appli	667	26.5	58.9	77	2	US-09-248-796A-27395	Sequence 27395, A
595	27	60.0	578	2	US-09-949-002-322	Sequence 322, App	668	26.5	58.9	938	2	US-09-252-991A-23882	Sequence 23882, A
596	27	60.0	578	4	PCT-US93-1163B-2	Sequence 2, Appli	669	26	57.8	16	2	US-09-233-086-8	Sequence 8, Appli
597	27	60.0	579	2	US-09-540-236-2373	Sequence 2373, Ap	670	26	57.8	52	2	US-09-470-512A-5	Sequence 5, Appli
598	27	60.0	580	2	US-09-949-016-9905	Sequence 9905, Ap	671	26	57.8	60	2	US-08-936-165A-322	Sequence 322, App
599	27	60.0	590	2	US-09-949-016-6405	Sequence 6405, Ap	672	26	57.8	62	2	US-09-270-767-41266	Sequence 41266, A
600	27	60.0	590	2	US-09-310-463-22	Sequence 22, Appl	673	26	57.8	62	2	US-09-270-767-56482	Sequence 56482, A
601	27	60.0	590	2	US-08-842-248A-22	Sequence 22, Appl	674	26	57.8	62	2	US-09-248-796A-26061	Sequence 26061, A
602	27	60.0	594	2	US-09-949-002-393	Sequence 393, App	675	26	57.8	64	2	US-09-134-001C-3186	Sequence 3186, Ap
603	27	60.0	594	2	US-09-468-872-2	Sequence 2, Appli	676	26	57.8	65	2	US-09-328-352-8245	Sequence 8245, Ap
604	27	60.0	608	2	US-09-949-016-9905	Sequence 9905, Ap	677	26	57.8	67	2	US-09-248-796A-27378	Sequence 27378, A
605	27	60.0	610	2	US-09-949-016-9964	Sequence 9964, Ap	678	26	57.8	67	2	US-09-248-796A-25535	Sequence 25535, A
606	27	60.0	612	2	US-09-949-002-450	Sequence 450, App	679	26	57.8	69	2	US-09-134-001C-4527	Sequence 4527, Ap
607	27	60.0	615	2	US-09-134-001C-3284	Sequence 3284, Ap	680	26	57.8	76	2	US-09-248-796A-24296	Sequence 24296, A
608	27	60.0	615	2	US-09-248-796A-20833	Sequence 20833, A	681	26	57.8	79	2	US-09-248-796A-26376	Sequence 26376, A
609	27	60.0	616	2	US-09-949-016-6889	Sequence 6889, Ap	682	26	57.8	81	2	US-09-248-796A-24288	Sequence 24288, A
610	27	60.0	616	2	US-09-949-016-7740	Sequence 7740, Ap	683	26	57.8	85	2	US-09-732-210-1703	Sequence 1703, Ap
611	27	60.0	618	1	US-08-332-312-2	Sequence 2, Appli	684	26	57.8	87	2	US-09-902-540-9916	Sequence 9916, Ap

685	26	57.8	97	2	US-09-107-532A-4024	Sequence 4024, Ap	758	26	57.8	293	2	US-09-270-767-61531	Sequence 61531, A
686	26	57.8	97	2	US-09-270-767-40231	Sequence 40231, A	759	26	57.8	293	2	US-10-402-818-8	Sequence 8, Appli
687	26	57.8	97	2	US-09-270-767-55447	Sequence 55447, A	760	26	57.8	294	2	US-09-674-741-6	Sequence 6, Appli
688	26	57.8	103	2	US-09-248-796A-26113	Sequence 26113, A	761	26	57.8	294	2	US-09-674-741-17	Sequence 17, Appli
689	26	57.8	106	2	US-09-248-796A-17434	Sequence 17434, A	762	26	57.8	294	2	US-09-270-767-45782	Sequence 45782, A
690	26	57.8	109	2	US-09-270-767-35586	Sequence 35586, A	763	26	57.8	294	2	US-10-402-818-7	Sequence 7, Appli
691	26	57.8	109	2	US-09-270-767-50803	Sequence 50803, A	764	26	57.8	294	2	US-10-379-010-6	Sequence 6, Appli
692	26	57.8	117	2	US-09-107-532A-3818	Sequence 3818, Ap	765	26	57.8	294	2	US-10-379-010-17	Sequence 17, Appli
693	26	57.8	122	2	US-09-134-000C-3932	Sequence 3932, Ap	766	26	57.8	294	2	US-10-151-832-7	Sequence 7, Appli
694	26	57.8	127	2	US-09-513-999C-4122	Sequence 4122, Ap	767	26	57.8	295	2	US-09-328-352-5192	Sequence 5192, Ap
695	26	57.8	131	2	US-09-270-767-33060	Sequence 33060, A	768	26	57.8	300	2	US-09-543-681A-6670	Sequence 6670, Ap
696	26	57.8	131	2	US-09-270-767-48277	Sequence 48277, A	769	26	57.8	300	2	US-09-248-796A-14785	Sequence 14785, A
697	26	57.8	134	2	US-09-455-960-6	Sequence 455, A	770	26	57.8	305	2	US-09-270-767-44944	Sequence 44944, A
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701	26	57.8	137	2	US-09-605-703B-2772	Sequence 2772, Ap	774	26	57.8	312	2	US-10-402-818-2	Sequence 2, Appli
702	26	57.8	143	2	US-09-830-230A-222	Sequence 222, Ap	775	26	57.8	312	2	US-10-379-010-18	Sequence 18, Appli
703	26	57.8	144	2	US-10-101-464A-756	Sequence 756, Ap	776	26	57.8	312	2	US-10-151-832-9	Sequence 9, Appli
704	26	57.8	145	2	US-09-107-532A-7292	Sequence 7292, Ap	777	26	57.8	314	2	US-09-270-767-41822	Sequence 41822, A
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707	26	57.8	150	2	US-09-270-767-54260	Sequence 54260, A	780	26	57.8	318	1	US-08-537-942A-1	Sequence 1, Appli
708	26	57.8	153	2	US-09-902-540-13845	Sequence 13845, A	781	26	57.8	318	2	US-08-997-252A-1	Sequence 1, Appli
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710	26	57.8	157	2	US-09-107-433-5026	Sequence 5026, Ap	783	26	57.8	318	2	US-09-935-720A-1	Sequence 1, Appli
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745	26	57.8	270	2	US-09-134-001C-4376	Sequence 4376, A	818	26	57.8	377	2	US-09-568-189A-65	Sequence 65, Appli
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755	26	57.8	286	2	US-10-379-010-12	Sequence 12, Appli	828	26	57.8	416	2	US-09-489-039A-7538	Sequence 7538, Ap
756	26	57.8	288	2	US-09-949-016-10862	Sequence 10862, A	829	26	57.8	416	2	US-09-270-767-45333	Sequence 45333, A
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874	26	57.8	424	2	US-09-257-770-6	Sequence 6, Appli	947	26	57.8	861	2	US-09-873-737A-6	Sequence 6, Appli
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898	26	57.8	424	1	US-08-268-161A-107	Sequence 107, App	971	26	57.8	1196	2	US-09-252-991A-18261	Sequence 7, Appli
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985 26 57.8 1464 2 US-08-940-035A-11  
986 26 57.8 1464 2 US-08-935-105A-11  
987 26 57.8 1464 2 US-09-648-797-11  
988 26 57.8 1464 2 US-08-217-704C-2  
989 26 57.8 1464 2 US-09-386-123-11  
990 26 57.8 1464 2 US-09-949-016-8311  
991 26 57.8 1464 2 US-10-038-937-11  
992 26 57.8 1464 2 US-10-007-747-11  
993 26 57.8 1464 2 US-09-922-011-1  
994 26 57.8 1464 2 US-09-945-901-11  
995 26 57.8 1480 2 US-09-922-011-10  
996 26 57.8 1482 1 US-08-026-138E-2  
997 26 57.8 1484 1 US-08-231-193A-56  
998 26 57.8 1484 1 US-08-486-273A-56  
999 26 57.8 1484 2 US-08-940-086A-56  
1000 26 57.8 1484 2 US-08-940-035A-56

ALIGNMENTS

RESULT 1  
US-08-905-223-453  
; Sequence 453, Application US/08905223  
; Patent No. 6222029  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste D.  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Lacroix, Bruno  
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS  
; NUMBER OF SEQUENCES: 503  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Knobb, Martens, Olson & Bear  
; STREET: 501 West Broadway  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-3505  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Win95  
; SOFTWARE: Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/905,223  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 235-8550  
; TELEFAX: (619) 235-0176  
; INFORMATION FOR SEQ ID NO: 453:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 65 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; TISSUE TYPE: Brain  
; FEATURE:  
; NAME/KEY: sig\_peptide

Sequence 26785, A  
Sequence 9603, Ap  
Sequence 8, Appl  
Sequence 1, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 2, Appl  
Sequence 11, Appl  
Sequence 8311, Ap  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 10, Appl  
Sequence 2, Appl  
Sequence 56, Appl  
Sequence 56, Appl  
Sequence 56, Appl

; LOCATION: -21...-1  
; IDENTIFICATION METHOD: Von Heijne matrix  
; OTHER INFORMATION: seq LVLSLQFLLLSYD/LF  
US-08-905-223-453

Query Match 77.8%; Score 35; DB 2; Length 65;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
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Db 18 LSYDLFV 24

RESULT 2  
US-09-513-999C-5304  
; Sequence 5304, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59 US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5304  
; LENGTH: 85  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 68  
; OTHER INFORMATION: Xaa=Ala or Pro or Ser or Thr  
US-09-513-999C-5304

Query Match 77.8%; Score 35; DB 2; Length 85;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
|||||  
Db 18 LSYDLFV 24

RESULT 3  
US-09-663-600A-126  
; Sequence 126, Application US/09663600A  
; Patent No. 6573068  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: 31.US3.CIP  
; CURRENT APPLICATION NUMBER: US/09/663,600A  
; CURRENT FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: 1998-04-13

; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent.pm  
; SEQ ID NO 126  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -21...-1  
US-09-663-600A-126

Query Match 77.8%; Score 35; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLFV 8  
| | | | |  
Db 18 LSYDLFV 24

## RESULT 4

US-09-663-600A-220  
; Sequence 220, Application US/09663600A  
; Patent No. 6573068

; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: 31 US3 CIP  
; CURRENT APPLICATION NUMBER: US/09/663,600A

; CURRENT FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent.pm  
; SEQ ID NO 220  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -94...-1  
US-09-663-600A-220

Query Match 77.8%; Score 35; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLFV 8  
| | | | |  
Db 18 LSYDLFV 24

## RESULT 5

US-09-149-476-462  
; Sequence 462, Application US/09149476

; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588

; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,881  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,908  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,669  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/049,610  
; EARLIER FILING DATE: 1997-06-13  
; EARLIER APPLICATION NUMBER: 60/061,060  
; EARLIER FILING DATE: 1997-10-02

Query Match 77.8%; Score 35; DB 2; Length 163;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLFV 8  
      |||||  
Db 18 LSYDLFV 24

RESULT 6  
US-09-766-055A-4  
; Sequence 4, Application US/09766055A  
; Patent No. 6403354  
; GENERAL INFORMATION:  
; APPLICANT: XU, SHUANG-YONG  
; APPLICANT: SAMUELSON, JAMES  
; APPLICANT: PELLETIER, JOHN  
; APPLICANT: SIBLEY, MARION  
; APPLICANT: WILSON, GEOFFREY G.

```
; TITLE OF INVENTION: METHOD FOR CLONING AND EXPRESSION OF BstYI RESTRICTION
; TITLE OF INVENTION: ENDONUCLEASE AND BstYI METHYLASE IN E. coli AND
; TITLE OF INVENTION: PURIFICATION OF BstYI AND M.BstYI ENZYMES
; FILE REFERENCE: NEB-185
; CURRENT APPLICATION NUMBER: US/09/766,055A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus Y406
US-09-766-055A-4

Query Match          77.8%; Score 35; DB 2; Length 203;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLSYDLFV 8
Db 136 FVAYDLFV 143

RESULT 7
US-09-270-767-38981
; Sequence 38981, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38981
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-38981

Query Match          77.8%; Score 35; DB 2; Length 231;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLFV 9
Db 172 ISYDLFII 179

RESULT 8
US-09-270-767-54198
; Sequence 54198, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54198
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-54198

Query Match          77.8%; Score 35; DB 2; Length 231;
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Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LSYDLFV 9
Db 172 ISYDLFII 179

RESULT 9
US-09-248-796A-18423
; Sequence 18423, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18423
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18423

Query Match          77.8%; Score 35; DB 2; Length 382;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLSYDLFV 9
Db 230 FLSYDLSII 238

RESULT 10
US-09-270-767-45072
; Sequence 45072, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45072
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45072

Query Match          75.6%; Score 34; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLSYDLFV 9
Db 86 FFSYDIFV 94

RESULT 11
US-09-270-767-35680
; Sequence 35680, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
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FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 35680  
LENGTH: 195  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-35680

Query Match 75.6%; Score 34; DB 2; Length 195;  
Best Local Similarity 44.4%; Pred. No. 52;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
:|:|:|:|:  
Db 66 YISYELFII 74

RESULT 12  
US-09-270-767-50897  
Sequence 50897, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 50897  
LENGTH: 195  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-50897

Query Match 75.6%; Score 34; DB 2; Length 195;  
Best Local Similarity 44.4%; Pred. No. 52;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
:|:|:|:|:  
Db 66 YISYELFII 74

RESULT 13  
US-09-328-352-5693  
Sequence 5693, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5693  
LENGTH: 363  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5693

Query Match 75.6%; Score 34; DB 2; Length 363;  
Best Local Similarity 66.7%; Pred. No. 97;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
:|:|:|:|:  
Db 39 FLVYDIFWV 47

RESULT 14  
US-09-543-681A-4764  
Sequence 4764, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709,1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 4764  
LENGTH: 103  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-4764

Query Match 73.3%; Score 33; DB 2; Length 103;  
Best Local Similarity 85.7%; Pred. No. 42;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
:|:|:|:|:  
Db 39 ISYDLFV 45

RESULT 15  
US-08-837-593-7  
Sequence 7, Application US/08837593  
Patent No. 5977442  
GENERAL INFORMATION:  
APPLICANT: Klessig, Daniel F.  
APPLICANT: Zhang Zhuqun  
TITLE OF INVENTION: "NO. 5977442el Salicylic Acid Induced  
TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman,  
ADDRESS: P.C.  
STREET: 1601 Market Street, Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: United States of America  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,593  
FILING DATE: April 21, 1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,805  
FILING DATE: October 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
REFERENCE/DOCKET NUMBER: Rutgers 97-0016  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:



```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-7

Query Match 73.3%; Score 33; DB 1; Length 370;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 7
Db 21 FLSYDLFV 27
|:|||||
|:|||||

RESULT 16
US-09-248-796A-19856
; Sequence 19856, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19856
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-19856

Query Match 73.3%; Score 33; DB 2; Length 593;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
Db 515 FLSYQLPEV 523
|:|||||
|:|||||

RESULT 17
US-09-270-767-36909
; Sequence 36909, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36909
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-36909

Query Match 68.9%; Score 31; DB 2; Length 132;
```

```
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
Db 82 FTSYNLFV 89
|:|||||
|:|||||

RESULT 18
US-09-270-767-52126
; Sequence 52126, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52126
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-52126

Query Match 68.9%; Score 31; DB 2; Length 132;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8
Db 82 FTSYNLFV 89
|:|||||
|:|||||

RESULT 19
US-09-583-110-3871
; Sequence 3871, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3871
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-3871

Query Match 68.9%; Score 31; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLF 7
Db 63 LSYDLF 68
|:|||||
|:|||||

RESULT 20
US-09-438-185A-79
; Sequence 79, Application US/09438185A
```

; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 79  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: CPn0077  
US-09-438-185A-79

Query Match 68.9%; Score 31; DB 2; Length 160;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
|:|:|:|:|  
Db 2 FVSYPFV 9

RESULT 21  
US-09-107-433-3765  
; Sequence 3765, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/ 085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 3765:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (B) LOCATION 1...170  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3765:  
US-09-107-433-3765

Query Match 68.9%; Score 31; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLF 7  
|:|:|:|:|  
Db 75 LSYDLF 80

RESULT 22  
US-09-270-767-38485  
; Sequence 38485, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 38485  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-38485

Query Match 68.9%; Score 31; DB 2; Length 195;  
Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
|:|:|:|:|  
Db 126 FLKYDSFV 133

RESULT 23  
US-09-270-767-53702  
; Sequence 53702, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 53702  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-53702

Query Match 68.9%; Score 31; DB 2; Length 195;  
Best Local Similarity 75.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLSYDLFV 8  
||| |||

Db 126 FLKYDSFV 133

RESULT 24  
US-09-583-110-4242  
; Sequence 4242, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics  
; CURRENT APPLICATION NUMBER: US/09/583.110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 4242  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-4242

Query Match 68.9%; Score 31; DB 2; Length 246;  
Best Local Similarity 77.8%; Pred. No. 2.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLSYDLFV 9  
||| |||

Db 133 FLSFLLFV 141

RESULT 25  
US-09-107-433-4836  
; Sequence 4836, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: CD/ROM ISO9660  
COMPUTER: <Unknown>  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,433  
FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/ 085131  
FILING DATE: May 12, 1998  
APPLICATION NUMBER: 60/051553  
FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 4836:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...249  
SEQUENCE DESCRIPTION: SEQ ID NO: 4836:  
US-09-107-433-4836

Query Match 68.9%; Score 31; DB 2; Length 249;  
Best Local Similarity 77.8%; Pred. No. 2.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLSYDLFV 9  
||| |||

Db 136 FLSFLLFV 144

RESULT 26  
US-09-603-208A-188  
; Sequence 188, Application US/09603208A  
; Patent No. 6822084  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; APPLICANT: Lee, Heung-Shick  
; APPLICANT: Kim, Hyung-Joon  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,  
FILE REFERENCE: BGI-124CP  
; CURRENT APPLICATION NUMBER: US/09/603,208A  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142692  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: 60/151214  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930429.7  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931413.6  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931457.8  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931541.8  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932209.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932230.9  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932914.1  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19940764.9  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19941382.7  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 306  
; SEQ ID NO 188  
; LENGTH: 284  
; TYPE: PRT

```

; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5546:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...344
; SEQUENCE DESCRIPTION: SEQ ID NO: 5546:
US-09-107-532A-5546

Query Match      68.9%; Score 31; DB 2; Length 344;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LSYDLFVV 9
      |::|
DB      227 LAHDLFVV 234

RESULT 29
US-09-248-796A-15456
; Sequence 15456, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIORITY FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15456
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15456

Query Match      68.9%; Score 31; DB 2; Length 346;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLSYDLF 7
      |::|
DB      59 FISPDLF 65

RESULT 30
US-09-328-352-7078
; Sequence 7078, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252

```

```
; SEQ ID NO 7078
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7078

Query Match      68.9%; Score 31; DB 2; Length 349;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLSYDLFV 7
      ||| |||: ||
Db      279 FLKYDIF 285

RESULT 31
US-09-107-532A-6266
; Sequence 6266, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6266:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...400
; SEQUENCE DESCRIPTION: SEQ ID NO: 6266:
US-09-107-532A-6266

Query Match      68.9%; Score 31; DB 2; Length 400;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLSYDLFV 8
      ||| |||: ||
Db      197 FLSYGLFL 204
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RESULT 32
US-09-540-236-2207
; Sequence 2207, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA.
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2207
; LENGTH: 437
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2207

Query Match      68.9%; Score 31; DB 2; Length 437;
Best Local Similarity 75.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLSYDLFV 8
      ||| |||: ||
Db      141 FLDYDLLV 148

RESULT 33
US-09-184-964-3
; Sequence 3, Application US/09184964
; Patent No. 6391574
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper D.
; APPLICANT: Boyartchuk, Victor L.
; APPLICANT: Ashby, Matthew N.
; TITLE OF INVENTION: AFCl AND RCEl: ISOPRENLYATED CAAx
; TITLE OF INVENTION: PROCESSING ENZYMES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 2200 Sand Hill road, suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/184,964
; FILING DATE: 03-NOV-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/902,774
; FILING DATE: 30-JUL-1997
; APPLICATION NUMBER: 60/023,491
; FILING DATE: 07-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Suyat, Reginald J.
; REGISTRATION NUMBER: 28,172
; REFERENCE/DOCKET NUMBER: 09272-006004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/322-5070
; TELEFAX: 650/854-0875
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
```

;  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: 1...451  
; OTHER INFORMATION: /note = "The sequence of the Afclp  
; OTHER INFORMATION: protein from yeast presented as a polypeptide sequence"  
US-09-184-964-3

Query Match 68.9%; Score 31; DB 2; Length 451;  
Best Local Similarity 71.4%; Pred. No. 4.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7  
|: ||||  
Db 87 FIKYDLF 93

RESULT 34  
US-09-538-092-472  
; Sequence 472, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuraPatSeqFormatter Version 0.9  
; SEQ ID NO 472  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number YJR117W  
US-09-538-092-472

Query Match 68.9%; Score 31; DB 2; Length 453;  
Best Local Similarity 71.4%; Pred. No. 4.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7  
|: ||||  
Db 87 FIKYDLF 93

RESULT 35  
US-09-486-192-3  
; Sequence 3, Application US/09486192  
; Patent No. 6521440  
; GENERAL INFORMATION:  
; APPLICANT: Estell, David A.  
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms  
; FILE REFERENCE: GC386-US  
; CURRENT APPLICATION NUMBER: US/09/486,192  
; CURRENT FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/US98/18677  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: EP9719637.2  
; PRIOR FILING DATE: 1997-09-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-486-192-3

Query Match 68.9%; Score 31; DB 2; Length 472;  
Best Local Similarity 71.4%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7  
|: ||||  
Db 87 FIKYDLF 93

RESULT 36  
US-10-328-459A-3  
; Sequence 3, Application US/10328459A  
; Patent No. 6905868  
; GENERAL INFORMATION:  
; APPLICANT: Genencor International, Inc.  
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms  
; FILE REFERENCE: GC386-PCT  
; CURRENT APPLICATION NUMBER: US/10/328,459A  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: PCT/US98/  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: EP9719637.2  
; PRIOR FILING DATE: 1997-09-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: S. cerevisiae  
US-10-328-459A-3

Query Match 68.9%; Score 31; DB 2; Length 472;  
Best Local Similarity 71.4%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7  
|: ||||  
Db 87 FIKYDLF 93

RESULT 37  
US-09-537-357-7  
; Sequence 7, Application US/09537357  
; Patent No. 6271018  
; GENERAL INFORMATION:  
; APPLICANT: Alan Brash  
; APPLICANT: Nathalie Tijet  
; TITLE OF INVENTION: MUSKMELOX (CUCUMIS MELO) HYDROPEROXIDE  
; TITLE OF INVENTION: LYASE AND USES THEREOF  
; FILE REFERENCE: 06027.0002  
; CURRENT APPLICATION NUMBER: US/09/537,357  
; CURRENT FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 481  
; TYPE: PRT  
; ORGANISM: Cucumis melo  
US-09-537-357-7

Query Match 68.9%; Score 31; DB 2; Length 481;  
Best Local Similarity 66.7%; Pred. No. 4.8e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
|: ||||  
Db 450 FLRYDTFTV 458

RESULT 38  
US-09-537-357-15  
; Sequence 15, Application US/09537357

RESULT 40  
US-09-134-000C-5626  
; Sequence 5626, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lyvin Doucette-Stamm et al

```

; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6

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1 LENGTH: 126

2 TYPE: PRT

3 ORGANISM: Zea mays

4 FEATURE:

5 NAME/KEY: UNSURE

6 LOCATION: (117)

7 OTHER INFORMATION: Xaa = any amino acid

8 FEATURE:

9 NAME/KEY: UNSURE

10 LOCATION: (120)

11 OTHER INFORMATION: Xaa = any amino acid

US-09-889-463A-6

Query Match

Best Local Similarity 66.7%; Score 30; DB 2; Length 126;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8

118 FVXFDFV 125

119 FVXFDFV 125

RESULT 43

US-09-198-452A-528

Sequence 528, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 528

LENGTH: 130

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-528

Query Match

Best Local Similarity 66.7%; Score 30; DB 2; Length 130;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8

31 FYSYBIFV 38

RESULT 44

US-09-270-767-43152

Sequence 43152, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 43152

LENGTH: 156

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-43152

Query Match

Best Local Similarity 66.7%; Score 30; DB 2; Length 156;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;



```
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 685
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0683
US-09-438-185A-685

Query Match          66.7%; Score 30; DB 2; Length 328;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
   |:|:|:|
Db 219 FISHDLAW 227

RESULT 48
US-09-230-637-30
; Sequence 30, Application US/09230637
; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpes-like virus
US-09-230-637-30

Query Match          66.7%; Score 30; DB 2; Length 333;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
   |:|:|:|
Db 127 FVFYQLFW 135
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RESULT 49
US-09-489-039A-10892
; Sequence 10892, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
```

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; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10892
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10892
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Query Match          66.7%; Score 30; DB 2; Length 343;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
   |:|:|:|
Db 223 FISHDLVV 231
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RESULT 50
US-09-543-681A-6716
; Sequence 6716, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6716
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6716
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Query Match          66.7%; Score 30; DB 2; Length 346;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
   |:|:|:|
Db 230 FISHDLVV 238
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Job time : 35.2 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 02:25:44 ; Search time 80.8 Seconds  
(without alignments)  
46.540 Million cell updates/sec

Title: US-09-870-216C-9  
Perfect score: 45  
Sequence: 1 FLSYDLFVV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published Applications\_AA\_Main:\*

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6: /cgn2\_6/prodata1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	3	US-09-870-216C-9
2	45	100.0	9	4	US-10-017-327-9
3	36	80.0	51	3	US-09-833-245-2059
4	36	80.0	51	4	US-10-060-255-62
5	36	80.0	51	5	US-10-881-088-62
6	35	77.8	130	3	US-09-729-674-16
7	35	77.8	130	5	US-10-913-553-16
8	35	77.8	162	3	US-09-378-360A-732
9	35	77.8	162	4	US-10-319-763-126
10	35	77.8	162	4	US-10-319-763-220
11	35	77.8	162	4	US-10-170-385-53
12	35	77.8	162	4	US-10-264-237-1995
13	35	77.8	163	3	US-09-809-391-462
14	35	77.8	163	3	US-09-882-171-462
15	35	77.8	163	3	US-10-164-861-462
16	35	77.8	203	5	US-10-501-196-2
17	34	75.6	55	3	US-09-867-550-916
18	34	75.6	66	4	US-10-424-599-175697
19	34	75.6	98	4	US-10-106-698-4683
20	34	75.6	247	4	US-10-108-260A-3015
21	34	75.6	346	4	US-10-424-599-217530
22	34	75.6	412	3	US-09-882-227-396
23	34	75.6	516	5	US-10-732-923-11374
24	34	75.6	576	4	US-10-108-260A-3829
25	34	75.6	674	4	US-10-094-749-2686
26	33	73.3	56	4	US-10-424-599-278654
27	33	73.3	67	4	US-10-424-599-284635

28	33	73.3	88	4	US-10-425-115-318398	Sequence 318398,
29	33	73.3	100	4	US-10-425-115-195354	Sequence 195354,
30	33	73.3	211	4	US-10-083-357-691	Sequence 691, App
31	33	73.3	274	5	US-10-732-923-11305	Sequence 11305, A
32	33	73.3	559	5	US-10-732-923-11303	Sequence 11303, A
33	33	73.3	572	5	US-10-732-923-11301	Sequence 11301, A
34	33	73.3	573	4	US-10-369-493-2314	Sequence 2314, Ap
35	33	73.3	573	4	US-10-369-493-2320	Sequence 2320, Ap
36	33	73.3	573	5	US-10-732-923-11302	Sequence 11302, A
37	33	73.3	583	4	US-10-369-493-23678	Sequence 22678, A
38	33	73.3	583	5	US-10-732-923-11304	Sequence 11304, A
39	33	73.3	839	4	US-10-424-599-206656	Sequence 206656,
40	33	73.3	1507	4	US-10-424-599-206659	Sequence 206659,
41	32	71.1	62	4	US-10-437-963-177564	Sequence 177564,
42	32	71.1	80	4	US-10-425-115-256908	Sequence 256908,
43	32	71.1	153	4	US-10-424-599-147896	Sequence 147896,
44	32	71.1	165	4	US-10-156-761-8778	Sequence 8778, Ap
45	32	71.1	265	4	US-10-336-603A-52	Sequence 52, Appl
46	32	71.1	279	3	US-09-778-927A-64	Sequence 64, Appl
47	32	71.1	288	4	US-10-336-603A-48	Sequence 48, Appl
48	32	71.1	291	4	US-10-437-963-131686	Sequence 131686,
49	32	71.1	305	4	US-10-336-603A-46	Sequence 46, Appl
50	32	71.1	313	5	US-10-739-930-6831	Sequence 6831, Ap
51	32	71.1	328	4	US-10-336-603A-44	Sequence 44, Appl
52	32	71.1	328	4	US-10-336-603A-50	Sequence 50, Appl
53	32	71.1	337	4	US-10-437-963-113203	Sequence 113203,
54	32	71.1	413	4	US-10-282-122A-63647	Sequence 63647, A
55	32	71.1	891	4	US-10-424-599-220899	Sequence 220899,
56	31	68.9	9	5	US-10-705-459-353	Sequence 353, App
57	31	68.9	35	4	US-10-424-599-152078	Sequence 152078,
58	31	68.9	40	4	US-10-424-599-281803	Sequence 281803,
59	31	68.9	44	4	US-10-425-115-347677	Sequence 347677,
60	31	68.9	57	4	US-10-424-599-182421	Sequence 182421,
61	31	68.9	57	4	US-10-437-963-179795	Sequence 179795,
62	31	68.9	62	4	US-10-424-599-165551	Sequence 165551,
63	31	68.9	63	3	US-09-864-408A-5262	Sequence 5262, Ap
64	31	68.9	63	4	US-10-425-115-345878	Sequence 345878,
65	31	68.9	75	4	US-10-424-599-197220	Sequence 197220,
66	31	68.9	84	4	US-10-437-963-194827	Sequence 194827,
67	31	68.9	95	4	US-10-425-115-333625	Sequence 333625,
68	31	68.9	102	4	US-10-437-963-146502	Sequence 146502,
69	31	68.9	109	4	US-10-424-599-149860	Sequence 149860,
70	31	68.9	114	5	US-10-472-928-2390	Sequence 2390, Ap
71	31	68.9	127	4	US-10-437-963-134155	Sequence 134155,
72	31	68.9	134	4	US-10-424-599-282408	Sequence 282408,
73	31	68.9	138	4	US-10-425-115-289256	Sequence 289256,
74	31	68.9	170	5	US-10-617-320-3765	Sequence 3765, Ap
75	31	68.9	185	4	US-10-425-115-282443	Sequence 282443,
76	31	68.9	211	4	US-10-424-599-284442	Sequence 284442,
77	31	68.9	226	4	US-10-474-776-409	Sequence 409, App
78	31	68.9	226	5	US-10-472-928-4428	Sequence 4428, App
79	31	68.9	249	5	US-10-617-320-4836	Sequence 4836, Ap
80	31	68.9	284	3	US-09-738-626-3667	Sequence 3667, Ap
81	31	68.9	301	5	US-10-774-355A-2211	Sequence 2211, Ap
82	31	68.9	304	4	US-10-282-122A-57028	Sequence 57028, A
83	31	68.9	327	5	US-10-732-923-5974	Sequence 5974, Ap
84	31	68.9	330	4	US-10-369-493-21232	Sequence 21232, A
85	31	68.9	336	4	US-10-437-963-176816	Sequence 176816,
86	31	68.9	340	5	US-10-732-923-5982	Sequence 5982, Ap
87	31	68.9	352	5	US-10-732-923-5986	Sequence 5986, Ap
88	31	68.9	357	3	US-09-750-703-2	Sequence 2, Appl1
89	31	68.9	357	6	US-11-097-143-4728	Sequence 4728, Ap
90	31	68.9	360	4	US-10-425-114-36807	Sequence 36807, A
91	31	68.9	394	4	US-10-369-493-7747	Sequence 7747, Ap
92	31	68.9	420	4	US-10-282-122A-67136	Sequence 67136, A
93	31	68.9	440	5	US-10-732-923-11205	Sequence 11205, A
94	31	68.9	453	4	US-10-646-950-2	Sequence 2, Appl1
95	31	68.9	462	4	US-10-424-599-181814	Sequence 181814,
96	31	68.9	472	4	US-10-328-459-3	Sequence 3, Appl1
97	31	68.9	476	4	US-10-369-493-13447	Sequence 13447, A
98	31	68.9	476	5	US-10-732-923-11315	Sequence 11315, A
99	31	68.9	478	4	US-10-434-991-10	Sequence 10, Appl
100	31	68.9	478	5	US-10-732-923-9861	Sequence 9861, Ap

101	31	68.9	479	4	US-10-425-114-45822	Sequence 45822, A	174	30	66.7	305	5	US-10-821-273-50	Sequence 50, Appl
102	31	68.9	481	3	US-09-884-260A-7	Sequence 7, Appli	175	30	66.7	308	4	US-10-767-701-45144	Sequence 45144, A
103	31	68.9	481	4	US-10-434-931-9	Sequence 9, Appli	176	30	66.7	309	3	US-09-835-242-11717	Sequence 11717, A
104	31	68.9	487	3	US-09-884-260A-15	Sequence 15, Appli	177	30	66.7	310	3	US-09-761-288-4	Sequence 4, Appli
105	31	68.9	529	3	US-09-815-242-13935	Sequence 13935, A	178	30	66.7	310	3	US-09-761-288-22	Sequence 22, Appl
106	31	68.9	610	3	US-09-738-626-4495	Sequence 4495, Ap	179	30	66.7	310	3	US-09-761-288-38	Sequence 24, Appl
107	31	68.9	610	4	US-10-289-132A-53702	Sequence 53702, A	180	30	66.7	310	3	US-09-761-288-38	Sequence 38, Appl
108	31	68.9	613	5	US-10-494-541-94	Sequence 94, Appl	181	30	66.7	310	3	US-09-761-288-64	Sequence 64, Appl
109	31	68.9	695	3	US-09-738-626-5527	Sequence 5527, Ap	182	30	66.7	310	3	US-09-761-288-67	Sequence 67, Appl
110	31	68.9	951	6	US-11-097-143-30642	Sequence 30642, A	183	30	66.7	310	3	US-09-761-288-89	Sequence 89, Appli
111	31	68.9	1444	6	US-11-097-143-5604	Sequence 5604, Ap	184	30	66.7	310	3	US-09-898-586-4	Sequence 4, Appli
112	31	68.9	1837	6	US-11-097-143-15531	Sequence 15531, A	185	30	66.7	310	3	US-09-898-586-22	Sequence 22, Appl
113	31	68.9	1934	4	US-10-437-963-204616	Sequence 204616, A	186	30	66.7	310	3	US-09-898-586-24	Sequence 24, Appl
114	31	68.9	2610	4	US-10-369-493-6553	Sequence 6553, Ap	187	30	66.7	310	3	US-09-898-586-38	Sequence 38, Appl
115	31	68.9	2610	4	US-10-369-493-6554	Sequence 6554, Ap	188	30	66.7	310	3	US-09-898-586-64	Sequence 64, Appl
116	30	66.7	42	4	US-10-001-879-153	Sequence 153, App	189	30	66.7	310	3	US-09-898-586-67	Sequence 67, Appl
117	30	66.7	43	4	US-10-424-599-275577	Sequence 275577, A	190	30	66.7	310	3	US-09-898-586-89	Sequence 89, Appl
118	30	66.7	49	4	US-10-424-599-192690	Sequence 192690, A	191	30	66.7	310	3	US-09-907-218-33	Sequence 33, Appl
119	30	66.7	49	4	US-10-425-115-254045	Sequence 254045, A	192	30	66.7	310	3	US-09-965-422-62	Sequence 62, Appl
120	30	66.7	50	4	US-10-425-114-60563	Sequence 60563, A	193	30	66.7	310	3	US-09-965-422-65	Sequence 65, Appl
121	30	66.7	55	4	US-10-437-963-169482	Sequence 169482, A	194	30	66.7	310	4	US-10-005-041A-77	Sequence 77, Appl
122	30	66.7	58	4	US-10-424-599-188899	Sequence 188899, A	195	30	66.7	310	4	US-10-005-041A-78	Sequence 78, Appl
123	30	66.7	58	4	US-10-425-115-246364	Sequence 246364, A	196	30	66.7	310	5	US-10-935-190-19	Sequence 19, Appl
124	30	66.7	60	4	US-10-425-115-227883	Sequence 227883, A	197	30	66.7	312	3	US-09-886-055-137	Sequence 137, App
125	30	66.7	63	4	US-10-425-115-355137	Sequence 355137, A	198	30	66.7	312	3	US-09-804-291-137	Sequence 137, App
126	30	66.7	64	3	US-09-764-872-274	Sequence 274, App	199	30	66.7	312	4	US-10-017-161-328	Sequence 328, App
127	30	66.7	75	4	US-10-424-599-155255	Sequence 155255, A	200	30	66.7	312	4	US-10-300-846-30	Sequence 30, Appl
128	30	66.7	79	4	US-10-425-115-277200	Sequence 277200, A	201	30	66.7	312	4	US-10-024-212-86	Sequence 86, Appl
129	30	66.7	84	4	US-10-424-599-159676	Sequence 159676, A	202	30	66.7	312	4	US-10-024-212-88	Sequence 88, Appl
130	30	66.7	86	5	US-10-501-282-3736	Sequence 3736, Ap	203	30	66.7	312	4	US-10-292-798-294	Sequence 294, App
131	30	66.7	90	5	US-10-732-923-7364	Sequence 7364, Ap	204	30	66.7	312	4	US-10-343-650A-278	Sequence 278, App
132	30	66.7	91	4	US-10-425-115-220726	Sequence 220726, A	205	30	66.7	312	4	US-10-473-518-42	Sequence 42, Appl
133	30	66.7	91	4	US-10-425-115-269323	Sequence 269323, A	206	30	66.7	312	5	US-10-819-316-137	Sequence 137, App
134	30	66.7	106	4	US-10-767-701-55550	Sequence 55550, A	207	30	66.7	318	4	US-10-276-774-2199	Sequence 2199, App
135	30	66.7	111	4	US-10-424-599-148582	Sequence 148582, A	208	30	66.7	320	4	US-10-292-798-432	Sequence 432, App
136	30	66.7	117	4	US-10-425-115-355139	Sequence 355139, A	209	30	66.7	320	4	US-10-072-012-84	Sequence 84, Appl
137	30	66.7	126	4	US-10-727-936-6	Sequence 6, Appli	210	30	66.7	320	4	US-10-473-518-72	Sequence 72, Appl
138	30	66.7	130	4	US-10-289-762-528	Sequence 528, App	211	30	66.7	323	4	US-10-282-122A-47093	Sequence 47093, A
139	30	66.7	131	4	US-10-425-115-236585	Sequence 236585, A	212	30	66.7	323	4	US-10-282-122A-53566	Sequence 53566, A
140	30	66.7	132	4	US-10-424-599-216970	Sequence 216970, A	213	30	66.7	324	4	US-10-289-762-724	Sequence 724, App
141	30	66.7	137	4	US-10-296-115-1032	Sequence 1032, Ap	214	30	66.7	324	4	US-10-282-122A-54701	Sequence 54701, A
142	30	66.7	141	4	US-10-415-478A-74	Sequence 74, Appl	215	30	66.7	326	4	US-10-282-122A-66938	Sequence 66938, A
143	30	66.7	141	5	US-10-472-928-306	Sequence 306, App	216	30	66.7	327	3	US-09-815-242-11198	Sequence 11198, A
144	30	66.7	159	4	US-10-437-963-129587	Sequence 129587, A	217	30	66.7	327	4	US-10-282-122A-58436	Sequence 58436, A
145	30	66.7	165	4	US-10-425-114-39661	Sequence 39661, A	218	30	66.7	330	4	US-10-282-122A-72806	Sequence 72806, A
146	30	66.7	183	3	US-09-761-288-39	Sequence 39, Appl	219	30	66.7	333	4	US-10-282-122A-69154	Sequence 69154, A
147	30	66.7	183	3	US-09-761-288-81	Sequence 81, Appl	220	30	66.7	334	4	US-09-815-242-10381	Sequence 10381, A
148	30	66.7	183	3	US-09-761-288-90	Sequence 90, Appl	221	30	66.7	334	4	US-10-282-122A-55671	Sequence 55671, A
149	30	66.7	183	3	US-09-898-586-39	Sequence 39, Appl	222	30	66.7	334	4	US-10-282-122A-56738	Sequence 56738, A
150	30	66.7	183	3	US-09-898-586-81	Sequence 81, Appl	223	30	66.7	335	5	US-10-976-042-9	Sequence 9, Appli
151	30	66.7	183	3	US-09-898-586-90	Sequence 90, Appl	224	30	66.7	335	4	US-10-017-161-486	Sequence 486, App
152	30	66.7	183	4	US-10-424-599-150967	Sequence 150967, A	225	30	66.7	335	4	US-10-282-122A-78321	Sequence 78321, A
153	30	66.7	185	4	US-10-425-115-355136	Sequence 355136, A	226	30	66.7	335	4	US-10-072-012-82	Sequence 82, Appl
154	30	66.7	200	4	US-10-437-963-159247	Sequence 159247, A	227	30	66.7	336	5	US-10-871-385-4	Sequence 4, Appli
155	30	66.7	203	4	US-10-425-115-201688	Sequence 201688, A	228	30	66.7	337	3	US-09-815-242-13800	Sequence 13800, A
156	30	66.7	207	4	US-10-282-122A-52891	Sequence 52891, A	229	30	66.7	337	3	US-10-282-122A-60029	Sequence 60029, A
157	30	66.7	211	4	US-10-425-114-37166	Sequence 37166, A	230	30	66.7	337	4	US-10-282-122A-75472	Sequence 75472, A
158	30	66.7	217	4	US-10-425-115-248249	Sequence 248249, A	231	30	66.7	349	4	US-10-274-694-13	Sequence 13, Appl
159	30	66.7	219	4	US-10-437-963-126799	Sequence 126799, A	232	30	66.7	349	5	US-10-332-448-13	Sequence 13, Appl
160	30	66.7	223	4	US-10-425-115-355138	Sequence 355138, A	233	30	66.7	357	4	US-10-425-115-349899	Sequence 349899, A
161	30	66.7	230	5	US-10-739-930-10046	Sequence 10046, A	234	30	66.7	361	4	US-10-437-963-145811	Sequence 145811, A
162	30	66.7	231	4	US-10-425-114-37243	Sequence 37243, A	235	30	66.7	374	5	US-10-739-930-10432	Sequence 10432, A
163	30	66.7	250	4	US-10-029-386-33683	Sequence 33683, A	236	30	66.7	375	4	US-10-425-115-278680	Sequence 278680, A
164	30	66.7	260	3	US-09-761-288-35	Sequence 35, Appl	237	30	66.7	377	5	US-10-739-930-10431	Sequence 10431, A
165	30	66.7	260	3	US-09-761-288-36	Sequence 36, Appl	238	30	66.7	379	4	US-10-437-963-140288	Sequence 140288, A
166	30	66.7	260	3	US-09-898-586-35	Sequence 35, Appl	239	30	66.7	380	4	US-10-437-963-104457	Sequence 104457, A
167	30	66.7	260	3	US-09-898-586-36	Sequence 36, Appl	240	30	66.7	380	4	US-10-425-115-371212	Sequence 371212, A
168	30	66.7	265	3	US-09-833-218-1842	Sequence 1842, Ap	241	30	66.7	382	4	US-10-425-115-271215	Sequence 271215, A
169	30	66.7	272	3	US-09-907-218-35	Sequence 35, Appl	242	30	66.7	383	5	US-10-739-930-7988	Sequence 7988, Ap
170	30	66.7	286	4	US-10-296-115-1425	Sequence 1425, Ap	243	30	66.7	400	3	US-09-804-357-6	Sequence 6, Appli
171	30	66.7	290	4	US-10-282-122A-55054	Sequence 55054, A	244	30	66.7	400	3	US-09-804-357-6	Sequence 6, Appli
172	30	66.7	304	3	US-09-747-835A-58	Sequence 58, Appl	245	30	66.7	437	4	US-10-424-599-152894	Sequence 152894, A
173	30	66.7	304	4	US-10-312-312-58	Sequence 58, Appl	246	30	66.7	442	5	US-10-732-923-11206	Sequence 11206, A

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248	30	66.7	451	4	US-10-282-122A-48001	Sequence 48001, A	321	29	64.4	68	4	US-10-424-599-196509	Sequence 196509, A
249	30	66.7	453	4	US-10-282-122A-50423	Sequence 50423, A	322	29	64.4	72	3	US-09-984-245-317	Sequence 317, App
250	30	66.7	460	6	US-11-097-143-9705	Sequence 9705, App	323	29	64.4	72	3	US-09-966-262-317	Sequence 317, App
251	30	66.7	461	4	US-10-369-493-13465	Sequence 13465, A	324	29	64.4	72	3	US-09-983-966-317	Sequence 317, App
252	30	66.7	464	4	US-10-369-493-11038	Sequence 11038, A	325	29	64.4	72	4	US-10-059-395-317	Sequence 317, App
253	30	66.7	467	5	US-10-732-923-11352	Sequence 11352, A	326	29	64.4	72	4	US-10-143-090-317	Sequence 317, App
254	30	66.7	471	5	US-10-732-923-11208	Sequence 11208, A	327	29	64.4	72	4	US-10-425-115-258762	Sequence 258762, A
255	30	66.7	471	5	US-10-732-923-11314	Sequence 11314, A	328	29	64.4	72	5	US-10-960-251-317	Sequence 317, App
256	30	66.7	471	5	US-10-732-923-11351	Sequence 11351, A	329	29	64.4	75	4	US-10-425-115-249562	Sequence 249562, A
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258	30	66.7	476	4	US-10-369-493-18270	Sequence 18270, A	331	29	64.4	80	4	US-10-425-115-235889	Sequence 235889, A
259	30	66.7	476	5	US-10-732-923-11212	Sequence 11212, A	332	29	64.4	81	4	US-10-425-115-205924	Sequence 205924, A
260	30	66.7	476	5	US-10-732-923-11213	Sequence 11213, A	333	29	64.4	81	4	US-10-425-115-205924	Sequence 205924, A
261	30	66.7	482	4	US-10-424-599-193626	Sequence 193626, A	334	29	64.4	84	4	US-10-425-115-205961	Sequence 205961, A
262	30	66.7	495	4	US-10-425-115-257630	Sequence 257630, A	335	29	64.4	86	4	US-10-425-115-364740	Sequence 364740, A
263	30	66.7	496	4	US-10-437-963-156276	Sequence 156276, A	336	29	64.4	88	4	US-10-424-599-246148	Sequence 246148, A
264	30	66.7	496	5	US-10-739-930-10000	Sequence 10000, A	337	29	64.4	90	4	US-10-424-599-245893	Sequence 245893, A
265	30	66.7	525	4	US-10-282-122A-69979	Sequence 69979, A	338	29	64.4	95	4	US-10-425-115-365719	Sequence 365719, A
266	30	66.7	533	4	US-10-369-493-13789	Sequence 13789, A	339	29	64.4	96	4	US-10-437-963-129623	Sequence 129623, A
267	30	66.7	533	4	US-10-072-012-395	Sequence 395, App	340	29	64.4	103	3	US-09-764-872-254	Sequence 254, App
268	30	66.7	534	4	US-10-282-122A-67913	Sequence 67913, A	341	29	64.4	103	4	US-10-424-599-164093	Sequence 164093, A
269	30	66.7	536	3	US-09-815-242-11857	Sequence 11857, A	342	29	64.4	106	4	US-10-425-115-239960	Sequence 239960, A
270	30	66.7	536	3	US-10-282-122A-66331	Sequence 66331, A	343	29	64.4	108	4	US-10-424-599-230370	Sequence 230370, A
271	30	66.7	546	5	US-10-732-923-11313	Sequence 11313, A	344	29	64.4	111	4	US-10-425-115-277845	Sequence 277845, A
272	30	66.7	547	3	US-09-738-626-6176	Sequence 6176, App	345	29	64.4	116	4	US-10-424-599-188592	Sequence 188592, A
273	30	66.7	555	4	US-10-369-493-17661	Sequence 17661, A	346	29	64.4	122	4	US-10-282-122A-67111	Sequence 67111, A
274	30	66.7	556	4	US-10-369-493-4879	Sequence 4879, App	347	29	64.4	123	4	US-10-379-010-16	Sequence 16, App1
275	30	66.7	569	4	US-10-369-493-11530	Sequence 11530, A	348	29	64.4	123	4	US-10-425-115-338308	Sequence 338308, A
276	30	66.7	580	4	US-10-425-114-53250	Sequence 53250, A	349	29	64.4	126	4	US-10-424-599-18265	Sequence 18265, A
277	30	66.7	602	4	US-10-282-122A-44918	Sequence 44918, A	350	29	64.4	127	4	US-10-425-114-48838	Sequence 48838, A
278	30	66.7	604	4	US-10-369-493-294	Sequence 294, App	351	29	64.4	127	4	US-10-437-963-171706	Sequence 171706, A
279	30	66.7	630	4	US-10-282-122A-76503	Sequence 76503, A	352	29	64.4	132	4	US-10-424-599-256923	Sequence 256923, A
280	30	66.7	652	4	US-10-369-493-2655	Sequence 2655, App	353	29	64.4	138	4	US-10-437-963-107212	Sequence 107212, A
281	30	66.7	663	4	US-10-282-122A-46534	Sequence 46534, A	354	29	64.4	140	4	US-10-425-115-311867	Sequence 311867, A
282	30	66.7	713	4	US-10-437-963-176881	Sequence 176881, A	355	29	64.4	141	4	US-10-425-115-240025	Sequence 240025, A
283	30	66.7	785	4	US-10-363-616-459	Sequence 459, App	356	29	64.4	146	5	US-10-943-507-377	Sequence 377, App
284	30	66.7	846	4	US-10-369-493-18319	Sequence 18319, A	357	29	64.4	147	4	US-10-437-963-195082	Sequence 195082, A
285	30	66.7	868	4	US-10-425-115-324554	Sequence 324554, A	358	29	64.4	149	4	US-10-369-493-3722	Sequence 3722, App
286	30	66.7	907	4	US-10-437-963-176121	Sequence 176121, A	359	29	64.4	153	4	US-10-437-963-106426	Sequence 106426, A
287	30	66.7	960	4	US-10-039-073-1	Sequence 1, App1	360	29	64.4	154	3	US-09-954-987B-16	Sequence 16, App1
288	30	66.7	960	4	US-10-168-425-6	Sequence 6, App1	361	29	64.4	154	3	US-10-424-599-161006	Sequence 161006, A
289	30	66.7	1022	4	US-10-437-963-161988	Sequence 161988, A	362	29	64.4	154	6	US-11-084-777-16	Sequence 16, App1
290	30	66.7	1191	4	US-10-408-765A-2177	Sequence 2177, App	363	29	64.4	160	4	US-10-424-599-198580	Sequence 198580, A
291	30	66.7	1450	4	US-10-263-929-197	Sequence 197, App	364	29	64.4	187	4	US-10-369-493-13225	Sequence 13225, A
292	30	66.7	1493	4	US-10-017-161-2230	Sequence 2230, App	365	29	64.4	188	5	US-10-938-740-11	Sequence 11, App1
293	30	66.7	1493	4	US-10-292-798-1876	Sequence 1876, App	366	29	64.4	203	3	US-09-900-766-5	Sequence 5, App1
294	30	66.7	1737	4	US-10-263-929-195	Sequence 195, App	367	29	64.4	208	4	US-10-342-224-88	Sequence 88, App1
295	30	66.7	1774	4	US-10-466-720-6	Sequence 6, App1	368	29	64.4	214	5	US-10-501-282-2006	Sequence 2006, App
296	30	66.7	2854	4	US-10-085-198-16	Sequence 16, App1	369	29	64.4	215	4	US-10-424-599-277339	Sequence 277339, A
297	30	66.7	4064	5	US-10-661-398-14	Sequence 14, App1	370	29	64.4	217	4	US-10-424-599-198582	Sequence 198582, A
298	30	66.7	5002	6	US-11-097-143-17961	Sequence 17961, A	371	29	64.4	222	4	US-10-724-972A-6265	Sequence 6265, App
299	29	64.4	10	3	US-09-900-590-52	Sequence 52, App1	372	29	64.4	225	4	US-10-424-599-174550	Sequence 174550, A
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302	29	64.4	24	4	US-10-437-963-157469	Sequence 157469, A	375	29	64.4	236	3	US-09-938-671-183	Sequence 183, App
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305	29	64.4	34	4	US-10-425-115-305212	Sequence 305212, A	378	29	64.4	245	5	US-10-774-355A-2337	Sequence 2337, App
306	29	64.4	36	6	US-10-001-843-139	Sequence 139, App	379	29	64.4	251	4	US-10-767-701-51234	Sequence 51234, A
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312	29	64.4	52	4	US-10-437-963-116157	Sequence 116157, A	385	29	64.4	258	5	US-10-937-758A-14	Sequence 14, App1
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318	29	64.4	61	4	US-10-335-977-5358	Sequence 5358, App	391	29	64.4	268	4	US-10-428-817A-175	Sequence 175, App
319	29	64.4	62	4	US-10-767-701-54800	Sequence 54800, A	392	29	64.4	269	5	US-10-756-149-5538	Sequence 5538, App

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403	29	64.4	286	3	US-09-876-997-287	Sequence 287, App	476	29	64.4	568	4	US-10-319-236A-4	Sequence 4, Appl
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442	29	64.4	416	4	US-10-344-738-12	Sequence 12, Appl	515	29	64.4	836	5	US-10-496-011-65	Sequence 65, Appl
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452	29	64.4	465	4	US-10-032-585-7811	Sequence 7811, Ap	525	29	64.4	1011	4	US-10-174-333-159	Sequence 159, App
453	29	64.4	479	3	US-09-738-626-6048	Sequence 6048, Ap	526	29	64.4	1014	3	US-09-842-758-2	Sequence 2, Appl
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455	29	64.4	483	5	US-10-469-204-156	Sequence 152, App	528	29	64.4	1014	4	US-10-174-333-2	Sequence 2, Appl
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541	29	64.4	1032	4	US-10-175-737-552	Sequence 552, App	614	29	64.4	1032	4	US-10-196-756-552	Sequence 552, App
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588	29	64.4	1032	4	US-10-176-925-552	Sequence 552, App	661	29	64.4	1032	4	US-10-195-901-552	Sequence 552, App
589	29	64.4	1032	4	US-10-176-978-552	Sequence 552, App	662	29	64.4	1032	4	US-10-195-897-552	Sequence 552, App
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591	29	64.4	1032	4	US-10-180-543-552	Sequence 552, App	664	29	64.4	1032	4	US-10-196-743-552	Sequence 552, App
592	29	64.4	1032	4	US-10-180-544-552	Sequence 552, App	665	29	64.4	1032	4	US-10-196-760-552	Sequence 552, App
593	29	64.4	1032	4	US-10-180-546-552	Sequence 552, App	666	29	64.4	1032	4	US-10-173-708-552	Sequence 552, App
594	29	64.4	1032	4	US-10-180-547-552	Sequence 552, App	667	29	64.4	1032	4	US-10-176-479-552	Sequence 552, App
595	29	64.4	1032	4	US-10-180-549-552	Sequence 552, App	668	29	64.4	1032	4	US-10-176-748-552	Sequence 552, App
596	29	64.4	1032	4	US-10-180-555-552	Sequence 552, App	669	29	64.4	1032	4	US-10-176-916-552	Sequence 552, App
597	29	64.4	1032	4	US-10-180-559-552	Sequence 552, App	670	29	64.4	1032	4	US-10-173-507-552	Sequence 552, App
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609	29	64.4	1032	4	US-10-187-596-552	Sequence 552, App	682	29	64.4	1032	4	US-10-184-626-552	Sequence 552, App
610	29	64.4	1032	4	US-10-187-745-552	Sequence 552, App	683	29	64.4	1032	4	US-10-184-627-552	Sequence 552, App
611	29	64.4	1032	4	US-10-187-885-552	Sequence 552, App	684	29	64.4	1032	4	US-10-184-645-552	Sequence 552, App







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977 29 64.4 1032 4 US-10-205-508-552 Sequence 552, App
978 29 64.4 1032 4 US-10-205-905-552 Sequence 552, App
979 29 64.4 1032 4 US-10-206-918-552 Sequence 552, App
980 29 64.4 1032 4 US-10-208-025-552 Sequence 552, App
981 29 64.4 1032 4 US-10-198-760-552 Sequence 552, App
982 29 64.4 1032 4 US-10-201-772-552 Sequence 552, App
983 29 64.4 1032 4 US-10-184-613-552 Sequence 552, App
984 29 64.4 1032 4 US-10-187-739-552 Sequence 552, App
985 29 64.4 1032 4 US-10-206-907-552 Sequence 552, App
986 29 64.4 1032 4 US-10-088-567-2 Sequence 2, Appli
987 29 64.4 1032 4 US-10-088-567-4 Sequence 4, Appli
988 29 64.4 1032 4 US-10-183-009-552 Sequence 552, App
989 29 64.4 1032 4 US-10-187-755-552 Sequence 552, App
990 29 64.4 1032 4 US-10-272-502A-7 Sequence 7, Appli
991 29 64.4 1032 4 US-10-272-502A-9 Sequence 9, Appli
992 29 64.4 1032 4 US-10-199-672-552 Sequence 552, App
993 29 64.4 1032 4 US-10-187-749-552 Sequence 552, App
994 29 64.4 1032 4 US-10-194-457-552 Sequence 552, App
995 29 64.4 1032 4 US-10-184-642-552 Sequence 552, App
996 29 64.4 1032 4 US-10-196-747-552 Sequence 552, App
997 29 64.4 1032 4 US-10-265-072-6 Sequence 6, Appli
998 29 64.4 1032 4 US-10-265-072-8 Sequence 8, Appli
999 29 64.4 1032 4 US-10-173-689-552 Sequence 552, App
1000 29 64.4 1032 4 US-10-173-690-552 Sequence 552, App

ALIGNMENTS

RESULT 1
US-09-870-216C-9
; Sequence 9, Application US/09870216C
; Publication No. US20040138135A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881210100
; CURRENT APPLICATION NUMBER: US/09/870,216C
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/209,391
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/226,256
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/257,008
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-216C-9

Query Match 100.0%; Score 45; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
|:|||||
Db 1 FLSYDLFVV 9

RESULT 2
US-10-017-327-9
; Sequence 9, Application US/10017327
; Publication No. US20020155471A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND
; TITLE OF INVENTION: METHODS FOR USING SAME
; FILE REFERENCE: GZ 2101.20
; CURRENT APPLICATION NUMBER: US/10/017,327
; CURRENT FILING DATE: 2001-12-06

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-327-9

Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
|:|||||
Db 1 FLSYDLFVV 9

RESULT 3
US-09-833-245-2059
; Sequence 2059, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2059
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-2059

Query Match 80.0%; Score 36; DB 3; Length 51;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
|:|||||
Db 7 FVSVDYFIV 15

RESULT 4
US-10-060-255-62
; Sequence 62, Application US/10060255
; Publication No. US20030113840A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 25 Human secreted proteins
; FILE REFERENCE: PZ042P1
; CURRENT APPLICATION NUMBER: US/10/060,255
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/781,417
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/22325
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/149,182
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-255-62
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Query Match 80.0%; Score 36; DB 4; Length 51;  
Best Local Similarity 66.7%; Pred. No. 22;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLSYDLFW 9  
|:|:|:|:|:  
Db 7 FVSYDYFV 15

RESULT 5  
US-10-881-088-62  
; Sequence 62, Application US/10881088  
; Publication No. US20040241803A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 25 Human secreted proteins  
; FILE REFERENCE: P2043P1  
; CURRENT APPLICATION NUMBER: US/10/881,088  
; CURRENT FILING DATE: 2004-07-01  
; PRIOR APPLICATION NUMBER: US/09/781,417  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US00/22325  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: 60/149,182  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 62  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-881-088-62

Query Match 80.0%; Score 36; DB 5; Length 51;  
Best Local Similarity 66.7%; Pred. No. 22;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLSYDLFW 9  
|:|:|:|:|:  
Db 7 FVSYDYFV 15

RESULT 6  
US-09-729-674-16  
; Sequence 16, Application US/09729674  
; Patent No. US20010039335A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steininger II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 6055-64X  
; CURRENT APPLICATION NUMBER: US/09/729,674  
; CURRENT FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 09/539,330  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 283  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 130  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-729-674-16

Query Match 77.8%; Score 35; DB 3; Length 130;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFW 8  
|:|:|:|:|:  
Db 18 LSYDLFW 24

RESULT 7  
US-10-913-553-16  
; Sequence 16, Application US/10913553  
; Publication No. US20050003491A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steininger II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 6055-64X  
; CURRENT APPLICATION NUMBER: US/10/913,553  
; CURRENT FILING DATE: 2004-08-09  
; PRIOR APPLICATION NUMBER: US/09/539,330  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 283  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-913-553-16

Query Match 77.8%; Score 35; DB 5; Length 130;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFW 8  
|:|:|:|:|:  
Db 18 LSYDLFW 24

RESULT 8  
US-09-978-360A-732  
; Sequence 732, Application US/09978360A  
; Publication No. US20040110939A1  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; APPLICANT: Clusel, Catherine  
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
; FILE REFERENCE: 56.US4.CIP  
; CURRENT APPLICATION NUMBER: US/09/978,360A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: US 60/074,121

; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: US 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: US 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: US 60/099,273  
; PRIOR FILING DATE: -09-04  
; PRIOR APPLICATION NUMBER: US 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: US 09/215,435  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: PCT/IB98/02122  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: US 09/247,155  
; PRIOR FILING DATE: 1998-02-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 810  
; SOFTWARE: Patent.pm  
; SEQ ID NO 732  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -94...-1  
US-09-978-360A-732

Query Match 77.8%; Score 35; DB 3; Length 162;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24

RESULT 9  
US-10-319-763-126  
; Sequence 126, Application US/10319763  
; Publication No. US2003014490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bouquelert, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: G-031.US04.DIV  
; CURRENT APPLICATION NUMBER: US/10/319,763  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent.pm  
; SEQ ID NO 126  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -21...-1  
US-10-319-763-126

Query Match 77.8%; Score 35; DB 4; Length 162;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24

RESULT 10  
US-10-319-763-220  
; Sequence 220, Application US/10319763  
; Publication No. US2003014490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bouquelert, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: G-031.US04.DIV  
; CURRENT APPLICATION NUMBER: US/10/319,763  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent.pm  
; SEQ ID NO 220  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -94...-1  
US-10-319-763-220

Query Match 77.8%; Score 35; DB 4; Length 162;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24

RESULT 11  
US-10-170-385-53  
; Sequence 53, Application US/10170385  
; Publication No. US20030203372A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Neil Raymond  
; APPLICANT: Mundy, Christopher Robert  
; APPLICANT: Kan, On  
; APPLICANT: Harris, Robert Alan  
; APPLICANT: White, Jonathan  
; APPLICANT: Binley, Katie Mary  
; APPLICANT: Rayner, William Nigel  
; APPLICANT: Naylor, Stuart  
; APPLICANT: Kingsman, Susan Mary  
; APPLICANT: Krige, David  
; TITLE OF INVENTION: ANALYSIS METHOD  
; FILE REFERENCE: 532682000100  
; CURRENT APPLICATION NUMBER: US/10/170,385  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: PCT/GB02/01662  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: PCT/GB01/05458

; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 549  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-170-385-53

Query Match 77.8%; Score 35; DB 4; Length 162;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
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RESULT 12  
US-10-264-237-1995  
; Sequence 1995, Application US/10264237  
; Publication No. US2004009491A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 6/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 1995  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-237-1995

Query Match 77.8%; Score 35; DB 4; Length 162;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
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RESULT 13  
US-09-809-391-462  
; Sequence 462, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 462  
; LENGTH: 163  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (163)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-809-391-462

Query Match 77.8%; Score 35; DB 3; Length 163;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
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RESULT 14  
US-09-882-171-462  
; Sequence 462, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,334  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,336  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/047,600  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,615  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,597  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,502  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,633  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,583  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,617  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,618  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,503  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,592  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,581  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,584  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,500  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,587  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,492  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,598  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,613  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,582

; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,596  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,612  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,632  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,601  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,580  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,568  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,314  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,569  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,311  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,671  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,674  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,669  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,312  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,313  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,672  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,315  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,877  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,889  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,893  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,630  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,878  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,662  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,872  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,882  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,637  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,903  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,888  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,879  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,880  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,894  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,911  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,874  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,910  
; PRIOR FILING DATE: 1997-08-22

; PRIOR APPLICATION NUMBER: 60/056,864  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,631  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,761  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/047,595  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,599  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,588  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,585  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,586  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,590  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,594  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,589  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,593  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,614  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,578  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/047,501  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/056,632  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,876  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,881  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,909  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,875  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,862  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,887  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,908  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,669  
; PRIOR FILING DATE: 1997-09-05

Query Match 77.8%; Score 35; DB 3; Length 163;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
Db 18 LSYDLFV 24  
|||||

RESULT 15  
US-10-164-861-462  
; Sequence 462, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/10/164,861  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 462  
; LENGTH: 163  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (163)  
; OTHER INFORMATION: Xaa equals stop translation  
US-10-164-861-462

Query Match 77.8%; Score 35; DB 4; Length 163;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
|:|:|:|:|  
DB 18 LSYDLFV 24

RESULT 16  
US-10-501-196-2  
; Sequence 2, Application US/10501196  
; Publication No. US20050164186A1  
; GENERAL INFORMATION:  
; APPLICANT: NEW ENGLAND BIOLABS, INC.  
; APPLICANT: SAMUELSON, JAMES  
; APPLICANT: XU, SHUANG-YONG  
; TITLE OF INVENTION: ALTERATION OF RESTRICTION ENDONUCLEASE SPECIFICITY BY GENETIC SE  
; FILE REFERENCE: NEB-198-PCT  
; CURRENT APPLICATION NUMBER: US/10/501,196  
; CURRENT FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US 60/347,403  
; PRIOR FILING DATE: 2002-01-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Bacillus stearothermophilus Y406  
US-10-501-196-2

Query Match 77.8%; Score 35; DB 5; Length 203;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
|:|:|:|:|  
DB 136 FVAYDLFV 143

RESULT 17  
US-09-867-550-916  
; Sequence 916, Application US/09867550  
; Patent No. US20020082206A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.

; APPLICANT: Mehraban, Fuad,  
; APPLICANT: Conley, Pamela  
; APPLICANT: Law, Debbie  
; APPLICANT: Topper, James  
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and  
; FILE REFERENCE: 21402-013 (Cura-313)  
; CURRENT APPLICATION NUMBER: US/09/867,550  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: USSN 60/208,427  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 2125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 916  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-867-550-916

Query Match 75.6%; Score 34; DB 3; Length 55;  
Best Local Similarity 77.8%; Pred. No. 56;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
|:|:|:|:|  
DB 16 FLSLDLFLV 24

RESULT 18  
US-10-424-599-175697  
; Sequence 175697, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 175697  
; LENGTH: 66  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_129672C.1.pep  
US-10-424-599-175697

Query Match 75.6%; Score 34; DB 4; Length 66;  
Best Local Similarity 66.7%; Pred. No. 67;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
|:|:|:|:|  
DB 30 FKXNDMEV 38

RESULT 19  
US-10-106-698-4683  
; Sequence 4683, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137

; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 4683  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-106-698-4683

Query Match 75.6%; Score 34; DB 4; Length 98;  
Best Local Similarity 77.8%; Pred. No. 98;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLSYDLFVW 9  
Db 16 FLSLDFVL 24  
|||||:

RESULT 20  
US-10-108-260A-3015  
; Sequence 3015, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3015  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-3015

Query Match 75.6%; Score 34; DB 4; Length 247;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLSYDLFVW 9  
Db 47 FLSFLMWI 55  
|||||:

RESULT 21  
US-10-424-599-217530  
; Sequence 217530, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 217530  
; LENGTH: 346  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MBT3847\_38457C.1.pcp  
US-10-424-599-217530

Query Match 75.6%; Score 34; DB 4; Length 346;  
Best Local Similarity 77.8%; Pred. No. 3.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLSYDLFVW 9  
Db 293 FLSYELHVW 301  
|||||:

RESULT 22  
US-09-882-227-396  
; Sequence 396, Application US/09882227  
; Publication No. US20030158396A1  
; GENERAL INFORMATION:  
; APPLICANT: Kleanthous, Harold  
; APPLICANT: Al-Garawi, Amal  
; APPLICANT: Miller, Charles  
; APPLICANT: Tomb, Jean-Francois  
; APPLICANT: Ooomen, Raymond P.  
; TITLE OF INVENTION: Identification of Polynucleotides  
; TITLE OF INVENTION: Encoding No. US20030158396A1el Helicobacter Polypeptides in the  
; FILE REFERENCE: 06132/047002  
; CURRENT APPLICATION NUMBER: US/09/882,227  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 08/902,615  
; PRIOR FILING DATE: 1997-07-29  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 396  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Helicobacter pylori  
US-09-882-227-396

Query Match 75.6%; Score 34; DB 3; Length 412;  
Best Local Similarity 77.8%; Pred. No. 4.1e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLSYDLFVW 9  
Db 253 FLSKDFVW 261  
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RESULT 23  
US-10-732-923-11374  
; Sequence 11374, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 11374  
; LENGTH: 516  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-732-923-11374

Query Match 75.6%; Score 34; DB 5; Length 516;  
Best Local Similarity 85.7%; Pred. No. 5.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYDLFVW 9  
Db 37 SYDLFVI 43  
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RESULT 24  
US-10-108-260A-3829  
; Sequence 3829, Application US/10108260A  
; Publication No. US20040005560A1



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; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560a1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3829
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-108-260A-3829

Query Match          75.6%; Score 34; DB 4; Length 576;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
   |||:| |
Db 376 FLSFDLMVI 384

RESULT 25
US-10-094-749-2686
; Sequence 2686, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2686
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-094-749-2686

Query Match          75.6%; Score 34; DB 4; Length 674;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
   |||:| |
Db 474 FLSFDLMVI 482

RESULT 26
US-10-424-599-278654
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; Sequence 278654, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278654
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(56)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93647C.1.pep
; US-10-424-599-278654

Query Match          73.3%; Score 33; DB 4; Length 56;
Best Local Similarity 77.8%; Pred. No. 87;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
   |||:| |
Db 4 FLSYELSVV 12

RESULT 27
US-10-424-599-284635
; Sequence 284635, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284635
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99050C.1.pep
; US-10-424-599-284635

Query Match          73.3%; Score 33; DB 4; Length 67;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
   |||:| |
Db 15 FLSYELSVV 23

RESULT 28
US-10-425-115-318398
; Sequence 318398, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 318398  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MPT4577\_53454C.1.pcp  
US-10-425-115-318398

Query Match 73.3%; Score 33; DB 4; Length 88;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
|::||| |::  
Db 37 FLYDTFII 45

RESULT 29  
US-10-425-115-195354  
; Sequence 195354, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 195354  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MPT4577\_109751C.1.pcp  
US-10-425-115-195354

Query Match 73.3%; Score 33; DB 4; Length 100;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7  
||| |  
Db 15 FLYQDLF 21

RESULT 30  
US-10-083-357-691  
; Sequence 691, Application US/10083357  
; Publication No. US20030054370A1  
; GENERAL INFORMATION:  
; APPLICANT: Qiangdong Zeng et al.  
; TITLE OF INVENTION: Systemic Discovery of New Genes  
; FILE REFERENCE: 032796-090  
; CURRENT APPLICATION NUMBER: US/10/083,357  
; CURRENT FILING DATE: 2002-02-27  
; NUMBER OF SEQ ID NOS: 1346  
; SEQ ID NO 691  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-083-357-691

Query Match 73.3%; Score 33; DB 4; Length 211;  
Best Local Similarity 75.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 9  
||||| |  
Db 20 LSYDLFLL 27

RESULT 31  
US-10-732-923-11305  
; Sequence 11305, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 11305  
; LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-732-923-11305

Query Match 73.3%; Score 33; DB 5; Length 274;  
Best Local Similarity 71.4%; Pred. No. 4.2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFV 9  
||||| |  
Db 59 SYDLFII 65

RESULT 32  
US-10-732-923-11303  
; Sequence 11303, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 11303  
; LENGTH: 559  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-732-923-11303

Query Match 73.3%; Score 33; DB 5; Length 559;  
Best Local Similarity 71.4%; Pred. No. 8.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFV 9  
||||| |  
Db 57 SYDLFII 63

RESULT 33  
US-10-732-923-11301  
; Sequence 11301, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 11301  
; LENGTH: 572  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-732-923-11301

Query Match 73.3%; Score 33; DB 5; Length 572;  
Best Local Similarity 71.4%; Pred. No. 8.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
Db 59 SYDLFII 65

## RESULT 34

US-10-369-493-2314  
; Sequence 2314, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 2314  
; LENGTH: 573  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-2314

Query Match 73.3%; Score 33; DB 4; Length 573;  
Best Local Similarity 71.4%; Pred. No. 8.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
Db 59 SYDLFII 65

## RESULT 35

US-10-369-493-2320  
; Sequence 2320, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 2320

; LENGTH: 573  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-2320

Query Match 73.3%; Score 33; DB 4; Length 573;  
Best Local Similarity 71.4%; Pred. No. 8.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
Db 59 SYDLFII 65

## RESULT 36

US-10-732-923-11302  
; Sequence 11302, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 11302  
; LENGTH: 573  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-732-923-11302

Query Match 73.3%; Score 33; DB 5; Length 573;  
Best Local Similarity 71.4%; Pred. No. 8.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
Db 59 SYDLFII 65

## RESULT 37

US-10-369-493-22678  
; Sequence 22678, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22678  
; LENGTH: 583  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-22678

Query Match 73.3%; Score 33; DB 4; Length 583;  
Best Local Similarity 71.4%; Pred. No. 8.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
Db 53 SYDLFII 59

```

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206659
; LENGTH: 1507
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28640C.1.pap
US-10-424-599-206659

Query Match      73.3%; Score 33; DB 4; Length 1507;
Best Local Similarity 55.6%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLSYDLFVV 9
      :|||||:
Db      824 YLDYDMFVL 832

RESULT 41
US-10-437-963-177564
; Sequence 177564, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 177564
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_75202C.1.pap
US-10-437-963-177564

Query Match      71.1%; Score 32; DB 4; Length 62;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LSYDLFV 8
      :|||||:
Db      40 LSYDLFL 46

RESULT 42
US-10-425-115-256908
; Sequence 256908, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256908

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206656
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28638C.1.pap
US-10-424-599-206656

Query Match      73.3%; Score 33; DB 4; Length 839;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLSYDLFVV 9
      :|||||:
Db      286 YLDYDMFVL 294

RESULT 40
US-10-424-599-206659
; Sequence 206659, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

```
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(80)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165889C.1.pep
US-10-425-115-256908

Query Match          71.1%; Score 32; DB 4; Length 80;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFW 9
Db 70 YMSYHLFIV 78

RESULT 43
US-10-424-599-147896
; Sequence 147896, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 147896
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104572C.1.pep
US-10-424-599-147896

Query Match          71.1%; Score 32; DB 4; Length 153;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLF 7
Db 47 FLSHDLF 53

RESULT 44
US-10-156-761-8778
; Sequence 8778, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
```

```
; SEQ ID NO 8778
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8778

Query Match          71.1%; Score 32; DB 4; Length 165;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7
Db 46 FLRYDLF 52

RESULT 45
US-10-336-603A-52
; Sequence 52, Application US/10336603A
; Publication No. US20040072997A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
; FILE REFERENCE: 21402-533A
; CURRENT APPLICATION NUMBER: US/10/336,603A
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: 09/746,491
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 10/055,569
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 52
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-336-603A-52

Query Match          71.1%; Score 32; DB 4; Length 265;
Best Local Similarity 55.6%; Pred. No. 6.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9
Db 219 YMSYHLFIV 227

RESULT 46
US-09-778-927A-64
; Sequence 64, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(279)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-64
```

Query Match 71.1%; Score 32; DB 3; Length 279;  
Best Local Similarity 55.6%; Pred. No. 6.5e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
::|||::|  
Db 233 YMSYHLFIV 241

RESULT 47  
US-10-336-603A-48  
; Sequence 48, Application US/10336603A  
; Publication No. US20040072997A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-533A  
; CURRENT APPLICATION NUMBER: US/10/336,603A  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: 09/746,491  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 10/055,569  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 48  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-336-603A-48

Query Match 71.1%; Score 32; DB 4; Length 288;  
Best Local Similarity 55.6%; Pred. No. 6.7e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
::|||::|  
Db 219 YMSYHLFIV 227

RESULT 48  
US-10-437-963-131686  
; Sequence 131686, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 131686  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_33729C.1.pep  
US-10-437-963-131686

Query Match 71.1%; Score 32; DB 4; Length 291;  
Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
| ||||::

Db 23 FVSYDLXI 30

RESULT 49  
US-10-336-603A-46  
; Sequence 46, Application US/10336603A  
; Publication No. US20040072997A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-533A  
; CURRENT APPLICATION NUMBER: US/10/336,603A  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: 09/746,491  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 10/055,569  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 46  
; LENGTH: 305  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-336-603A-46

Query Match 71.1%; Score 32; DB 4; Length 305;  
Best Local Similarity 55.6%; Pred. No. 7.1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
::|||::|  
Db 259 YMSYHLFIV 267

RESULT 50  
US-10-739-930-6831  
; Sequence 6831, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 6831  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Brassica napus  
; FEATURE:  
; OTHER INFORMATION: Clone ID: BRANA-23APR03-C10529\_1.p  
US-10-739-930-6831

Query Match 71.1%; Score 32; DB 5; Length 313;  
Best Local Similarity 85.7%; Pred. No. 7.3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
|:||||  
Db 171 LNYDLFV 177

Search completed: May 9, 2006, 02:35:03  
Job time : 96.8 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:28:58 ; Search time 12.8 Seconds  
(without alignments)  
32.544 Million cell updates/sec

Title: US-09-870-216C-9

Perfect score: 45

Sequence: 1 FLSYDLFVV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA.New.\*

- 1: /SIDSS/ptodata/2/pubpaa/US06\_NEW\_PUB.pep1.\*
- 2: /SIDSS/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /SIDSS/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /SIDSS/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /SIDSS/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 6: /SIDSS/ptodata/2/pubpaa/US03\_NEW\_PUB.pep1.\*
- 7: /SIDSS/ptodata/2/pubpaa/US09\_NEW\_PUB.pep1.\*
- 8: /SIDSS/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 9: /SIDSS/ptodata/2/pubpaa/US10\_NEW\_PUB.pep1.\*
- 10: /SIDSS/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 11: /SIDSS/ptodata/2/pubpaa/US11\_NEW\_PUB.pep1.\*
- 12: /SIDSS/ptodata/2/pubpaa/US60\_NEW\_PUB.pep1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	35	77.8	162	7	US-09-378-360A-732
3	35	77.8	163	11	US-11-144-947-462
4	34	75.6	280	11	US-11-188-298-934
5	34	75.6	313	11	US-11-188-298-10140
6	34	75.6	347	11	US-11-188-298-19812
7	34	75.6	382	11	US-11-188-298-845
8	34	75.6	516	11	US-11-188-298-15430
9	33	73.3	237	11	US-11-188-298-13289
10	33	73.3	238	11	US-11-188-298-14738
11	33	73.3	274	11	US-11-188-298-5952
12	33	73.3	559	11	US-11-188-298-4981
13	33	73.3	572	11	US-11-188-298-4278
14	33	73.3	573	11	US-11-188-298-14889
15	33	73.3	583	11	US-11-188-298-22471
16	32	71.1	865	9	US-10-467-962B-33
17	32	71.1	1038	11	US-11-096-568A-31273
18	32	71.1	1158	11	US-11-096-568A-31272
19	32	71.1	1549	11	US-11-096-568A-31271
20	31	68.9	275	9	US-10-485-517-347
21	31	68.9	284	9	US-10-703-799B-188
22	31	68.9	312	11	US-11-188-298-5816
23	31	68.9	357	11	US-11-108-088-62
24	31	68.9	441	11	US-11-188-298-17875
25	31	68.9	472	11	US-11-008-331-3
26	31	68.9	627	11	US-11-079-463-6971
27	30	66.7	81	11	US-11-079-463-8050
28	30	66.7	102	11	US-11-096-568A-14201
29	30	66.7	106	11	US-11-096-568A-14200
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35	30	66.7	334	11	US-11-165-226-63
36	30	66.7	392	11	US-11-079-463-7885
37	30	66.7	413	11	US-11-079-463-10384
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39	30	66.7	467	11	US-11-188-298-6866
40	30	66.7	471	11	US-11-188-298-16982
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93	29	64.4	1206	11	US-11-096-568A-31287
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96	29	64.4	1336	9	US-10-912-971-10	Sequence 10, Appl	169	28	62.2	680	11	US-11-245-400-27	Sequence 27, Appl
97	28	62.2	161	9	US-10-487-468A-6	Sequence 6, Appl	170	28	62.2	684	11	US-11-188-298-18036	Sequence 18036, A
98	28	62.2	166	11	US-11-087-099-10258	Sequence 10258, A	171	28	62.2	701	11	US-11-188-298-20373	Sequence 20373, A
99	28	62.2	178	9	US-10-793-626-1176	Sequence 1176, Ap	172	28	62.2	739	11	US-11-188-189-12	Sequence 12, Appl
100	28	62.2	196	11	US-11-087-099-8913	Sequence 8913, Ap	173	28	62.2	812	11	US-11-051-720-1339	Sequence 1339, Ap
101	28	62.2	224	11	US-11-087-099-7035	Sequence 7035, Ap	174	28	62.2	886	9	US-10-821-234-1329	Sequence 1329, Ap
102	28	62.2	224	11	US-11-087-099-11763	Sequence 11763, A	175	28	62.2	892	11	US-11-079-463-8461	Sequence 8461, Ap
103	28	62.2	225	11	US-11-087-099-9680	Sequence 9680, Ap	176	28	62.2	907	11	US-11-079-463-8461	Sequence 1337, Ap
104	28	62.2	225	11	US-11-087-099-10176	Sequence 10176, A	177	28	62.2	919	11	US-11-051-720-1336	Sequence 1336, Ap
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106	28	62.2	233	11	US-11-202-507A-1	Sequence 1, Appl	179	28	62.2	931	11	US-11-051-720-1437	Sequence 1437, Ap
107	28	62.2	233	11	US-11-202-507A-3	Sequence 3, Appl	180	28	62.2	1076	11	US-11-109-157A-5	Sequence 5, Appl
108	28	62.2	242	11	US-11-096-568A-236	Sequence 236, App	181	28	62.2	1686	11	US-11-109-157A-1	Sequence 1, Appl
109	28	62.2	277	11	US-11-108-172-693	Sequence 693, App	182	28	62.2	1686	11	US-11-226-701-2	Sequence 2, Appl
110	28	62.2	290	11	US-11-045-004-1481	Sequence 1481, Ap	183	28	62.2	1907	11	US-11-039-398-25	Sequence 25, Appl
111	28	62.2	294	11	US-11-045-004-1428	Sequence 1428, Ap	184	27	60.0	9	9	US-10-530-061-367	Sequence 367, App
112	28	62.2	310	11	US-11-087-099-5412	Sequence 5412, Ap	185	27	60.0	9	11	US-11-026-403-25	Sequence 25, Appl
113	28	62.2	318	9	US-10-793-626-3118	Sequence 3118, Ap	186	27	60.0	10	9	US-10-530-061-690	Sequence 690, App
114	28	62.2	340	11	US-11-096-568A-235	Sequence 235, App	187	27	60.0	15	9	US-10-530-061-2103	Sequence 2103, Ap
115	28	62.2	340	11	US-11-096-568A-237	Sequence 237, App	188	27	60.0	15	9	US-10-530-061-2104	Sequence 2104, Ap
116	28	62.2	344	11	US-11-188-298-12614	Sequence 12614, A	189	27	60.0	43	9	US-10-982-727-76	Sequence 76, Appl
117	28	62.2	345	11	US-11-096-568A-234	Sequence 234, App	190	27	60.0	44	9	US-10-982-727-75	Sequence 75, Appl
118	28	62.2	374	11	US-11-188-298-16425	Sequence 16425, A	191	27	60.0	47	9	US-10-467-657-2746	Sequence 2746, Ap
119	28	62.2	376	11	US-11-188-298-1996	Sequence 1996, Ap	192	27	60.0	75	11	US-11-264-096-516	Sequence 516, App
120	28	62.2	376	11	US-11-188-298-9945	Sequence 9945, Ap	193	27	60.0	102	11	US-11-096-568A-6875	Sequence 6875, Ap
121	28	62.2	383	11	US-11-188-298-21651	Sequence 21651, A	194	27	60.0	108	11	US-11-045-004-665	Sequence 665, App
122	28	62.2	385	11	US-11-079-463-6139	Sequence 6139, Ap	195	27	60.0	119	9	US-10-956-008-74	Sequence 74, Appl
123	28	62.2	391	11	US-11-072-512-2353	Sequence 2353, Ap	196	27	60.0	131	9	US-10-793-626-52	Sequence 52, Appl
124	28	62.2	398	11	US-11-079-463-6994	Sequence 6994, Ap	197	27	60.0	131	9	US-10-793-626-738	Sequence 738, App
125	28	62.2	397	9	US-10-793-626-1244	Sequence 1244, Ap	198	27	60.0	135	11	US-11-098-686-11098	Sequence 11098, A
126	28	62.2	407	9	US-10-873-628-14	Sequence 14, Appl	199	27	60.0	137	11	US-11-045-004-1233	Sequence 1233, Ap
127	28	62.2	416	11	US-11-188-298-4739	Sequence 4739, Ap	200	27	60.0	138	9	US-10-511-130-32	Sequence 32, Appl
128	28	62.2	416	11	US-11-188-298-12806	Sequence 12806, A	201	27	60.0	142	9	US-10-856-751-37	Sequence 37, Appl
129	28	62.2	416	11	US-11-188-298-19453	Sequence 19453, A	202	27	60.0	143	9	US-10-467-657-1802	Sequence 1802, Ap
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131	28	62.2	426	11	US-11-188-298-13376	Sequence 13376, A	204	27	60.0	157	11	US-11-123-241-32	Sequence 32, Appl
132	28	62.2	428	9	US-10-485-517-371	Sequence 371, App	205	27	60.0	163	11	US-11-096-568A-21919	Sequence 21919, A
133	28	62.2	498	11	US-11-079-463-6018	Sequence 6018, Ap	206	27	60.0	174	11	US-11-079-463-9631	Sequence 9631, Ap
134	28	62.2	499	11	US-11-188-298-19084	Sequence 19084, A	207	27	60.0	186	9	US-10-980-388-105	Sequence 105, App
135	28	62.2	505	9	US-10-194-487-450	Sequence 450, App	208	27	60.0	201	11	US-11-082-389-138	Sequence 138, App
136	28	62.2	505	9	US-10-195-883-450	Sequence 450, App	209	27	60.0	211	11	US-11-274-910-34	Sequence 34, Appl
137	28	62.2	505	9	US-10-195-888-450	Sequence 450, App	210	27	60.0	214	11	US-11-079-463-7410	Sequence 7410, Ap
138	28	62.2	505	9	US-10-195-888-450	Sequence 450, App	211	27	60.0	215	11	US-11-096-568A-30243	Sequence 30243, A
139	28	62.2	506	11	US-11-188-298-13908	Sequence 13908, A	212	27	60.0	220	11	US-11-096-568A-18400	Sequence 18400, A
140	28	62.2	506	11	US-11-188-298-17812	Sequence 17812, A	213	27	60.0	224	11	US-11-096-568A-18399	Sequence 18399, A
141	28	62.2	512	9	US-10-242-586-110	Sequence 110, App	214	27	60.0	235	11	US-11-096-568A-9710	Sequence 9710, Ap
142	28	62.2	512	9	US-10-242-902-110	Sequence 110, App	215	27	60.0	236	11	US-11-096-568A-9709	Sequence 9709, Ap
143	28	62.2	512	9	US-10-243-116-110	Sequence 110, App	216	27	60.0	240	11	US-11-197-488-35	Sequence 35, Appl
144	28	62.2	512	9	US-10-243-136-110	Sequence 110, App	217	27	60.0	243	9	US-10-467-657-310	Sequence 310, App
145	28	62.2	512	9	US-10-243-189-110	Sequence 110, App	218	27	60.0	248	11	US-11-096-568A-9708	Sequence 9708, Ap
146	28	62.2	512	9	US-10-243-215-110	Sequence 110, App	219	27	60.0	251	9	US-10-467-657-608	Sequence 608, App
147	28	62.2	512	9	US-10-243-236-110	Sequence 110, App	220	27	60.0	255	11	US-11-197-488-37	Sequence 37, Appl
148	28	62.2	512	9	US-10-243-298-110	Sequence 110, App	221	27	60.0	260	11	US-11-197-488-39	Sequence 39, Appl
149	28	62.2	512	9	US-10-243-304-110	Sequence 110, App	222	27	60.0	261	11	US-11-096-568A-30242	Sequence 30242, A
150	28	62.2	512	9	US-10-243-338-110	Sequence 110, App	223	27	60.0	263	9	US-10-510-386-234	Sequence 234, App
151	28	62.2	512	9	US-10-243-345-110	Sequence 110, App	224	27	60.0	282	11	US-11-096-568A-32848	Sequence 32848, A
152	28	62.2	512	9	US-10-243-357-110	Sequence 110, App	225	27	60.0	284	11	US-11-096-568A-14948	Sequence 14948, A
153	28	62.2	512	9	US-10-245-083-110	Sequence 110, App	226	27	60.0	296	9	US-10-793-626-1674	Sequence 1674, Ap
154	28	62.2	512	9	US-10-247-015-110	Sequence 110, App	227	27	60.0	297	11	US-11-096-568A-17245	Sequence 17245, A
155	28	62.2	512	11	US-11-108-172-1093	Sequence 1093, Ap	228	27	60.0	315	9	US-10-878-556A-178	Sequence 178, App
156	28	62.2	521	11	US-11-188-298-19470	Sequence 19470, A	229	27	60.0	316	9	US-10-455-772-314	Sequence 314, App
157	28	62.2	557	11	US-11-087-099-3168	Sequence 3168, Ap	230	27	60.0	316	11	US-11-190-188-18	Sequence 18, Appl
158	28	62.2	563	11	US-11-188-298-22102	Sequence 22102, A	231	27	60.0	324	9	US-10-455-772-312	Sequence 312, Appl
159	28	62.2	568	11	US-11-188-298-2609	Sequence 2609, Ap	232	27	60.0	324	9	US-10-455-772-318	Sequence 318, App
160	28	62.2	568	11	US-11-188-298-2613	Sequence 2613, Ap	233	27	60.0	324	9	US-10-455-772-320	Sequence 320, App
161	28	62.2	574	11	US-11-188-298-1848	Sequence 1848, Ap	234	27	60.0	324	9	US-10-455-772-322	Sequence 322, App
162	28	62.2	575	11	US-11-188-298-17885	Sequence 17885, A	235	27	60.0	327	9	US-10-467-657-2408	Sequence 2408, Ap
163	28	62.2	577	11	US-11-188-298-753	Sequence 753, App	236	27	60.0	328	11	US-11-096-568A-20428	Sequence 20428, A
164	28	62.2	587	11	US-11-188-298-296	Sequence 296, App	237	27	60.0	332	9	US-10-455-772-316	Sequence 316, App
165	28	62.2	599	11	US-11-109-157A-3	Sequence 3, Appl	238	27	60.0	333	9	US-10-821-234-1036	Sequence 1036, Ap
166	28	62.2	649	11	US-11-109-157A-7	Sequence 7, Appl	239	27	60.0	333	11	US-11-096-568A-14947	Sequence 14947, A
167	28	62.2	671	11	US-11-202-507A-14	Sequence 14, Appl	240	27	60.0	334	11	US-11-096-568A-20427	Sequence 20427, A



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243	27	60.0	345	11	US-11-096-568A-32847	Sequence 32847, A	316	27	60.0	590	11	US-11-299-182-22	Sequence 22, Appl
244	27	60.0	364	9	US-10-995-561-699	Sequence 699, App	317	27	60.0	592	9	US-10-840-688-22	Sequence 22, Appl
245	27	60.0	367	11	US-11-045-004-1309	Sequence 1309, Ap	318	27	60.0	612	11	US-11-079-463-7921	Sequence 7921, Ap
246	27	60.0	377	11	US-11-096-568A-1804	Sequence 1804, Ap	319	27	60.0	616	11	US-11-155-452-3	Sequence 3, Appli
247	27	60.0	377	11	US-11-096-568A-27181	Sequence 27181, A	320	27	60.0	616	11	US-11-045-004-1213	Sequence 1213, Ap
248	27	60.0	378	11	US-11-096-568A-12553	Sequence 12553, A	321	27	60.0	627	11	US-11-079-463-8819	Sequence 8819, Ap
249	27	60.0	379	11	US-11-096-568A-26197	Sequence 26197, A	322	27	60.0	653	11	US-11-079-463-6965	Sequence 6965, Ap
250	27	60.0	380	11	US-11-096-568A-10708	Sequence 10708, A	323	27	60.0	708	11	US-11-174-150-25	Sequence 25, Appl
251	27	60.0	381	11	US-11-188-298-3140	Sequence 3140, Ap	324	27	60.0	735	11	US-11-188-298-19064	Sequence 19064, A
252	27	60.0	387	11	US-11-045-004-106	Sequence 106, App	325	27	60.0	736	11	US-11-174-150-26	Sequence 26, Appl
253	27	60.0	409	11	US-11-096-568A-7256	Sequence 7256, Ap	326	27	60.0	736	11	US-11-078-189-9	Sequence 9, Appli
254	27	60.0	410	11	US-11-096-568A-7255	Sequence 7255, Ap	327	27	60.0	816	9	US-10-216-161A-375	Sequence 375, App
255	27	60.0	418	11	US-11-096-568A-1803	Sequence 1803, Ap	328	27	60.0	816	11	US-11-188-298-8103	Sequence 8103, Ap
256	27	60.0	418	11	US-11-096-568A-27180	Sequence 27180, A	329	27	60.0	816	11	US-11-188-298-22193	Sequence 22193, A
257	27	60.0	421	11	US-11-096-568A-10707	Sequence 10707, A	330	27	60.0	852	9	US-10-645-441-15	Sequence 15, Appl
258	27	60.0	424	9	US-10-793-626-2756	Sequence 2756, Ap	331	27	60.0	852	9	US-10-725-475-7	Sequence 7, Appli
259	27	60.0	424	11	US-11-188-298-13015	Sequence 13015, A	332	27	60.0	852	11	US-11-050-804-6	Sequence 6, Appli
260	27	60.0	424	11	US-11-188-298-19444	Sequence 19444, A	333	27	60.0	858	9	US-10-645-441-18	Sequence 18, Appl
261	27	60.0	428	11	US-11-096-568A-7254	Sequence 7254, Ap	334	27	60.0	858	9	US-10-645-441-20	Sequence 20, Appl
262	27	60.0	443	11	US-11-188-298-11903	Sequence 11903, A	335	27	60.0	858	9	US-10-645-441-23	Sequence 23, Appl
263	27	60.0	447	11	US-11-096-568A-32846	Sequence 32846, A	336	27	60.0	858	9	US-10-645-441-25	Sequence 25, Appl
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265	27	60.0	451	11	US-11-087-099-4574	Sequence 4574, Ap	338	27	60.0	908	9	US-10-467-657-1070	Sequence 1070, Ap
266	27	60.0	453	11	US-11-087-099-8802	Sequence 8802, Ap	339	27	60.0	924	9	US-10-467-657-4290	Sequence 4290, Ap
267	27	60.0	453	11	US-11-188-298-21923	Sequence 21923, A	340	27	60.0	939	11	US-11-188-298-17641	Sequence 17641, A
268	27	60.0	456	11	US-11-188-298-11242	Sequence 11242, A	341	27	60.0	1006	9	US-10-793-626-154	Sequence 154, App
269	27	60.0	456	11	US-11-188-298-16609	Sequence 16609, A	342	27	60.0	1032	11	US-11-079-463-10074	Sequence 10074, A
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271	27	60.0	457	11	US-11-188-298-12706	Sequence 12706, A	344	27	60.0	1227	11	US-11-079-463-9512	Sequence 9512, Ap
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273	27	60.0	460	11	US-11-188-298-22519	Sequence 22519, A	346	26	57.8	22	11	US-11-155-164-1	Sequence 1, Appli
274	27	60.0	464	11	US-11-188-298-1372	Sequence 1372, Ap	347	26	57.8	33	9	US-10-467-657-8326	Sequence 8326, Ap
275	27	60.0	464	11	US-11-188-298-7589	Sequence 7589, Ap	348	26	57.8	120	9	US-10-982-440-47	Sequence 47, Appl
276	27	60.0	466	11	US-11-188-298-856	Sequence 856, App	349	26	57.8	123	9	US-10-980-388-72	Sequence 72, Appl
277	27	60.0	466	11	US-11-188-298-7618	Sequence 7618, Ap	350	26	57.8	149	9	US-10-530-253-18	Sequence 18, Appl
278	27	60.0	471	11	US-11-188-298-8321	Sequence 8321, Ap	351	26	57.8	169	11	US-11-188-298-5623	Sequence 5623, Ap
279	27	60.0	475	11	US-11-188-298-13871	Sequence 13871, A	352	26	57.8	169	11	US-11-188-298-5928	Sequence 5928, Ap
280	27	60.0	476	11	US-11-188-298-21620	Sequence 21620, A	353	26	57.8	174	9	US-10-980-388-88	Sequence 88, Appl
281	27	60.0	477	11	US-11-188-298-3156	Sequence 3156, Ap	354	26	57.8	178	9	US-10-467-657-2220	Sequence 2220, Ap
282	27	60.0	477	11	US-11-188-298-11172	Sequence 11172, A	355	26	57.8	179	11	US-11-188-298-5150	Sequence 5150, Ap
283	27	60.0	477	11	US-11-188-298-13574	Sequence 13574, A	356	26	57.8	192	9	US-10-506-454-436	Sequence 436, App
284	27	60.0	478	11	US-11-076-733-13	Sequence 13, Appl	357	26	57.8	192	11	US-11-079-463-6430	Sequence 6430, Ap
285	27	60.0	478	11	US-11-188-298-2074	Sequence 2074, Ap	358	26	57.8	192	11	US-11-188-298-20967	Sequence 20967, A
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289	27	60.0	487	11	US-11-076-733-15	Sequence 15, Appl	362	26	57.8	216	11	US-11-096-568A-9205	Sequence 9205, Ap
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291	27	60.0	506	11	US-11-188-298-19543	Sequence 19543, A	364	26	57.8	223	9	US-10-793-626-3078	Sequence 3078, Ap
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293	27	60.0	516	11	US-11-096-568A-1802	Sequence 1802, Ap	366	26	57.8	253	9	US-10-793-626-928	Sequence 928, App
294	27	60.0	516	11	US-11-096-568A-27179	Sequence 27179, A	367	26	57.8	253	9	US-10-793-626-1196	Sequence 1196, Ap
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296	27	60.0	519	11	US-11-096-568A-30772	Sequence 30772, A	369	26	57.8	254	11	US-11-266-444-1469	Sequence 1469, Ap
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298	27	60.0	521	11	US-11-188-298-18154	Sequence 18154, A	371	26	57.8	255	11	US-11-188-298-13975	Sequence 13975, A
299	27	60.0	521	11	US-11-188-298-19766	Sequence 19766, A	372	26	57.8	262	11	US-11-096-568A-9204	Sequence 9204, Ap
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303	27	60.0	524	11	US-11-188-298-19975	Sequence 19975, A	376	26	57.8	266	11	US-11-079-463-8657	Sequence 8657, Ap
304	27	60.0	524	11	US-11-188-298-21006	Sequence 21006, A	377	26	57.8	273	11	US-11-079-463-8657	Sequence 8657, Ap
305	27	60.0	529	11	US-11-033-039-487	Sequence 487, App	378	26	57.8	275	11	US-11-096-568A-17112	Sequence 17112, A
306	27	60.0	529	11	US-11-155-288-1	Sequence 1, Appli	379	26	57.8	276	9	US-10-873-528-134	Sequence 134, App
307	27	60.0	529	11	US-11-132-947-8	Sequence 8, Appli	380	26	57.8	286	11	US-11-057-012-93	Sequence 93, Appl
308	27	60.0	529	11	US-11-197-498-10	Sequence 10, Appl	381	26	57.8	287	11	US-11-096-568A-17110	Sequence 17110, A
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310	27	60.0	533	11	US-11-188-298-15389	Sequence 15389, A	383	26	57.8	291	11	US-11-045-004-391	Sequence 391, App
311	27	60.0	567	11	US-11-096-568A-30771	Sequence 30771, A	384	26	57.8	293	11	US-11-188-298-20182	Sequence 20182, A
312	27	60.0	574	11	US-11-079-463-5591	Sequence 5591, Ap	385	26	57.8	306	9	US-10-055-877-195	Sequence 195, App
313	27	60.0	577	11	US-11-082-389-134	Sequence 134, App	386	26	57.8	307	11	US-11-055-822-528	Sequence 528, App

387	26	57.8	311	11	US-11-188-298-10501	Sequence 10501, A	460	26	57.8	479	11	US-11-087-099-10492	Sequence 10492, A
388	26	57.8	318	11	US-11-058-924-8	Sequence 8, Appli	461	26	57.8	479	11	US-11-188-298-9712	Sequence 9712, Ap
389	26	57.8	318	11	US-11-096-568A-19733	Sequence 19733, A	462	26	57.8	480	11	US-11-188-298-2910	Sequence 2910, Ap
390	26	57.8	321	11	US-11-096-568A-19510	Sequence 19510, A	463	26	57.8	484	11	US-11-188-298-16845	Sequence 16845, A
391	26	57.8	325	9	US-10-506-454-447	Sequence 447, App	464	26	57.8	495	11	US-11-096-568A-31474	Sequence 31474, A
392	26	57.8	325	11	US-11-096-568A-19732	Sequence 19732, A	465	26	57.8	495	11	US-11-096-568A-33210	Sequence 33210, A
393	26	57.8	328	11	US-11-188-298-15447	Sequence 15447, A	466	26	57.8	499	11	US-11-096-568A-31473	Sequence 31473, A
394	26	57.8	329	11	US-11-087-099-2299	Sequence 2299, Ap	467	26	57.8	499	11	US-11-096-568A-33209	Sequence 33209, A
395	26	57.8	334	11	US-11-096-568A-19731	Sequence 19731, A	468	26	57.8	508	11	US-11-096-568A-22465	Sequence 22465, A
396	26	57.8	334	11	US-11-188-298-4714	Sequence 4714, Ap	469	26	57.8	509	11	US-11-188-298-3938	Sequence 3938, Ap
397	26	57.8	334	11	US-11-188-298-8278	Sequence 8278, Ap	470	26	57.8	515	9	US-10-507-720-49	Sequence 49, Appl
398	26	57.8	335	11	US-11-188-298-4341	Sequence 4341, Ap	471	26	57.8	517	9	US-10-506-454-1083	Sequence 1083, Ap
399	26	57.8	335	11	US-11-188-298-11669	Sequence 11669, A	472	26	57.8	521	11	US-11-188-298-9148	Sequence 9148, Ap
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402	26	57.8	348	9	US-10-195-883-94	Sequence 94, Appl	475	26	57.8	525	11	US-11-188-298-3920	Sequence 3920, Ap
403	26	57.8	348	9	US-10-195-888-94	Sequence 94, Appl	476	26	57.8	525	11	US-11-188-298-4941	Sequence 4941, Ap
404	26	57.8	348	9	US-10-195-889-94	Sequence 94, Appl	477	26	57.8	525	11	US-11-188-298-5543	Sequence 5543, Ap
405	26	57.8	348	9	US-10-216-161A-380	Sequence 380, App	478	26	57.8	525	11	US-11-188-298-11936	Sequence 11936, A
406	26	57.8	348	11	US-11-188-298-9636	Sequence 9636, Ap	479	26	57.8	525	11	US-11-188-298-14735	Sequence 14735, A
407	26	57.8	356	9	US-10-506-454-105	Sequence 105, App	480	26	57.8	525	11	US-11-188-298-20701	Sequence 20701, A
408	26	57.8	358	11	US-11-045-004-1787	Sequence 1787, Ap	481	26	57.8	525	11	US-11-188-298-21434	Sequence 21434, A
409	26	57.8	364	11	US-11-098-686-10327	Sequence 10327, A	482	26	57.8	526	11	US-11-188-298-5033	Sequence 5033, Ap
410	26	57.8	366	11	US-11-188-298-1792	Sequence 1792, Ap	483	26	57.8	526	11	US-11-188-298-6566	Sequence 6566, Ap
411	26	57.8	369	11	US-11-188-298-6906	Sequence 6906, Ap	484	26	57.8	526	11	US-11-188-298-8364	Sequence 8364, Ap
412	26	57.8	371	11	US-11-188-298-559	Sequence 559, App	485	26	57.8	526	11	US-11-188-298-18948	Sequence 18948, A
413	26	57.8	371	11	US-11-188-298-13966	Sequence 13966, A	486	26	57.8	526	11	US-11-188-298-20205	Sequence 20205, A
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415	26	57.8	379	11	US-11-188-298-6617	Sequence 6617, Ap	488	26	57.8	527	11	US-11-098-686-10494	Sequence 10494, A
416	26	57.8	382	11	US-11-079-463-8093	Sequence 8093, Ap	489	26	57.8	527	11	US-11-188-298-1546	Sequence 1546, Ap
417	26	57.8	386	11	US-11-188-298-2005	Sequence 2005, Ap	490	26	57.8	527	11	US-11-188-298-6052	Sequence 6052, Ap
418	26	57.8	387	11	US-11-079-463-6801	Sequence 6801, Ap	491	26	57.8	527	11	US-11-188-298-12326	Sequence 12326, A
419	26	57.8	387	11	US-11-188-298-5669	Sequence 5669, Ap	492	26	57.8	528	11	US-11-188-298-5387	Sequence 5387, Ap
420	26	57.8	388	11	US-11-188-298-7030	Sequence 7030, Ap	493	26	57.8	528	11	US-11-188-298-12286	Sequence 12286, A
421	26	57.8	390	11	US-11-188-298-3780	Sequence 3780, Ap	494	26	57.8	528	11	US-11-188-298-19860	Sequence 19860, A
422	26	57.8	390	11	US-11-188-298-6308	Sequence 6308, Ap	495	26	57.8	531	11	US-11-076-074-11	Sequence 11, Appl
423	26	57.8	390	11	US-11-188-298-7340	Sequence 7340, Ap	496	26	57.8	532	11	US-11-188-298-1854	Sequence 1854, Ap
424	26	57.8	390	11	US-11-188-298-9548	Sequence 9548, Ap	497	26	57.8	533	11	US-11-096-568A-14987	Sequence 14987, A
425	26	57.8	391	11	US-11-188-298-21687	Sequence 21687, A	498	26	57.8	533	11	US-11-188-298-618	Sequence 618, App
426	26	57.8	391	11	US-11-188-298-1549	Sequence 1549, Ap	499	26	57.8	533	11	US-11-188-298-2314	Sequence 2314, Ap
427	26	57.8	393	11	US-11-188-298-5111	Sequence 5111, Ap	500	26	57.8	534	11	US-11-188-298-10767	Sequence 10767, A
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430	26	57.8	396	11	US-11-188-298-3139	Sequence 3139, Ap	503	26	57.8	534	11	US-11-188-298-17428	Sequence 17428, A
431	26	57.8	396	11	US-11-188-298-5062	Sequence 5062, Ap	504	26	57.8	534	11	US-11-188-298-18905	Sequence 18905, A
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433	26	57.8	397	11	US-11-188-298-15977	Sequence 15977, A	506	26	57.8	535	11	US-11-188-298-6117	Sequence 6117, Ap
434	26	57.8	405	11	US-11-188-298-1876	Sequence 21876, A	507	26	57.8	535	11	US-11-188-298-13691	Sequence 13691, A
435	26	57.8	409	11	US-11-096-568A-19509	Sequence 19509, A	508	26	57.8	535	11	US-11-188-298-17170	Sequence 17170, A
436	26	57.8	414	11	US-11-096-568A-19508	Sequence 19508, A	509	26	57.8	535	11	US-11-188-298-18481	Sequence 18481, A
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438	26	57.8	430	11	US-11-096-568A-28190	Sequence 28190, A	511	26	57.8	536	11	US-11-076-074-2	Sequence 2, Appl
439	26	57.8	430	11	US-11-079-463-6976	Sequence 6976, Ap	512	26	57.8	536	11	US-11-188-298-12565	Sequence 12565, A
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441	26	57.8	437	11	US-11-045-004-756	Sequence 756, App	514	26	57.8	536	11	US-11-188-298-21419	Sequence 21419, A
442	26	57.8	442	11	US-11-096-568A-28189	Sequence 28189, A	515	26	57.8	537	11	US-11-188-298-17514	Sequence 17514, A
443	26	57.8	452	11	US-11-096-568A-28188	Sequence 28188, A	516	26	57.8	537	11	US-11-188-298-18313	Sequence 18313, A
444	26	57.8	454	11	US-11-096-568A-18178	Sequence 18178, A	517	26	57.8	537	11	US-11-188-298-20479	Sequence 20479, A
445	26	57.8	456	11	US-11-188-298-17994	Sequence 17994, A	518	26	57.8	537	11	US-11-188-298-22308	Sequence 22308, A
446	26	57.8	459	11	US-11-188-298-4044	Sequence 4044, Ap	519	26	57.8	538	11	US-11-188-298-13698	Sequence 13698, A
447	26	57.8	460	11	US-11-188-298-18177	Sequence 18177, A	520	26	57.8	538	11	US-11-188-298-16173	Sequence 16173, A
448	26	57.8	463	11	US-11-096-568A-14988	Sequence 14988, A	521	26	57.8	538	11	US-11-188-298-17860	Sequence 17860, A
449	26	57.8	465	11	US-11-082-389-284	Sequence 284, App	522	26	57.8	538	11	US-11-188-298-18680	Sequence 18680, A
450	26	57.8	469	9	US-10-793-626-2204	Sequence 2204, App	523	26	57.8	539	11	US-11-096-568A-22464	Sequence 22464, A
451	26	57.8	471	11	US-11-188-298-12279	Sequence 12279, A	524	26	57.8	539	11	US-11-188-298-1395	Sequence 1395, Ap
452	26	57.8	474	11	US-11-188-298-800	Sequence 800, App	525	26	57.8	539	11	US-11-188-298-6582	Sequence 6582, Ap
453	26	57.8	474	11	US-11-188-298-13296	Sequence 13296, A	526	26	57.8	539	11	US-11-188-298-8468	Sequence 8468, Ap
454	26	57.8	475	11	US-11-188-298-8902	Sequence 8902, Ap	527	26	57.8	539	11	US-11-188-298-11452	Sequence 11452, A
455	26	57.8	475	11	US-11-188-298-12536	Sequence 12536, A	528	26	57.8	539	11	US-11-188-298-14032	Sequence 14032, A
456	26	57.8	477	11	US-11-188-298-4271	Sequence 4271, Ap	529	26	57.8	539	11	US-11-188-298-20081	Sequence 20081, A
457	26	57.8	477	11	US-11-188-298-7305	Sequence 7305, Ap	530	26	57.8	540	11	US-11-079-463-9721	Sequence 9721, Ap
458	26	57.8	477	11	US-11-188-298-19121	Sequence 19121, A	531	26	57.8	540	11	US-11-188-298-2688	Sequence 2688, Ap
459	26	57.8	478	11	US-11-188-298-8782	Sequence 8782, Ap	532	26	57.8	540	11	US-11-188-298-10355	Sequence 10355, A

533	26	57.8	540	11	US-11-188-298-12453	Sequence 12453, A	606	26	57.8	1480	11	US-11-076-074-10	Sequence 10, Appl
534	26	57.8	540	11	US-11-188-298-13778	Sequence 19778, A	607	26	57.8	1482	11	US-11-181-330-2	Sequence 2, Appl
535	26	57.8	541	11	US-11-188-298-12545	Sequence 19778, A	608	26	57.8	1484	9	US-10-912-971-6	Sequence 6, Appl
536	26	57.8	541	11	US-11-188-298-12545	Sequence 5545, A	609	26	57.8	1484	11	US-11-181-330-6	Sequence 6, Appl
537	26	57.8	541	11	US-11-188-298-13712	Sequence 13712, A	610	25	56.7	590	11	US-11-188-298-8744	Sequence 8744, Ap
538	26	57.8	541	11	US-11-188-298-17156	Sequence 17156, A	611	25	55.6	10	9	US-10-530-061-518	Sequence 518, App
539	26	57.8	542	11	US-11-188-298-1634	Sequence 1634, Ap	612	25	55.6	10	9	US-10-530-061-519	Sequence 519, App
540	26	57.8	542	11	US-11-188-298-13845	Sequence 3845, Ap	613	25	55.6	15	9	US-10-530-061-1660	Sequence 1660, Ap
541	26	57.8	542	11	US-11-188-298-17077	Sequence 17077, A	614	25	55.6	15	9	US-10-530-061-1661	Sequence 1661, Ap
542	26	57.8	542	11	US-11-188-298-19307	Sequence 19307, A	615	25	55.6	15	11	US-11-004-399-1498	Sequence 1498, Ap
543	26	57.8	543	11	US-11-188-298-1686	Sequence 1686, Ap	616	25	55.6	48	11	US-11-004-399-1406	Sequence 1406, Ap
544	26	57.8	543	11	US-11-188-298-14697	Sequence 14697, A	617	25	55.6	49	11	US-11-096-568A-7008	Sequence 7008, Ap
545	26	57.8	545	11	US-11-188-298-2597	Sequence 2597, Ap	618	25	55.6	64	11	US-11-000-463-312	Sequence 312, App
546	26	57.8	545	11	US-11-188-298-10682	Sequence 10682, A	619	25	55.6	64	11	US-11-000-463-784	Sequence 784, App
547	26	57.8	552	11	US-11-188-298-2216	Sequence 2216, Ap	620	25	55.6	79	9	US-10-972-233-2	Sequence 2, Appl
548	26	57.8	554	11	US-11-188-298-17498	Sequence 17498, A	621	25	55.6	83	11	US-11-079-463-9805	Sequence 9805, Ap
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551	26	57.8	563	11	US-11-188-298-21311	Sequence 21311, A	624	25	55.6	100	11	US-11-264-096-1359	Sequence 1559, Ap
552	26	57.8	568	11	US-11-188-298-3686	Sequence 3686, Ap	625	25	55.6	103	11	US-11-045-004-1482	Sequence 1482, Ap
553	26	57.8	576	11	US-11-096-568A-13469	Sequence 13469, A	626	25	55.6	108	11	US-10-925-366A-97	Sequence 97, Appl
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556	26	57.8	583	11	US-11-188-298-9008	Sequence 9008, Ap	629	25	55.6	140	11	US-11-052-554A-240	Sequence 240, App
557	26	57.8	588	11	US-11-079-463-6487	Sequence 6487, Ap	630	25	55.6	144	9	US-10-821-234-1255	Sequence 1255, App
558	26	57.8	591	11	US-11-045-004-724	Sequence 724, App	631	25	55.6	158	9	US-10-530-253-15	Sequence 15, Appl
559	26	57.8	612	11	US-11-098-686-10390	Sequence 10390, A	632	25	55.6	164	11	US-11-096-568A-22678	Sequence 22678, A
560	26	57.8	615	9	US-10-525-907-54	Sequence 54, Appl	633	25	55.6	166	9	US-10-506-454-824	Sequence 824, App
561	26	57.8	615	11	US-11-087-099-9420	Sequence 9420, Ap	634	25	55.6	167	8	US-10-505-928-682	Sequence 682, App
562	26	57.8	615	11	US-11-188-298-13754	Sequence 13754, A	635	25	55.6	167	8	US-10-511-937-2949	Sequence 2949, Ap
563	26	57.8	623	9	US-10-467-657-6260	Sequence 6260, Ap	636	25	55.6	168	11	US-11-096-568A-594	Sequence 594, App
564	26	57.8	624	9	US-10-467-657-1740	Sequence 1740, Ap	637	25	55.6	172	11	US-11-096-568A-593	Sequence 593, App
565	26	57.8	642	9	US-10-991-285-891	Sequence 891, App	638	25	55.6	176	11	US-11-087-099-571	Sequence 571, App
566	26	57.8	647	11	US-11-096-568A-27741	Sequence 27741, A	639	25	55.6	182	11	US-11-087-099-11294	Sequence 11294, A
567	26	57.8	654	11	US-11-096-568A-27740	Sequence 27740, A	640	25	55.6	198	11	US-11-087-099-12073	Sequence 12073, A
568	26	57.8	659	11	US-11-096-568A-6605	Sequence 6605, Ap	641	25	55.6	212	11	US-11-045-004-1172	Sequence 1172, App
569	26	57.8	665	11	US-11-169-087-2	Sequence 88, Appl	642	25	55.6	215	11	US-11-188-298-592	Sequence 592, App
570	26	57.8	671	9	US-10-506-454-88	Sequence 2408, Ap	643	25	55.6	218	9	US-10-878-556A-92	Sequence 92, Appl
571	26	57.8	671	11	US-11-045-004-2408	Sequence 107, App	644	25	55.6	224	9	US-10-537-003-46	Sequence 46, Appl
572	26	57.8	682	11	US-11-154-227-107	Sequence 696, App	645	25	55.6	226	11	US-11-264-096-1453	Sequence 1453, Ap
573	26	57.8	684	11	US-11-090-617-686	Sequence 2, Appl	646	25	55.6	227	11	US-11-170-653-27	Sequence 27, Appl
574	26	57.8	684	11	US-11-072-512-2418	Sequence 2, Appl	647	25	55.6	227	11	US-11-045-004-698	Sequence 698, App
575	26	57.8	698	11	US-11-119-569-2	Sequence 113, App	648	25	55.6	229	9	US-10-986-405-296	Sequence 296, App
576	26	57.8	703	11	US-11-069-642-113	Sequence 19, Appl	649	25	55.6	233	11	US-11-022-562-226	Sequence 226, App
577	26	57.8	703	11	US-11-119-569-19	Sequence 16110, A	650	25	55.6	233	11	US-11-202-507A-4	Sequence 4, Appl
578	26	57.8	703	11	US-11-188-298-16110	Sequence 16110, A	651	25	55.6	233	11	US-11-202-507A-2	Sequence 2, Appl
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581	26	57.8	748	8	US-10-511-937-3012	Sequence 3012, Ap	654	25	55.6	242	11	US-11-096-568A-16198	Sequence 16198, A
582	26	57.8	751	9	US-10-467-657-1418	Sequence 1418, Ap	655	25	55.6	242	11	US-11-264-096-1885	Sequence 1885, Ap
583	26	57.8	754	11	US-11-188-298-17153	Sequence 17153, A	656	25	55.6	248	11	US-11-188-298-11119	Sequence 11119, A
584	26	57.8	801	9	US-10-532-153-9	Sequence 9, Appl	657	25	55.6	249	11	US-11-054-515-1956	Sequence 1956, Ap
585	26	57.8	801	9	US-10-532-153-18	Sequence 18, Appl	658	25	55.6	249	11	US-11-096-568A-16197	Sequence 16197, A
586	26	57.8	804	11	US-11-096-568A-27739	Sequence 27739, A	659	25	55.6	249	11	US-11-266-444-1956	Sequence 1956, Ap
587	26	57.8	811	11	US-11-188-298-2220	Sequence 2220, Ap	660	25	55.6	251	11	US-11-188-298-2902	Sequence 2902, Ap
588	26	57.8	821	9	US-10-784-004-362	Sequence 362, App	661	25	55.6	251	11	US-11-188-298-6841	Sequence 6841, Ap
589	26	57.8	821	9	US-10-784-004-371	Sequence 371, App	662	25	55.6	251	11	US-11-188-298-9862	Sequence 9862, Ap
590	26	57.8	829	11	US-11-072-512-3439	Sequence 3439, Ap	663	25	55.6	253	11	US-11-096-568A-16196	Sequence 16196, A
591	26	57.8	836	11	US-11-154-227-105	Sequence 105, App	664	25	55.6	257	9	US-10-467-657-1522	Sequence 1522, Ap
592	26	57.8	837	11	US-11-079-463-8217	Sequence 8217, Ap	665	25	55.6	257	11	US-11-188-298-20351	Sequence 20351, A
593	26	57.8	849	11	US-11-087-099-1756	Sequence 1756, Ap	666	25	55.6	258	11	US-11-096-568A-28028	Sequence 28028, A
594	26	57.8	857	11	US-11-079-463-5544	Sequence 5544, Ap	667	25	55.6	259	11	US-11-140-416-33	Sequence 33, Appl
595	26	57.8	904	11	US-11-154-227-97	Sequence 97, Appl	668	25	55.6	265	9	US-10-793-626-1976	Sequence 1976, Ap
596	26	57.8	946	11	US-11-096-568A-29105	Sequence 29105, A	669	25	55.6	266	9	US-10-506-454-1414	Sequence 1414, Ap
597	26	57.8	954	9	US-10-467-9628-31	Sequence 31, Appl	670	25	55.6	268	11	US-11-188-298-2969	Sequence 2969, Ap
598	26	57.8	959	11	US-11-096-568A-29104	Sequence 29104, A	671	25	55.6	268	11	US-11-188-298-16002	Sequence 16002, A
599	26	57.8	966	11	US-11-096-568A-29103	Sequence 29103, A	672	25	55.6	274	9	US-10-883-512-108	Sequence 108, App
600	26	57.8	1185	9	US-10-877-346-7	Sequence 7, Appl	673	25	55.6	274	11	US-11-087-099-2499	Sequence 2499, Ap
601	26	57.8	1244	11	US-11-181-330-4	Sequence 4, Appl	674	25	55.6	275	11	US-11-172-740-60	Sequence 60, Appl
602	26	57.8	1273	11	US-11-181-330-8	Sequence 8, Appl	675	25	55.6	275	11	US-11-079-463-8197	Sequence 8197, Ap
603	26	57.8	1464	9	US-10-912-971-4	Sequence 4, Appl	676	25	55.6	275	11	US-11-079-463-9318	Sequence 9318, Ap
604	26	57.8	1464	11	US-11-076-074-1	Sequence 1, Appl	677	25	55.6	277	9	US-10-063-703-28	Sequence 28, Appl
605	26	57.8	1464	11	US-11-124-367A-262	Sequence 262, App	678	25	55.6	277	9	US-10-194-487-144	Sequence 144, App

679	25	55.6	277	9	US-10-195-883-144	Sequence 144, App	752	25	55.6	407	11	US-11-082-389-48	Sequence 48, Appl
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681	25	55.6	277	9	US-10-195-889-144	Sequence 144, App	754	25	55.6	411	11	US-11-087-099-6317	Sequence 6317, Ap
682	25	55.6	277	11	US-11-102-240-28	Sequence 28, Appl	755	25	55.6	411	11	US-11-087-099-7760	Sequence 7760, Ap
683	25	55.6	277	11	US-11-096-568A-2388	Sequence 2388, Ap	756	25	55.6	412	11	US-11-282-495-2	Sequence 2, Appl
684	25	55.6	277	11	US-11-096-568A-6766	Sequence 6766, Ap	757	25	55.6	415	9	US-10-506-454-750	Sequence 750, App
685	25	55.6	277	11	US-11-103-195-28	Sequence 28, Appl	758	25	55.6	417	9	US-10-915-002-326	Sequence 326, App
686	25	55.6	277	11	US-11-172-740-2172	Sequence 2172, Ap	759	25	55.6	422	9	US-10-632-150-4	Sequence 4, Appl
687	25	55.6	281	11	US-11-087-099-9922	Sequence 9922, Ap	760	25	55.6	422	10	US-11-106-014-4	Sequence 4, Appl
688	25	55.6	281	11	US-11-172-740-61	Sequence 61, Appl	761	25	55.6	422	11	US-11-073-457-4	Sequence 4, Appl
689	25	55.6	289	11	US-11-096-568A-23059	Sequence 23059, A	762	25	55.6	422	11	US-11-073-460-4	Sequence 4, Appl
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691	25	55.6	296	11	US-11-096-568A-6765	Sequence 6765, Ap	764	25	55.6	429	11	US-11-188-298-17588	Sequence 17588, A
692	25	55.6	300	11	US-11-188-298-18518	Sequence 18518, A	765	25	55.6	430	11	US-11-188-298-18807	Sequence 18807, A
693	25	55.6	302	9	US-10-793-626-2380	Sequence 2380, Ap	766	25	55.6	431	11	US-11-096-568A-2385	Sequence 2385, Ap
694	25	55.6	302	11	US-11-024-959-387	Sequence 387, App	767	25	55.6	435	11	US-11-098-686-10376	Sequence 10376, A
695	25	55.6	304	11	US-11-156-084-274	Sequence 274, App	768	25	55.6	439	11	US-11-096-568A-20092	Sequence 20092, A
696	25	55.6	305	11	US-11-096-568A-11194	Sequence 11194, A	769	25	55.6	442	11	US-11-188-298-13068	Sequence 13068, A
697	25	55.6	308	11	US-11-004-399-87	Sequence 87, Appl	770	25	55.6	450	11	US-11-122-396-9	Sequence 9, Appl
698	25	55.6	308	11	US-11-004-399-457	Sequence 457, App	771	25	55.6	451	11	US-11-079-463-9559	Sequence 9559, Ap
699	25	55.6	308	11	US-11-004-399-3890	Sequence 3890, Ap	772	25	55.6	475	11	US-11-087-099-3174	Sequence 3174, Ap
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701	25	55.6	309	11	US-11-096-568A-18130	Sequence 18130, A	774	25	55.6	475	11	US-11-188-298-3009	Sequence 3009, Ap
702	25	55.6	311	11	US-11-096-568A-11193	Sequence 11193, A	775	25	55.6	475	11	US-11-188-298-15161	Sequence 15161, A
703	25	55.6	312	9	US-10-873-528-69	Sequence 69, Appl	776	25	55.6	478	11	US-11-098-686-10246	Sequence 10246, A
704	25	55.6	314	9	US-10-506-454-1061	Sequence 1061, Ap	777	25	55.6	479	11	US-11-264-096-1886	Sequence 1886, Ap
705	25	55.6	314	11	US-11-096-568A-11685	Sequence 11685, A	778	25	55.6	487	11	US-11-024-959-495	Sequence 495, App
706	25	55.6	316	11	US-11-096-568A-17301	Sequence 17301, A	779	25	55.6	487	11	US-11-188-298-2223	Sequence 2223, Ap
707	25	55.6	322	9	US-10-793-626-586	Sequence 586, App	780	25	55.6	491	9	US-10-793-626-2770	Sequence 2770, Ap
708	25	55.6	322	9	US-10-793-626-984	Sequence 984, App	781	25	55.6	496	11	US-11-079-463-8528	Sequence 8528, Ap
709	25	55.6	329	11	US-11-096-568A-11684	Sequence 11684, A	782	25	55.6	498	11	US-11-079-463-10282	Sequence 10282, A
710	25	55.6	331	9	US-10-505-590-22	Sequence 22, Appl	783	25	55.6	499	11	US-11-079-463-6095	Sequence 6095, Ap
711	25	55.6	334	11	US-11-096-568A-14707	Sequence 14707, A	784	25	55.6	500	11	US-11-087-100-24	Sequence 24, Appl
712	25	55.6	334	11	US-11-096-568A-17212	Sequence 17212, A	785	25	55.6	500	11	US-11-087-085-24	Sequence 24, Appl
713	25	55.6	335	11	US-11-188-298-9303	Sequence 9303, Ap	786	25	55.6	500	11	US-11-188-298-6067	Sequence 6067, Ap
714	25	55.6	338	11	US-11-096-568A-17211	Sequence 17211, A	787	25	55.6	502	11	US-11-188-298-15145	Sequence 15145, A
715	25	55.6	342	11	US-11-096-568A-14706	Sequence 14706, A	788	25	55.6	506	11	US-11-188-298-15145	Sequence 15145, A
716	25	55.6	342	11	US-11-079-463-7032	Sequence 7032, Ap	789	25	55.6	508	11	US-11-188-298-20231	Sequence 20231, A
717	25	55.6	343	11	US-11-079-463-6210	Sequence 6210, Ap	790	25	55.6	508	11	US-11-188-298-22338	Sequence 22338, A
718	25	55.6	345	11	US-11-079-463-6197	Sequence 6197, Ap	791	25	55.6	509	11	US-11-087-099-10350	Sequence 10350, A
719	25	55.6	347	11	US-11-096-568A-18129	Sequence 18129, A	792	25	55.6	509	11	US-11-188-298-20560	Sequence 20560, A
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721	25	55.6	350	11	US-11-087-099-10266	Sequence 10266, A	794	25	55.6	510	9	US-10-242-902-18	Sequence 18, Appl
722	25	55.6	353	11	US-11-096-568A-11192	Sequence 11192, A	795	25	55.6	510	9	US-10-243-116-18	Sequence 18, Appl
723	25	55.6	355	11	US-11-096-568A-14705	Sequence 14705, A	796	25	55.6	510	9	US-10-243-136-18	Sequence 18, Appl
724	25	55.6	358	11	US-11-079-463-10222	Sequence 10222, A	797	25	55.6	510	9	US-10-243-136-18	Sequence 18, Appl
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726	25	55.6	365	11	US-11-188-298-445	Sequence 2445, Ap	799	25	55.6	510	9	US-10-243-236-18	Sequence 18, Appl
727	25	55.6	367	11	US-11-096-568A-17299	Sequence 17299, A	800	25	55.6	510	9	US-10-243-298-18	Sequence 18, Appl
728	25	55.6	371	11	US-11-096-568A-18128	Sequence 18128, A	801	25	55.6	510	9	US-10-243-304-18	Sequence 18, Appl
729	25	55.6	376	11	US-11-188-298-5536	Sequence 5536, Ap	802	25	55.6	510	9	US-10-243-338-18	Sequence 18, Appl
730	25	55.6	384	11	US-11-188-298-19094	Sequence 19094, A	803	25	55.6	510	9	US-10-243-345-18	Sequence 18, Appl
731	25	55.6	386	11	US-11-096-568A-2387	Sequence 2387, Ap	804	25	55.6	510	9	US-10-243-357-18	Sequence 18, Appl
732	25	55.6	386	11	US-11-096-568A-28218	Sequence 28218, A	805	25	55.6	510	9	US-10-245-083-18	Sequence 18, Appl
733	25	55.6	386	11	US-11-045-004-1268	Sequence 1268, Ap	806	25	55.6	510	9	US-10-247-015-18	Sequence 18, Appl
734	25	55.6	390	11	US-11-079-463-8590	Sequence 8590, Ap	807	25	55.6	513	11	US-11-096-568A-28217	Sequence 28217, A
735	25	55.6	390	11	US-11-188-298-16844	Sequence 16844, A	808	25	55.6	513	11	US-11-096-568A-34187	Sequence 34187, A
736	25	55.6	391	11	US-11-129-143-176	Sequence 176, App	809	25	55.6	521	11	US-11-096-568A-34186	Sequence 34186, A
737	25	55.6	394	11	US-11-096-568A-8620	Sequence 8620, Ap	810	25	55.6	523	11	US-11-188-298-16556	Sequence 16556, A
738	25	55.6	394	11	US-11-188-298-10033	Sequence 10033, A	811	25	55.6	523	11	US-11-188-298-18815	Sequence 18815, A
739	25	55.6	394	11	US-11-045-004-1365	Sequence 1365, Ap	812	25	55.6	524	8	US-10-505-928-770	Sequence 770, App
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ALIGNMENTS

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; PRIOR FILING DATE: 2005-11-02  
; PRIOR APPLICATION NUMBER: 09/833,245  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229,358  
; PRIOR FILING DATE: 2000-04-12  
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; Sequence 732, Application US/09978360A

; Publication No. US20060009633A9  
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; APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
; APPLICANT: Duclet, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; APPLICANT: Clusel, Catherine  
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
; FILE REFERENCE: 56.US4.CIP  
; CURRENT APPLICATION NUMBER: US/09/978,360A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
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; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: US 60/099,273  
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; PRIOR APPLICATION NUMBER: US 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: US 09/215,435  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: PCT/IB98/02122  
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; PRIOR FILING DATE: 1999-02-09  
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; APPLICANT: Ruben et al.  
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; FILE REFERENCE: PZ002P2C2  
; CURRENT APPLICATION NUMBER: US/11/144,947  
; CURRENT FILING DATE: 2005-06-06  
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; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
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; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
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; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
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; PRIOR FILING DATE: 2004-07-31
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; NAME/KEY: unsure
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Query Match          75.6%; Score 34; DB 11; Length 313;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
Db 260 FLSYELFV 268

RESULT 6
US-11-188-298-19812
; Sequence 19812, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19812
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Glycine max
US-11-188-298-19812

Query Match          75.6%; Score 34; DB 11; Length 347;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9
Db 293 FLSYELFV 301

RESULT 7
US-11-188-298-845
; Sequence 845, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 845
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-188-298-845

Query Match          75.6%; Score 34; DB 11; Length 382;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFV 9
Db 18 SYDLFVI 24
```

```
RESULT 8
US-11-188-298-15430
; Sequence 15430, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 15430
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-188-298-15430

Query Match          75.6%; Score 34; DB 11; Length 516;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYDLFVV 9
      |||||:
Db      37 SYDLFVI 43

RESULT 9
US-11-188-298-13289
; Sequence 13289, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13289
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(237)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-13289

Query Match          73.3%; Score 33; DB 11; Length 237;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLSYDLFVV 9
      |||||:
Db      185 FLSYELSVV 193

RESULT 10
US-11-188-298-14738
; Sequence 14738, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
```

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; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14738
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Glycine max
US-11-188-298-14738

Query Match          73.3%; Score 33; DB 11; Length 238;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLSYDLFVV 9
      |||||:
Db      186 FLSYELSVV 194

RESULT 11
US-11-188-298-5952
; Sequence 5952, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 5952
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-188-298-5952

Query Match          73.3%; Score 33; DB 11; Length 274;
Best Local Similarity 71.4%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYDLFVV 9
      |||||:
Db      59 SYDLFII 65

RESULT 12
US-11-188-298-4981
; Sequence 4981, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 4981
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-188-298-4981

Query Match          73.3%; Score 33; DB 11; Length 559;
Best Local Similarity 71.4%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYDLFVV 9
      |||||:
Db      57 SYDLFII 63

RESULT 13
```



```
US-11-188-298-4278
; Sequence 4278, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; PRIOR FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 4278
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-188-298-4278

Query Match      73.3%; Score 33; DB 11; Length 572;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYDLFVV 9
      |||||::
Db      59 SYDLFII 65

RESULT 14
US-11-188-298-14889
; Sequence 14889, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14889
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-188-298-14889

Query Match      73.3%; Score 33; DB 11; Length 573;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYDLFVV 9
      |||||::
Db      59 SYDLFII 65

RESULT 15
US-11-188-298-22471
; Sequence 22471, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 22471
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-188-298-22471

US-11-096-568A-31273
; Sequence 31273, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31273
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1038)
; OTHER INFORMATION: Ceres Seq. ID no. 13579190
US-11-096-568A-31273

Query Match      71.1%; Score 32; DB 11; Length 1038;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LSYDLFV 8
      |||||::
Db      358 LSYDVFV 364

RESULT 17
US-11-096-568A-31273
; Sequence 31273, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31273
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1038)
; OTHER INFORMATION: Ceres Seq. ID no. 13579190
US-11-096-568A-31273

Query Match      71.1%; Score 32; DB 11; Length 1038;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LSYDLFV 8
      |||||::
Db      531 LSYDVFV 537
```

```
RESULT 18
US-11-096-568A-31272
; Sequence 31272, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31272
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1158)
; OTHER INFORMATION: Ceres Seq. ID no. 13579189
US-11-096-568A-31272

Query Match          71.1%; Score 32; DB 11; Length 1158;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LSYDLFV 8
Db      651 LSYDVFV 657

RESULT 19
US-11-096-568A-31271
; Sequence 31271, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31271
; LENGTH: 1549
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1549)
; OTHER INFORMATION: Ceres Seq. ID no. 13579188
US-11-096-568A-31271

Query Match          71.1%; Score 32; DB 11; Length 1549;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LSYDLFV 8
Db      1042 LSYDVFV 1048

RESULT 20
US-10-485-517-347
; Sequence 347, Application US/10485517
; Publication No. US2005025629A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
```

```
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 347
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-347

Query Match          68.9%; Score 31; DB 9; Length 275;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LSYDLF 7
Db      29 LSYDLF 34

RESULT 21
US-10-703-799B-188
; Sequence 188, Application US/10703799B
; Publication No. US20060078884A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; APPLICANT: Lee, Heung-Joon
; APPLICANT: Kim, Hyung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
; FILE REFERENCE: BGI-124PCPN
; CURRENT APPLICATION NUMBER: US/10/703,799B
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 09/603,208
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142692
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/151214
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930429.7
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931457.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931541.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 306
; SEQ ID NO 188
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-703-799B-188

Query Match          68.9%; Score 31; DB 9; Length 284;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLSYDL 6
```

Db 73 FLSYDL 78  
|||||

## RESULT 22

US-11-188-298-5816  
; Sequence 5816, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 5816  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Burkholderia fungorum  
US-11-188-298-5816

Query Match 68.9%; Score 31; DB 11; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSYDLF 7  
|||||

Db 28 LSYDLF 33  
|||||

## RESULT 23

US-11-108-088-62  
; Sequence 62, Application US/11108088  
; Publication No. US20060040353A1  
; GENERAL INFORMATION:  
; APPLICANT: DAVIDSON, ROBERT  
; APPLICANT: GERNGROSS, TILLMAN  
; APPLICANT: WILDT, STEFAN  
; APPLICANT: CHOI, BYUNG-KWON  
; APPLICANT: NETT, JUERGEN  
; APPLICANT: BOBROWICZ, PIOTR  
; APPLICANT: HAMILTON, STEPHEN  
; TITLE OF INVENTION: PRODUCTION OF GALACTOSYLATED GLYCOPROTEINS IN LOWER  
; FILE REFERENCE: GFI-12  
; CURRENT APPLICATION NUMBER: US/11/108,088  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: 60/214,358  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/215,638  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/279,997  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US02/41510  
; PRIOR FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: 60/344,169  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/562,424  
; PRIOR FILING DATE: 2004-04-15  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 62  
; LENGTH: 357  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-11-108-088-62

Query Match 68.9%; Score 31; DB 11; Length 357;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
|||||

Db 256 FKGYDLFV 263  
|||||

## RESULT 24

US-11-188-298-17875  
; Sequence 17875, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 17875  
; LENGTH: 441  
; TYPE: PRT  
; ORGANISM: Coxiella burnetii RSA 493  
US-11-188-298-17875

Query Match 68.9%; Score 31; DB 11; Length 441;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
:|||||

Db 37 AYDLFVI 43  
|||||

## RESULT 25

US-11-008-331-3  
; Sequence 3, Application US/11008331  
; Publication No. US20050244925A1  
; GENERAL INFORMATION:  
; APPLICANT: Genencor International, Inc.  
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms  
; FILE REFERENCE: GC386-PCT  
; CURRENT APPLICATION NUMBER: US/11/008,331  
; CURRENT FILING DATE: 2004-12-08  
; PRIOR APPLICATION NUMBER: EP9719637.2  
; PRIOR FILING DATE: 1997-09-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: S. cerevisiae  
US-11-008-331-3

Query Match 68.9%; Score 31; DB 11; Length 472;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7  
:|||||

Db 87 FKYDLF 93  
|||||

## RESULT 26

US-11-079-463-6971  
; Sequence 6971, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR  
; FILE REFERENCE: PAT00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 6971  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-11-079-463-6971

Query Match 68.9%; Score 31; DB 11; Length 627;  
Best Local Similarity 62.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 8  
|||::|||  
Db 384 FLGYBIFV 391

RESULT 27  
US-11-079-463-8050  
; Sequence 8050, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR

; FILE REFERENCE: PATH00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 8050  
; LENGTH: 81  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-11-079-463-8050

Query Match 66.7%; Score 30; DB 11; Length 81;  
Best Local Similarity 44.4%; Pred. No. 42; Mismatches 5; Conservative 4; Gaps 0;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
|::|::|  
Db 23 FMSFDLYLM 31

RESULT 28  
US-11-096-568A-14201  
; Sequence 14201, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 14201  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(102)  
; OTHER INFORMATION: Ceres Seq. ID no. 2786661  
; FEATURE:  
; NAME/KEY: misc\_feature

; LOCATION: (97)..(97)  
; OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-14201

Query Match 66.7%; Score 30; DB 11; Length 102;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YDLFVV 9  
|||||  
Db 18 YDLFVI 23

RESULT 29  
US-11-096-568A-14200  
; Sequence 14200, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 14200  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(106)  
; OTHER INFORMATION: Ceres Seq. ID no. 2786660  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (101)..(101)  
; OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-14200

Query Match 66.7%; Score 30; DB 11; Length 106;  
Best Local Similarity 83.3%; Pred. No. 55;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YDLFVV 9  
|||||  
Db 22 YDLFVI 27

RESULT 30  
US-11-079-463-5646  
; Sequence 5646, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR

; FILE REFERENCE: PATH00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 5646  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-11-079-463-5646

Query Match 66.7%; Score 30; DB 11; Length 111;  
Best Local Similarity 83.3%; Pred. No. 57;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFV 8  
|||||  
Db 57 SYDLFI 62

## RESULT 31

US-11-096-568A-14199  
; Sequence 14199, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 14199  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(133)  
; OTHER INFORMATION: Ceres Seq. ID no. 2786659  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (128)..(128)  
; OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-14199

Query Match 66.7%; Score 30; DB 11; Length 133;  
Best Local Similarity 83.3%; Pred. No. 69;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YDLFV 9  
|||||  
Db 49 YDLFI 54

## RESULT 32

US-11-264-096-1842  
; Sequence 1842, Application US/11264096  
; Publication No. US20060084794A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546D1  
; CURRENT APPLICATION NUMBER: US/11/264,096  
; CURRENT FILING DATE: 2005-11-02  
; PRIOR APPLICATION NUMBER: 09/833,245  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199, 384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1842  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (22)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-11-264-096-1842

Query Match 66.7%; Score 30; DB 11; Length 265;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLSYDLF 7  
:|||||  
Db 166 YLEVDLF 172

## RESULT 33

US-11-098-686-11233  
; Sequence 11233, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: US 60/416,395  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11233  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-11233

Query Match 66.7%; Score 30; DB 11; Length 330;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
:|||||  
Db 213 FISHDLAV 221

## RESULT 34

US-11-165-211-53  
; Sequence 53, Application US/11165211  
; Publication No. US20050287626A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Process for producing dipeptides  
; FILE REFERENCE: 4093-14  
; CURRENT APPLICATION NUMBER: US/11/165,211  
; CURRENT FILING DATE: 2005-06-24  
; PRIOR APPLICATION NUMBER: JP2004-189012  
; PRIOR FILING DATE: 2004-06-25  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-11-165-211-53

Query Match 66.7%; Score 30; DB 11; Length 334;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFV 9  
:|||||  
Db 217 FISHDLAV 225

## RESULT 35

US-11-165-226-63  
; Sequence 63, Application US/11165226  
; Publication No. US20050287627A1  
; GENERAL INFORMATION:

```
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Process for producing dipeptides or dipeptide derivatives
; FILE REFERENCE: 4093-13
; CURRENT APPLICATION NUMBER: US/11/165,226
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: JP2004-189007
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-165-226-63

Query Match      66.7%; Score 30; DB 11; Length 334;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLSYDLFVV 9
       |:|:|:|:|
Db      217 FISHDLSSV 225

RESULT 36
US-11-079-463-7885
; Sequence 7885, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7885
; LENGTH: 392
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-7885

Query Match      66.7%; Score 30; DB 11; Length 392;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 YDLFVV 9
       |:|:|:|:|
Db      113 YDLFVI 118

RESULT 37
US-11-079-463-10384
; Sequence 10384, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 10384
; LENGTH: 413
```

```
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-10384

Query Match      66.7%; Score 30; DB 11; Length 413;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLSYDLFVV 9
       |:|:|:|:|
Db      160 FIAPDLFLL 168

RESULT 38
US-11-188-298-7549
; Sequence 7549, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7549
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Coxiella burnetii RSA 493
US-11-188-298-7549

Query Match      66.7%; Score 30; DB 11; Length 442;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYDLFVV 9
       |:|:|:|:|
Db      33 AYDLFII 39

RESULT 39
US-11-188-298-6866
; Sequence 6866, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6866
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Ferropasma acidarmanus
US-11-188-298-6866

Query Match      66.7%; Score 30; DB 11; Length 467;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYDLFVV 9
       |:|:|:|:|
Db      33 AYDLFII 39

RESULT 40
US-11-188-298-16982
; Sequence 16982, Application US/11188298
; Publication No. US20060075522A1
```

; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 16982  
; LENGTH: 471  
; TYPE: PRT  
; ORGANISM: Ferropasma acidarmanus  
US-11-188-298-16982

Query Match 66.7%; Score 30; DB 11; Length 471;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYDLFVV 9  
:||||:  
Db 39 AYDLFVI 45

## RESULT 41

US-11-096-568A-9990  
; Sequence 9990, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 9990  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(497)  
; OTHER INFORMATION: Ceres Seq. ID no. 13496284  
US-11-096-568A-9990

Query Match 66.7%; Score 30; DB 11; Length 497;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YDLFVV 9  
:||||:  
Db 24 YDLFVI 29

## RESULT 42

US-11-096-568A-9989  
; Sequence 9989, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 9989  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc\_feature

; LOCATION: (1)..(501)  
; OTHER INFORMATION: Ceres Seq. ID no. 13496283  
US-11-096-568A-9989

Query Match 66.7%; Score 30; DB 11; Length 501;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YDLFVV 9  
:||||:  
Db 28 YDLFVI 33

## RESULT 43

US-11-082-389-182  
; Sequence 182, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; FILE REFERENCE: BGI-131CPCN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 182  
; LENGTH: 547  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-082-389-182

Query Match 66.7%; Score 30; DB 11; Length 547;  
Best Local Similarity 66.7%; Pred. No. 2.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
:||||:  
Db 485 FISHLAVV 493

## RESULT 44

US-11-087-099-3291  
; Sequence 3291, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 3291  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Coxiella burnetii RSA 493  
US-11-087-099-3291

Query Match 66.7%; Score 30; DB 11; Length 560;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
|:|:|  
Db 440 FLSFMLEVV 448

RESULT 45  
US-11-188-298-14097  
; Sequence 14097, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 14097  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Coxiella burnetii RSA 493  
US-11-188-298-14097

Query Match 66.7%; Score 30; DB 11; Length 560;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLFVV 9  
|:|:|  
Db 440 FLSFMLEVV 448

RESULT 46  
US-11-078-189-15  
; Sequence 15, Application US/11078189  
; Publication No. US20050277167A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachinger, Hans Peter  
; APPLICANT: Vranka, Janice  
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES  
; FILE REFERENCE: 08062-020001  
; CURRENT APPLICATION NUMBER: US/11/078,189  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US 60/552,409  
; PRIOR FILING DATE: 2004-03-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 725  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-11-078-189-15

Query Match 66.7%; Score 30; DB 11; Length 725;  
Best Local Similarity 71.4%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLSYDLF 7

Db 370 FFSYDVF 376  
|:|:|

RESULT 47  
US-11-169-041-177  
; Sequence 177, Application US/11169041  
; Publication No. US20060019284A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF  
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE  
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 10001 NP  
; CURRENT APPLICATION NUMBER: US/11/169,041  
; CURRENT FILING DATE: 2005-06-28  
; PRIOR APPLICATION NUMBER: 60/584,405  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 527  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 177  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-169-041-177

Query Match 66.7%; Score 30; DB 11; Length 960;  
Best Local Similarity 85.7%; Pred. No. 5e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSYDLFV 8  
|:|:|  
Db 76 LHYDLFV 82

RESULT 48  
US-11-116-881A-514  
; Sequence 514, Application US/11116881A  
; Publication No. US20060041949A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Dongmei  
; APPLICANT: Nielsen, Mark T.  
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof  
; FILE REFERENCE: 07678/141014  
; CURRENT APPLICATION NUMBER: US/11/116,881A  
; CURRENT FILING DATE: 2005-04-27  
; PRIOR APPLICATION NUMBER: 60/665,451  
; PRIOR FILING DATE: 2005-03-24  
; PRIOR APPLICATION NUMBER: 60/665,097  
; PRIOR FILING DATE: 2005-03-24  
; PRIOR APPLICATION NUMBER: 60/646,764  
; PRIOR FILING DATE: 2005-01-25  
; PRIOR APPLICATION NUMBER: 60/607,357  
; PRIOR FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: 60/566,235  
; PRIOR FILING DATE: 2004-04-29  
; PRIOR APPLICATION NUMBER: 10/934,944  
; PRIOR FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: 10/943,507  
; PRIOR FILING DATE: 2004-09-17  
; PRIOR APPLICATION NUMBER: 60/503,989  
; PRIOR FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: 60/485,368  
; PRIOR FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: 60/418,933  
; PRIOR FILING DATE: 2002-10-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2300  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 514  
; LENGTH: 146  
; TYPE: PRT



```
; ORGANISM: Nicotiana tabacum
US-11-116-881A-514

Query Match      64.4%; Score 29; DB 11; Length 146;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 PLSYDLFW 9
Db      118 FMYDTFTV 126

RESULT 49
US-11-096-568A-6972
; Sequence 6972, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6972
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(324)
; OTHER INFORMATION: Ceres Seq. ID no. 15169353
US-11-096-568A-6972

Query Match      64.4%; Score 29; DB 11; Length 324;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 PLSYDLFW 9
Db      173 FLGFDVFFV 181

RESULT 50
US-11-096-568A-25297
; Sequence 25297, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25297
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(329)
; OTHER INFORMATION: Ceres Seq. ID no. 12567161
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (287)..(287)
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; LOCATION: (293)..(293)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (297)..(297)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (309)..(309)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; NAME/KEY: misc_feature
; LOCATION: (317)..(317)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-25297

Query Match      64.4%; Score 29; DB 11; Length 329;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LSYDLFW 9
Db      63 LCFDLFVI 70

Search completed: May 9, 2006, 02:36:05
Job time : 21.8 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 02:05:23 ; Search time 98.4 Seconds  
(without alignments)  
40.187 Million cell updates/sec

Title: US-09-870-216C-11  
Perfect score: 43  
Sequence: 1 NLQLMDRV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

- A\_Geneseq\_21.\*
  - 1: Geneseq1980s.\*
  - 2: Geneseq1990s.\*
  - 3: Geneseq2000s.\*
  - 4: Geneseq2001s.\*
  - 5: Geneseq2002s.\*
  - 6: Geneseq2003as.\*
  - 7: Geneseq2003bs.\*
  - 8: Geneseq2004s.\*
  - 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	43	100.0	9	7	AbR82217 Human ant
3	43	100.0	256	3	Aab56775 Human pro
4	43	100.0	302	7	Ade29060 Human Eif
5	43	100.0	347	7	Ade29059 Human Eif
6	43	100.0	352	5	Abb08360 Human eif
7	43	100.0	352	7	AbR82212 Human ant
8	43	100.0	352	7	AdJ68541 Human hea
9	43	100.0	352	8	Abm81006 Tumour-as
10	43	100.0	352	8	AdS34462 POSH prot
11	43	100.0	352	9	Adw08703 Human pro
12	43	100.0	352	9	Adx06453 Cyclin-de
13	43	100.0	368	7	AdC31312 Human nov
14	36	83.7	260	3	Aag57646 Arabidops
15	36	83.7	311	3	Aag57645 Arabidops
16	36	83.7	311	8	Adt56346 Plant pol
17	36	83.7	334	3	Aag57644 Arabidops
18	35	81.4	133	4	Aab92665 Human pro
19	35	81.4	133	8	Adp55533 Human pro
20	35	81.4	152	3	Aag01149 Human sec
21	35	81.4	180	2	Aay28922 Human reg
22	35	81.4	180	5	Abb89507 Human pol
23	35	81.4	180	7	AdD22442 HLA-B46 T
24	35	81.4	180	7	Adi15876 Human PP

98	30	69.8	231	8	ADL04391	Adl04391 M. catarr	171	29	67.4	209	9	AEC10502	Aec10502 Streptoco
99	30	69.8	315	8	ADT57494	Adt57494 Plant pol	172	29	67.4	209	9	AEC10500	Aec10500 Streptoco
100	30	69.8	340	2	AAW20513	Aaw20513 Helicobac	173	29	67.4	228	5	ABP39849	Abp39849 Staphyloc
101	30	69.8	340	2	AAW24679	Aaw24679 H. pylori	174	29	67.4	228	5	ABP40650	Abp40650 Staphyloc
102	30	69.8	340	2	AAU36033	Aau36033 Helicobac	175	29	67.4	228	8	ADS06881	Ads06881 Staphyloc
103	30	69.8	354	4	AAW20865	Aaw20865 H. pylori	176	29	67.4	228	8	ADS07893	Ads07893 Staphyloc
104	30	69.8	367	6	ABU21639	Abu21639 Protein e	177	29	67.4	265	6	ABM68402	Abm68402 Photorhab
105	30	69.8	386	3	AG49075	Ag49075 Arabidops	178	29	67.4	269	7	ADD24634	Add24634 DNA polym
106	30	69.8	406	3	AG49074	Ag49074 Arabidops	179	29	67.4	278	6	ABM68345	Abm68345 Photorhab
107	30	69.8	412	7	ADH88781	Adh88781 Enterococ	180	29	67.4	280	7	ASO81603	Aso81603 Pseudomon
108	30	69.8	434	6	ABM68878	Abm68878 Photorhab	181	29	67.4	284	4	AAW46328	Aaw46328 H. pylori
109	30	69.8	467	5	ABE93351	Abbe93351 Herbicida	182	29	67.4	285	4	AAW46385	Aaw46385 H. pylori
110	30	69.8	487	5	ABE93673	Abbe93673 Herbicida	183	29	67.4	289	2	AAW10977	Aaw10977 H. pylori
111	30	69.8	518	8	ADT59662	Adt59662 Plant pol	184	29	67.4	291	2	AAW21018	Aaw21018 H. pylori
112	30	69.8	520	3	AG49073	Ag49073 Arabidops	185	29	67.4	292	4	ABM68530	Abm68530 Human GNP
113	30	69.8	522	8	ADI45359	Adi45359 Rice isop	186	29	67.4	292	5	AAU79300	Aau79300 Accessory
114	30	69.8	540	6	ABU42118	Abu42118 Protein e	187	29	67.4	298	8	ADU98847	Adu98847 Borrelia
115	30	69.8	593	4	ABG27989	Abg27989 Novel hum	188	29	67.4	320	6	ABM70375	Abm70375 Photorhab
116	30	69.8	591	4	AU36222	Au36222 Pseudomon	189	29	67.4	322	6	ABU24086	Abu24086 Protein e
117	30	69.8	591	6	ABU38312	Abu38312 Protein e	190	29	67.4	328	5	ABP69626	Abp69626 Human pol
118	30	69.8	612	6	ABU50234	Abu50234 Protein e	191	29	67.4	328	8	ADY07537	Ady07537 Plant ful
119	30	69.8	656	7	ABO80829	Abu80829 Pseudomon	192	29	67.4	340	2	AAW98773	Aaw98773 H. pylori
120	30	69.8	670	6	ABU43077	Abu43077 Protein e	193	29	67.4	340	3	AAW52217	Aaw52217 Helicobac
121	30	69.8	673	5	ABP39635	Abp39635 Staphyloc	194	29	67.4	340	6	ABU31115	Abu31115 Protein e
122	30	69.8	673	8	ADS05691	Ads05691 Staphyloc	195	29	67.4	342	3	AAW53203	Aaw53203 Macsaca mu
123	30	69.8	681	4	ABE63032	Abbe63032 Drosophil	196	29	67.4	369	6	ABU21624	Abu21624 Protein e
124	30	69.8	701	8	ADS30828	Adbs30828 Bacterial	197	29	67.4	369	7	ABO74952	Abu74952 Pseudomon
125	30	69.8	705	4	ABW71548	Abw71548 Drosophil	198	29	67.4	420	7	ASO81363	Aso81363 Pseudomon
126	30	69.8	753	3	AAW58422	Aaw58422 Lung canc	199	29	67.4	424	5	ABW48922	Abw48922 Listeria
127	30	69.8	757	6	ABJ25904	Abj25904 Aspergill	200	29	67.4	425	6	ABU33346	Abu33346 Protein e
128	30	69.8	766	8	ADW77964	Adw77964 Plant ful	201	29	67.4	425	9	ABE41205	Abu41205 L. pneumo
129	30	69.8	771	6	ABU33311	Abu33311 Protein e	202	29	67.4	430	9	ABE37901	Abu37901 L. pneumo
130	30	69.8	771	9	ABE39430	Abu39430 L. pneumo	203	29	67.4	491	8	ADS14868	Adu14868 Pseudomon
131	30	69.8	778	9	ABE36001	Abu36001 L. pneumo	204	29	67.4	509	7	ABO73941	Abu73941 Pseudomon
132	30	69.8	808	7	ABO65030	Abu65030 Klebsiell	205	29	67.4	515	6	ABU19138	Abu19138 Protein e
133	30	69.8	837	6	ABO52992	Abu52992 Human put	206	29	67.4	515	8	ADU98849	Adu98849 Borrelia
134	30	69.8	891	6	ABJ26504	Abj26504 Aspergill	207	29	67.4	526	4	AAW92906	Aaw92906 Human pro
135	30	69.8	881	8	ADS29934	Adbs29934 Bacterial	208	29	67.4	539	8	ADW77127	Adw77127 Plant ful
136	30	69.8	1071	5	ABW92974	Abw92974 Herbicida	209	29	67.4	541	5	ABW55029	Abw55029 Lactococc
137	30	69.8	1091	8	ADW92141	Adw92141 S. pneumon	210	29	67.4	541	8	ADS29442	Adu29442 Bacterial
138	30	69.8	1116	6	ABU01290	Abu01290 S. pneumo	211	29	67.4	550	7	ADC14201	Adc14201 Human enz
139	30	69.8	1116	8	ADK48579	Adk48579 Streptoco	212	29	67.4	559	8	ADW80129	Adw80129 Plant ful
140	30	69.8	1120	8	ADR94967	Adr94967 Novel S.	213	29	67.4	563	8	ADM48239	Adm48239 Polypepti
141	30	69.8	1120	9	AEA58837	Aea58837 Streptoco	214	29	67.4	573	7	ABO69998	Abu69998 Pseudomon
142	30	69.8	1385	4	ABW60138	Abw60138 Drosophil	215	29	67.4	575	7	ABO80695	Abu80695 Pseudomon
143	30	69.8	1483	4	ABW61765	Abw61765 Drosophil	216	29	67.4	586	9	AEA62697	Aea62697 Mitochond
144	30	69.8	1522	8	ADL46156	Adl46156 Yeast sor	217	29	67.4	587	5	AAU76543	Aau76543 Human ami
145	30	69.8	1579	6	ABR53877	Abu53877 Protein s	218	29	67.4	587	5	AAU76544	Aau76544 Human ami
146	30	69.8	1579	7	ADK64870	Adk64870 Disease t	219	29	67.4	587	7	ADW79834	Adw79834 Rat eryth
147	30	69.8	1763	7	ADW85511	Adw85511 Human GIG	220	29	67.4	587	7	ADW79794	Adw79794 Rat eryth
148	30	69.8	1763	7	ADC16722	Adc16722 Human mod	221	29	67.4	587	8	ADP12398	Adp12398 Protein e
149	30	69.8	1784	2	AAW77223	Aaw77223 Tubercous	222	29	67.4	587	8	ADP12398	Adp12398 Protein e
150	30	69.8	1807	7	ADW85512	Adw85512 Human GIG	223	29	67.4	587	9	ADW80346	Adw80346 Human ami
151	30	69.8	1807	7	ADC16723	Adc16723 Human mod	224	29	67.4	587	9	AEA62694	Aea62694 Mitochond
152	30	69.8	1807	7	ADQ18517	Adq18517 Human sof	225	29	67.4	615	7	ABM85307	Abm85307 Human pro
153	29	67.4	74	7	ADQ18578	Adq18578 Soil meta	226	29	67.4	622	6	ABW67835	Abw67835 Photorhab
154	29	67.4	86	6	ABU23125	Abu23125 Protein e	227	29	67.4	655	6	ABU25241	Abu25241 Protein e
155	29	67.4	107	5	ABW90676	Abw90676 Chlamydia	228	29	67.4	655	8	ADS29754	Adu29754 Bacterial
156	29	67.4	115	5	ABG37774	Abg37774 Human pep	229	29	67.4	726	9	ABE91417	Abu91417 Microbial
157	29	67.4	119	4	AAU32007	Aau32007 Novel hum	230	29	67.4	739	7	ADW67677	Adw67677 Novel hum
158	29	67.4	127	4	AAO05028	Aao05028 Human pol	231	29	67.4	739	7	ADJ69194	Adj69194 Human hea
159	29	67.4	127	5	ABW89220	Abw89220 Human pol	232	29	67.4	743	4	ABW70788	Abw70788 Drosophil
160	29	67.4	127	6	ABU18001	Abu18001 Human exp	233	29	67.4	763	7	ADC31085	Adc31085 Human nov
161	29	67.4	130	4	ABW18001	Abu18001 Human ner	234	29	67.4	800	4	ABG16794	Abg16794 Novel hum
162	29	67.4	140	9	AEA30984	Aea30984 Duck inte	235	29	67.4	814	8	ADR05176	Adr05176 Human ser
163	29	67.4	140	9	AEA30983	Aea30983 Duck inte	236	29	67.4	814	8	ADP23813	Adp23813 PRO polyP
164	29	67.4	160	8	ABW95870	Abw95870 M. xanthu	237	29	67.4	856	7	ABO72698	Abu72698 Pseudomon
165	29	67.4	165	8	ADS30321	Adbs30321 Bacterial	238	29	67.4	858	4	ABW68562	Abw68562 Drosophil
166	29	67.4	192	9	ADW17720	Adw17720 Pinus rad	239	29	67.4	879	6	ABJ25894	Abj25894 Aspergill
167	29	67.4	198	5	ABU51517	Abu51517 Helicobac	240	29	67.4	1011	6	ABU20937	Abu20937 Protein e
168	29	67.4	209	6	ABU01438	Abu01438 S. pneumo	241	29	67.4	1032	6	ABU26494	Abu26494 Aspergill
169	29	67.4	209	7	ADG73324	Adg73324 Streptoco	242	29	67.4	1078	8	ABW87519	Abw87519 Mutant SC
170	29	67.4	209	7	ADG73326	Adg73326 Streptoco	243	29	67.4	1138	3	AAW81512	Aaw81512 Streptoco

244	29	67.4	1142	9	ADY20048	PRO polyp	317	29	67.4	2009	8	ADS87530	Mutant SC
245	29	67.4	1155	8	ADS24079	Bacterial	318	29	67.4	2009	8	ADS87532	Mutant SC
246	29	67.4	1214	8	ADS87520	Mutant SC	319	29	67.4	2009	8	ADS87502	Mutant SC
247	29	67.4	1216	4	AUU37719	Streptoco	320	29	67.4	2009	8	ADS87510	Mutant SC
248	29	67.4	1216	4	AUU38105	Streptoco	321	29	67.4	2009	8	ADS87531	Mutant SC
249	29	67.4	1216	6	ABU01575	S. pneumo	322	29	67.4	2009	8	ADS87507	Mutant SC
250	29	67.4	1216	6	ABU46053	Protein e	323	29	67.4	2009	9	ADY27142	Human SCN
251	29	67.4	1216	8	ADK47309	Streptoco	324	29	67.4	2009	9	ADY27140	Human SCN
252	29	67.4	1224	8	ADR95712	Novel S.	325	29	67.4	2009	9	ADY27141	Human SCN
253	29	67.4	1224	8	AEA59582	Streptoco	326	29	67.4	2009	9	ADY27139	Human SCN
254	29	67.4	1277	8	ADQ65753	Novel hum	327	29	67.4	2009	9	ADY27144	Human SCN
255	29	67.4	1358	8	ADS87521	Mutant SC	328	29	67.4	2009	9	ADX26412	Novel cel
256	29	67.4	1381	5	AAE20513	Human ion	329	29	67.4	2028	8	ADT56126	Plant pol
257	29	67.4	1387	5	AAE20514	Human ion	330	29	67.4	3477	9	ADX83191	Human REG
258	29	67.4	1392	5	AAE20518	Human ion	331	29	67.4	3477	9	ADY19286	PRO polyp
259	29	67.4	1398	5	AAE20519	Human ion	332	29	67.4	3477	9	ADY19286	PRO polyp
260	29	67.4	1406	9	ADY27143	Human SCN	333	29	67.4	4413	8	ADN20924	Bacterial
261	29	67.4	1415	9	AEA19933	Novel hum	334	29	67.4	19938	6	ABP76682	Streptomy
262	29	67.4	1426	8	ADS87524	Mutant SC	335	28	65.1	29	4	AAW20160	Peptide #
263	29	67.4	1430	4	ABB58602	Drosophil	336	28	65.1	29	4	ABM20160	Peptide #
264	29	67.4	1442	5	AAE20512	Human ion	337	28	65.1	29	4	AAW34103	Peptide #
265	29	67.4	1448	4	ABB62325	Drosophil	338	28	65.1	29	4	ABB24769	Protein #
266	29	67.4	1453	5	AAE20517	Human ion	339	28	65.1	29	4	AAW73924	Human bon
267	29	67.4	1510	8	ADS87522	Mutant SC	340	28	65.1	29	4	ABG55676	Human liv
268	29	67.4	1681	5	AAU78573	Mouse voi	341	28	65.1	29	5	ABG43812	Human pep
269	29	67.4	1687	8	ADO17156	Novel exp	342	28	65.1	79	4	AAW86940	Human imm
270	29	67.4	1757	2	AAW84351	Murine ub	343	28	65.1	82	3	AAW12751	Arabidops
271	29	67.4	1757	4	AAW84351	Murine ub	344	28	65.1	35	8	ADO42773	Leader se
272	29	67.4	1757	8	ADJ95455	Mouge Ubi	345	28	65.1	46	8	ADO42774	Leader se
273	29	67.4	1757	8	ADS86877	Murine E3	346	28	65.1	46	8	ADO42768	Leader se
274	29	67.4	1757	8	ADZ75835	Mouse E3a	347	28	65.1	58	4	ABG17849	Novel hum
275	29	67.4	1795	7	ADB78596	Human sod	348	28	65.1	79	4	AAW86940	Human imm
276	29	67.4	1855	7	ADB78597	Human sod	349	28	65.1	82	3	AAW12751	Arabidops
277	29	67.4	1891	9	ADY27145	Human SCN	350	28	65.1	82	7	ADF30904	Soil meta
278	29	67.4	1942	8	ADS87534	Mutant SC	351	28	65.1	82	7	ADF30909	Soil meta
279	29	67.4	1942	5	AAE20511	Human ion	352	28	65.1	82	7	ADF30912	Soil meta
280	29	67.4	1973	5	AAE20516	Human ion	353	28	65.1	94	8	ADT39371	hsARS vir
281	29	67.4	1981	7	ABR83185	Human SCN	354	28	65.1	94	8	ADT39371	hsARS vir
282	29	67.4	1998	5	AAE20510	Human ion	355	28	65.1	94	8	ADT36901	hsARS vir
283	29	67.4	1998	7	ABR83184	Human SCN	356	28	65.1	103	3	AAW12750	Arabidops
284	29	67.4	1998	9	ADX26269	Novel cel	357	28	65.1	118	7	ABO78393	Pseudomon
285	29	67.4	1998	9	ABE43184	Human poc	358	28	65.1	120	5	ABW08648	Human ATP
286	29	67.4	1999	5	ABB06026	Human sod	359	28	65.1	128	2	AAV37734	Protein i
287	29	67.4	1999	8	ADU78366	Human voi	360	28	65.1	133	6	ABU46375	Protein e
288	29	67.4	2000	9	ADY17682	PRO polyp	361	28	65.1	135	2	AAV30531	Recombina
289	29	67.4	2009	4	ABY99674	Human adu	362	28	65.1	136	2	AAW22132	Sequence
290	29	67.4	2009	5	AAE20515	Human ion	363	28	65.1	146	3	AAW06875	Arabidops
291	29	67.4	2009	5	ABG69292	Human sod	364	28	65.1	155	1	AAW00091	Sequence
292	29	67.4	2009	5	ABG69291	Human sod	365	28	65.1	155	1	AAW00091	Sequence
293	29	67.4	2009	5	ABG69293	Human sod	366	28	65.1	155	2	AAW22131	Sequence
294	29	67.4	2009	5	ABG69289	Human sod	367	28	65.1	155	2	AAW22131	Sequence
295	29	67.4	2009	5	ABG69290	Human sod	368	28	65.1	156	3	ABO76437	Pseudomon
296	29	67.4	2009	5	ABR83626	Human GEP	369	28	65.1	157	3	ABW1249	Human ORF
297	29	67.4	2009	5	AAE16776	Human tra	370	28	65.1	157	8	ADY23915	Plant ful
298	29	67.4	2009	7	ADB78599	Human sod	371	28	65.1	162	2	AAW98608	Human nov
299	29	67.4	2009	7	ADB78595	Human sod	372	28	65.1	165	7	ADC31299	Human nov
300	29	67.4	2009	7	ADB78593	Human sod	373	28	65.1	165	9	ADX16349	N-termina
301	29	67.4	2009	7	ADB78594	Human sod	374	28	65.1	165	9	ADX16347	N-termina
302	29	67.4	2009	7	ADB78598	Human sod	375	28	65.1	165	9	ADX16384	N-termina
303	29	67.4	2009	7	ABR83180	Human SCN	376	28	65.1	165	9	ADX16398	N-termina
304	29	67.4	2009	7	ADE57563	Human Pro	377	28	65.1	165	9	ADX16366	N-termina
305	29	67.4	2009	7	ADE57561	Rat Prote	378	28	65.1	165	9	ADX16383	N-termina
306	29	67.4	2009	8	ADS87509	Mutant SC	379	28	65.1	165	9	ADX16348	N-termina
307	29	67.4	2009	8	ADS87512	Mutant SC	380	28	65.1	165	9	ADX16353	N-termina
308	29	67.4	2009	8	ADS87515	Mutant SC	381	28	65.1	165	9	ADX16395	N-termina
309	29	67.4	2009	8	ADS87514	Mutant SC	382	28	65.1	165	9	ADX16368	N-termina
310	29	67.4	2009	8	ADS87503	Mutant SC	383	28	65.1	165	9	ADX16382	N-termina
311	29	67.4	2009	8	ADS87505	Mutant SC	384	28	65.1	165	9	ADX16365	N-termina
312	29	67.4	2009	8	ADS87508	Mutant SC	385	28	65.1	165	9	ADX16380	N-termina
313	29	67.4	2009	8	ADS87511	Mutant SC	386	28	65.1	165	9	ADX16346	N-termina
314	29	67.4	2009	8	ADS87506	Mutant SC	387	28	65.1	165	9	ADX16350	N-termina
315	29	67.4	2009	8	ADS87504	Mutant SC	388	28	65.1	165	9	ADX16351	N-termina
316	29	67.4	2009	8	ADS87513	Mutant SC	389	28	65.1	165	9	ADX16352	N-termina

390	28	65.1	165	9	ADXL16369	Adxl16369 N-termina	463	28	65.1	199	9	ADXL16409	Adxl16409 Full leng
391	28	65.1	165	9	ADXL16399	Adxl16399 N-termina	464	28	65.1	199	9	ADXL16377	Adxl16377 Full leng
392	28	65.1	165	9	ADXL16347	Adxl16347 N-termina	465	28	65.1	199	9	ADXL16405	Adxl16405 Full leng
393	28	65.1	165	9	ADXL16354	Adxl16354 N-termina	466	28	65.1	199	9	ADXL16376	Adxl16376 Full leng
394	28	65.1	165	9	ADXL16396	Adxl16396 N-termina	467	28	65.1	199	9	ADXL16378	Adxl16378 Full leng
395	28	65.1	165	9	ADXL16397	Adxl16397 N-termina	468	28	65.1	199	9	ADY93813	Human int
396	28	65.1	165	9	ADXL16381	Adxl16381 N-termina	469	28	65.1	204	9	ADW38527	Humunomcd
397	28	65.1	165	9	ADXL16381	Adxl16381 N-termina	470	28	65.1	210	7	ADC31301	Human nov
398	28	65.1	177	2	AAR43261	Aar43261 Human adi	471	28	65.1	211	9	ABM92893	M. xanthu
399	28	65.1	177	2	AAR43262	Aar43262 Human adi	472	28	65.1	219	4	ABBS59974	Drosophil
400	28	65.1	178	6	ABW73076	Abm73076 Staphyloc	473	28	65.1	225	6	ABU38499	Protein e
401	28	65.1	178	2	AAW02202	Aaw02202 Human int	474	28	65.1	229	6	ABU38499	Protein e
402	28	65.1	178	2	AAW02202	Aaw02202 Human int	475	28	65.1	229	7	ADC31300	Human nov
403	28	65.1	178	9	ADXL16357	Adxl16357 N-termina	476	28	65.1	241	6	ABM70404	Photorhab
404	28	65.1	178	9	ADXL16389	Adxl16389 N-termina	477	28	65.1	262	7	ADH86636	Enterococ
405	28	65.1	178	9	ADXL16403	Adxl16403 N-termina	478	28	65.1	263	6	ADH86636	Enterococ
406	28	65.1	178	9	ADXL16359	Adxl16359 N-termina	479	28	65.1	264	2	AAW53324	P-selecti
407	28	65.1	178	9	ADXL16404	Adxl16404 N-termina	480	28	65.1	265	4	AAU35032	Enterococ
408	28	65.1	178	9	ADXL16387	Adxl16387 N-termina	481	28	65.1	265	4	ADH86542	Enterococ
409	28	65.1	178	9	ADXL16370	Adxl16370 N-termina	482	28	65.1	268	7	ADH86542	Enterococ
410	28	65.1	178	9	ADXL16371	Adxl16371 N-termina	483	28	65.1	270	7	ADH86542	Enterococ
411	28	65.1	178	9	ADXL16372	Adxl16372 N-termina	484	28	65.1	270	8	ADH86542	Enterococ
412	28	65.1	178	9	ADXL16388	Adxl16388 N-termina	485	28	65.1	273	8	ADH86542	Enterococ
413	28	65.1	178	9	ADXL16374	Adxl16374 N-termina	486	28	65.1	277	6	ABU18434	Protein e
414	28	65.1	178	9	ADXL16386	Adxl16386 N-termina	487	28	65.1	277	7	ABO69689	Pseudomon
415	28	65.1	178	9	ADXL16385	Adxl16385 N-termina	488	28	65.1	280	4	AAU36886	Staphyloc
416	28	65.1	178	9	ADXL16356	Adxl16356 N-termina	489	28	65.1	280	4	ABM60757	Drosophil
417	28	65.1	178	9	ADXL16373	Adxl16373 N-termina	490	28	65.1	281	6	ABR42489	Conuermc
418	28	65.1	178	9	ADXL16402	Adxl16402 N-termina	491	28	65.1	289	9	ABM91537	M. xanthu
419	28	65.1	178	9	ADXL16401	Adxl16401 N-termina	492	28	65.1	296	2	AAU26213	Fuslon pr
420	28	65.1	178	9	ADXL16355	Adxl16355 N-termina	493	28	65.1	296	2	AAU26213	Fuslon pr
421	28	65.1	178	9	ADXL16358	Adxl16358 N-termina	494	28	65.1	296	2	AAU26213	Fuslon pr
422	28	65.1	179	8	ADJ49475	Adj49475 Oil-assoc	495	28	65.1	296	2	AAU26213	Fuslon pr
423	28	65.1	180	7	ADM04919	Adm04919 Human pro	496	28	65.1	296	2	AAU26213	Fuslon pr
424	28	65.1	183	8	ADN92060	Adn92060 Plant ful	497	28	65.1	296	2	AAU26213	Fuslon pr
425	28	65.1	184	8	ADN22981	Adn22981 Bacterial	498	28	65.1	300	6	ABM70389	Photorhab
426	28	65.1	185	4	AAU23307	Aau23307 Fibre kno	499	28	65.1	302	8	ADX92976	Plant ful
427	28	65.1	185	6	AAO23307	Aao23307 Fibre kno	500	28	65.1	303	8	ADX92976	Plant ful
428	28	65.1	185	9	ADXL16421	Adxl16421 Mutated F	501	28	65.1	303	8	ADX92976	Plant ful
429	28	65.1	185	9	ADXL16421	Adxl16421 Mutated F	502	28	65.1	304	4	ADM19689	Protein e
430	28	65.1	185	9	ADXL16419	Adxl16419 Parental	503	28	65.1	307	7	ADC94999	E. faeciu
431	28	65.1	192	4	AAU19536	Aau19536 Human dia	504	28	65.1	308	6	ABM67730	Photorhab
432	28	65.1	192	4	AAU19536	Aau19536 Human dia	505	28	65.1	309	6	ABM67730	Photorhab
433	28	65.1	192	4	AAU19536	Aau19536 Human dia	506	28	65.1	310	4	ABM67730	Photorhab
434	28	65.1	192	4	AAU19536	Aau19536 Human dia	507	28	65.1	311	4	ABM67730	Photorhab
435	28	65.1	192	4	AAU19536	Aau19536 Human dia	508	28	65.1	311	4	ABM67730	Photorhab
436	28	65.1	192	4	AAU19536	Aau19536 Human dia	509	28	65.1	311	4	ABM67730	Photorhab
437	28	65.1	192	4	AAU19536	Aau19536 Human dia	510	28	65.1	311	4	ABM67730	Photorhab
438	28	65.1	192	4	AAU19536	Aau19536 Human dia	511	28	65.1	311	4	ABM67730	Photorhab
439	28	65.1	192	4	AAU19536	Aau19536 Human dia	512	28	65.1	311	4	ABM67730	Photorhab
440	28	65.1	192	4	AAU19536	Aau19536 Human dia	513	28	65.1	311	4	ABM67730	Photorhab
441	28	65.1	192	4	AAU19536	Aau19536 Human dia	514	28	65.1	311	4	ABM67730	Photorhab
442	28	65.1	192	4	AAU19536	Aau19536 Human dia	515	28	65.1	311	4	ABM67730	Photorhab
443	28	65.1	192	4	AAU19536	Aau19536 Human dia	516	28	65.1	311	4	ABM67730	Photorhab
444	28	65.1	192	4	AAU19536	Aau19536 Human dia	517	28	65.1	311	4	ABM67730	Photorhab
445	28	65.1	192	4	AAU19536	Aau19536 Human dia	518	28	65.1	311	4	ABM67730	Photorhab
446	28	65.1	192	4	AAU19536	Aau19536 Human dia	519	28	65.1	311	4	ABM67730	Photorhab
447	28	65.1	192	4	AAU19536	Aau19536 Human dia	520	28	65.1	311	4	ABM67730	Photorhab
448	28	65.1	192	4	AAU19536	Aau19536 Human dia	521	28	65.1	311	4	ABM67730	Photorhab
449	28	65.1	192	4	AAU19536	Aau19536 Human dia	522	28	65.1	311	4	ABM67730	Photorhab
450	28	65.1	192	4	AAU19536	Aau19536 Human dia	523	28	65.1	311	4	ABM67730	Photorhab
451	28	65.1	192	4	AAU19536	Aau19536 Human dia	524	28	65.1	311	4	ABM67730	Photorhab
452	28	65.1	192	4	AAU19536	Aau19536 Human dia	525	28	65.1	311	4	ABM67730	Photorhab
453	28	65.1	192	4	AAU19536	Aau19536 Human dia	526	28	65.1	311	4	ABM67730	Photorhab
454	28	65.1	192	4	AAU19536	Aau19536 Human dia	527	28	65.1	311	4	ABM67730	Photorhab
455	28	65.1	192	4	AAU19536	Aau19536 Human dia	528	28	65.1	311	4	ABM67730	Photorhab
456	28	65.1	192	4	AAU19536	Aau19536 Human dia	529	28	65.1	311	4	ABM67730	Photorhab
457	28	65.1	192	4	AAU19536	Aau19536 Human dia	530	28	65.1	311	4	ABM67730	Photorhab
458	28	65.1	192	4	AAU19536	Aau19536 Human dia	531	28	65.1	311	4	ABM67730	Photorhab
459	28	65.1	192	4	AAU19536	Aau19536 Human dia	532	28	65.1	311	4	ABM67730	Photorhab
460	28	65.1	192	4	AAU19536	Aau19536 Human dia	533	28	65.1	311	4	ABM67730	Photorhab
461	28	65.1	192	4	AAU19536	Aau19536 Human dia	534	28	65.1	311	4	ABM67730	Photorhab
462	28	65.1	192	4	AAU19536	Aau19536 Human dia	535	28	65.1	311	4	ABM67730	Photorhab

536	28	65.1	413	8	ADJ48767	Adj48767 Oil-asso	609	28	65.1	570	8	ADL05248	AdL05248 M. catarr
537	28	65.1	419	6	ABU27357	Abu27357 Protein e	610	28	65.1	571	8	ADP04715	Adp04715 Sea squir
538	28	65.1	426	8	ADY12431	Ady12431 Plant ful	611	28	65.1	580	4	ADG70895	Adg70895 C albican
539	28	65.1	438	4	AUC36211	Auc36211 Pseudomon	612	28	65.1	582	8	ADN47488	Adn47488 Thermococ
540	28	65.1	441	7	ADC94998	Adc94998 E. faeciu	613	28	65.1	583	7	ADJ70094	Adj70094 Human hea
541	28	65.1	441	6	ADC94996	Adc94996 E. faeciu	614	28	65.1	609	6	ABP70527	Abp70527 Histone d
542	28	65.1	443	6	AOA23297	Aoa23297 Chimpanze	615	28	65.1	617	3	ABP70527	Abp70527 Histone d
543	28	65.1	443	9	ABE47164	Abe47164 Chimpanze	616	28	65.1	618	6	ABU40529	Abu40529 Protein e
544	28	65.1	443	9	ABE47170	Abe47170 Chimpanze	617	28	65.1	633	3	ADM19690	Adm19690 Protein e
545	28	65.1	446	5	ABP25955	Abp25955 Streptoco	618	28	65.1	635	3	ABP24787	Abp24787 Plant SDF
546	28	65.1	446	8	ADV83031	Adv83031 Streptoco	619	28	65.1	637	3	ADP06227	Adp06227 Bacterial
547	28	65.1	449	8	ADS29062	Ads29062 Bacterial	620	28	65.1	639	3	ABP24786	Abp24786 Plant SDF
548	28	65.1	462	8	ADQ08692	Adq08692 Clona inc	621	28	65.1	641	8	ADL81921	Adl81921 P. aerugi
549	28	65.1	464	2	AAV35231	Aav35231 Protein i	622	28	65.1	652	7	ABO77608	AbO77608 Pseudomon
550	28	65.1	464	6	ABU76819	Abu76819 Protein e	623	28	65.1	682	5	ABN93069	Abn93069 Herbicida
551	28	65.1	467	5	ABP73567	Abp73567 Candida a	624	28	65.1	699	8	AD841839	Ad841839 Bacterial
552	28	65.1	474	7	ABO80523	AbO80523 Pseudomon	625	28	65.1	710	8	ADQ65395	Adq65395 Novel hum
553	28	65.1	485	9	ADZ77672	Adz77672 Escherich	626	28	65.1	714	7	ADC95513	Adc95513 E. faeciu
554	28	65.1	485	9	ABE39815	Abe39815 L. pneumo	627	28	65.1	743	4	ABE65349	AbE65349 Drosophil
555	28	65.1	490	6	ABU42427	Abu42427 Protein e	628	28	65.1	762	9	AEA61936	Aea61936 Interleuk
556	28	65.1	490	6	ABM71034	Abm71034 Staphyloc	629	28	65.1	763	8	ADL16712	Adl16712 Human stu
557	28	65.1	492	6	ABU43625	Abu43625 Protein e	630	28	65.1	763	9	AEA61939	Aea61939 Albumin-i
558	28	65.1	494	8	ADS29911	Ads29911 Bacterial	631	28	65.1	786	9	AEA61935	Aea61935 Interleuk
559	28	65.1	499	5	ABP73254	Abp73254 Candida a	632	28	65.1	787	8	ADQ67638	Adq67638 Novel hum
560	28	65.1	500	3	AAV92051	Aav92051 HrPC9 po	633	28	65.1	787	9	AEA61938	Aea61938 Albumin-i
561	28	65.1	500	3	AAV92052	Aav92052 HrPCa10 p	634	28	65.1	838	5	AAW48735	Aaw48735 Human hel
562	28	65.1	500	3	AAV94626	Aav94626 Amino aci	635	28	65.1	838	8	ADO20283	Ado20283 Human PRO
563	28	65.1	500	4	ABN84841	Abn84841 Human FGF	636	28	65.1	917	4	AAU10980	Aau10980 Human PAR
564	28	65.1	500	7	ADK98680	Adk98680 Human PRO	637	28	65.1	920	6	ABP70827	Abp70827 Human C1Q
565	28	65.1	500	8	ADQ94618	Adq94618 Human tra	638	28	65.1	925	6	ABR43339	AbR43339 Caldicbaci
566	28	65.1	502	9	ABE36402	Abe36402 L. pneumo	639	28	65.1	925	6	ABR43321	AbR43321 Caldicbaci
567	28	65.1	507	7	ADC94759	Adc94759 E. faeciu	640	28	65.1	928	6	ABP55407	Abp55407 Human MDD
568	28	65.1	512	8	ADS27387	Ads27387 Bacterial	641	28	65.1	939	7	ABO70363	AbO70363 Pseudomon
569	28	65.1	523	3	ABP24025	Abp24025 Human PRO	642	28	65.1	940	5	ABE55167	AbE55167 Lactococc
570	28	65.1	523	3	AAV99419	Aav99419 Human PRO	643	28	65.1	969	9	ABE63009	AbE63009 Drosophil
571	28	65.1	523	4	ABE66168	Abe66168 Protein o	644	28	65.1	982	6	ADA55011	Ada55011 Human pro
572	28	65.1	523	4	ABE88348	AbE88348 Human mem	645	28	65.1	1000	9	ABM91063	Abm91063 M. xanthu
573	28	65.1	523	6	ABO33661	AbO33661 Novel hum	646	28	65.1	1016	3	ADJ70151	Adj70151 Human ORF
574	28	65.1	523	7	ABO44514	AbO44514 Human sec	647	28	65.1	1016	7	ADJ70151	Adj70151 Human hea
575	28	65.1	523	7	ABO33538	AbO33538 Novel hum	648	28	65.1	1016	8	ABM80282	Abm80282 Tumour-as
576	28	65.1	523	7	ADCI18151	Adci18151 Human PRO	649	28	65.1	1016	9	ADV70240	Adv70240 Tumour-ass
577	28	65.1	523	7	ADD70797	Add70797 Human sec	650	28	65.1	1032	8	ADR08889	Adr08889 Human pro
578	28	65.1	523	7	ADD39874	Add39874 Human sec	651	28	65.1	1085	6	ABU31244	Abu31244 Protein e
579	28	65.1	523	7	ADD70320	Add70320 Human sec	652	28	65.1	1085	6	ABU28426	Abu28426 Protein e
580	28	65.1	523	7	ADD38441	Add38441 Human sec	653	28	65.1	1086	2	AAW36051	Aaw36051 Hybrid Ma
581	28	65.1	523	7	ADD39397	Add39397 Human sec	654	28	65.1	1092	6	ADB10368	AdB10368 Alloiooc
582	28	65.1	523	7	ADD38920	Add38920 Human sec	655	28	65.1	1104	8	ADJ27131	Adj27131 Alloiooc
583	28	65.1	523	7	ADD40351	Add40351 Human sec	656	28	65.1	1140	4	ABJ69065	Abj69065 Drosophil
584	28	65.1	523	7	ADE50572	Ade50572 Human sec	657	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
585	28	65.1	523	7	ADE20184	Ade20184 Human sec	658	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
586	28	65.1	523	7	ADE50095	Ade50095 Human sec	659	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
587	28	65.1	523	7	ADE21653	Ade21653 Human sec	660	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
588	28	65.1	523	7	ADF30078	Adf30078 Human sec	661	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
589	28	65.1	523	7	ADF55971	Adf55971 Human sec	662	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
590	28	65.1	523	7	ADH99475	Adh99475 Human sec	663	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
591	28	65.1	523	8	ADP25966	Adp25966 Human sec	664	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
592	28	65.1	523	8	ADP25966	Adp25966 Human sec	665	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
593	28	65.1	523	8	ADP24865	Adp24865 Human sec	666	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
594	28	65.1	523	8	ADP29601	Adp29601 Human sec	667	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
595	28	65.1	523	8	ADH03170	Adh03170 Human sec	668	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
596	28	65.1	523	8	ADH03170	Adh03170 Human sec	669	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
597	28	65.1	523	8	ADH04124	Adh04124 Human sec	670	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
598	28	65.1	523	8	ADH03647	Adh03647 Human sec	671	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
599	28	65.1	523	8	ADH04601	Adh04601 Human sec	672	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
600	28	65.1	523	8	ADH61602	Adh61602 Human sec	673	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
601	28	65.1	523	8	ADL94801	Adl94801 Human sec	674	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
602	28	65.1	523	8	ADP99201	Adp99201 KIAA0830,	675	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
603	28	65.1	523	9	ADY63061	Ady63061 Human c1o	676	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
604	28	65.1	528	6	ADJ35335	Adj35335 Protein e	677	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
605	28	65.1	535	8	ADS21038	Ads21038 Bacterial	678	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
606	28	65.1	542	7	ADF94893	Adf94893 Human gen	679	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
607	28	65.1	542	8	ADL71719	Adl71719 Novel hum	680	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC
608	28	65.1	566	9	ABM95405	Abm95405 M. xanthu	681	28	65.1	1297	2	AAW3866	Aaw3866 ChimERIC

682	27	62.8	48	3	AAG48052	Aag48052	Arabidops	755	27	62.8	244	7	ADC10970	Adc10970	Human pro
683	27	62.8	53	4	AAO09394	Aao09394	Human pol	756	27	62.8	244	8	ADP07865	Adp07865	Human sec
684	27	62.8	82	3	AY84629	Ay84629	The colle	757	27	62.8	245	3	AAQ21293	Aaq21293	Arabidops
685	27	62.8	82	7	ADF30964	Adf30964	Soil meta	758	27	62.8	245	3	AAQ21293	Aaq21293	Arabidops
686	27	62.8	82	7	ADF30898	Adf30898	Soil meta	759	27	62.8	245	4	AAU12278	Aau12278	Human PRO
687	27	62.8	88	6	ADA34830	Ada34830	Acinetoba	760	27	62.8	245	6	ABO17722	Abol17722	Novel hum
688	27	62.8	90	2	AAW21828	Aaw21828	Rat RT1.B	761	27	62.8	245	6	ABU80976	Abu80976	Human PRO
689	27	62.8	93	2	AAW11929	Aaw11929	Human S'	762	27	62.8	245	6	ABU66676	Abu66676	Human PRO
690	27	62.8	93	4	AAU67813	Aau67813	Propionib	763	27	62.8	245	6	ABU59757	Abu59757	Novel sec
691	27	62.8	93	4	ABM64332	Abm64332	Propionib	764	27	62.8	245	6	ABO24947	Abol24947	Human sec
692	27	62.8	103	4	AAO09001	Aao09001	Human pol	765	27	62.8	245	6	ABU66952	Abu66952	Human sec
693	27	62.8	105	4	AAU39498	Aau39498	Propionib	766	27	62.8	245	6	ADA45733	Ada45733	Novel hum
694	27	62.8	105	6	ABM36017	Abm36017	Propionib	767	27	62.8	245	6	ADA76164	Ada76164	Human PRO
695	27	62.8	106	2	AAV12546	Aav12546	Human S'	768	27	62.8	245	6	ADA18814	Ada18814	Human PRO
696	27	62.8	110	4	AAW82529	Aaw82529	S. epider	769	27	62.8	245	6	ADA61437	Ada61437	Homo sapi
697	27	62.8	111	3	AAW52505	Aaw52505	Helicobac	770	27	62.8	245	6	ADB19222	Adb19222	Novel hum
698	27	62.8	121	2	AAW21827	Aaw21827	Rat RT1.B	771	27	62.8	245	6	ADB27763	Adb27763	Human PRO
699	27	62.8	121	4	AAU44635	Aau44635	Propionib	772	27	62.8	245	6	ADA86242	Ada86242	Novel hum
700	27	62.8	121	6	ABM41154	Abm41154	Propionib	773	27	62.8	245	6	ADB15806	Adb15806	Human PRO
701	27	62.8	125	4	AAU23322	Aau23322	Novel hum	774	27	62.8	245	6	ADA7592	Ada7592	Human PRO
702	27	62.8	129	2	AAW27843	Aaw27843	Staphyloc	775	27	62.8	245	6	ADA67387	Ada67387	Human PRO
703	27	62.8	132	2	AAW82564	Aaw82564	Rice glyc	776	27	62.8	245	6	ADB30394	Adb30394	Human PRO
704	27	62.8	132	4	AAW05245	Aaw05245	Rice glyc	777	27	62.8	245	6	ADA85690	Ada85690	Novel hum
705	27	62.8	132	5	AAU76199	Aau76199	Rice wate	778	27	62.8	245	6	ADA96902	Ada96902	Human PRO
706	27	62.8	132	7	AAE38779	Aae38779	Rice wate	779	27	62.8	245	6	ADA79206	Ada79206	Human PRO
707	27	62.8	136	8	ADW72833	Adw72833	Plant ful	780	27	62.8	245	6	ADA87345	Ada87345	Novel hum
708	27	62.8	138	7	ADM05291	Adm05291	Human pro	781	27	62.8	245	6	ADA16547	Ada16547	Human PRO
709	27	62.8	138	8	ABO54981	Abol54981	Human gen	782	27	62.8	245	6	ADA91639	Ada91639	Novel hum
710	27	62.8	143	5	ABP07026	Abp07026	Human ORF	783	27	62.8	245	6	ADB14702	Adb14702	Human PRO
711	27	62.8	148	4	ABG01189	Abg01189	Novel hum	784	27	62.8	245	6	ADB18663	Adb18663	Novel hum
712	27	62.8	149	9	ABE40143	Abe40143	L. pneumo	785	27	62.8	245	6	ADA93878	Ada93878	Human PRO
713	27	62.8	149	9	ABE36760	Abe36760	L. pneumo	786	27	62.8	245	6	ADB19774	Adb19774	Novel hum
714	27	62.8	155	6	ABO00481	Abol00481	Novel hum	787	27	62.8	245	6	ADB13086	Adb13086	Human PRO
715	27	62.8	156	3	ABE16346	Abel16346	E. grandi	788	27	62.8	245	6	ABO43255	Abol43255	Novel hum
716	27	62.8	156	5	ADW06656	Adw06656	Cell prot	789	27	62.8	245	6	ADA74340	Ada74340	Human PRO
717	27	62.8	157	7	ADP41522	Adp41522	Caffeic a	790	27	62.8	245	6	ADB24573	Adb24573	Human PRO
718	27	62.8	157	5	ABE50043	Abel50043	Listeria	791	27	62.8	245	6	ADA82097	Ada82097	Human PRO
719	27	62.8	160	5	ABU51074	Abu51074	Helicobac	792	27	62.8	245	6	ADA75060	Ada75060	Human PRO
720	27	62.8	163	3	AAW57769	Aaw57769	Arabidops	793	27	62.8	245	6	ADA85138	Ada85138	Novel hum
721	27	62.8	164	5	ABU51951	Abu51951	Helicobac	794	27	62.8	245	6	ADA84586	Ada84586	Novel hum
722	27	62.8	165	4	ABG12127	Abg12127	Novel hum	795	27	62.8	245	6	ADB29842	Adb29842	Human PRO
723	27	62.8	166	6	ABU25874	Abu25874	Protein e	796	27	62.8	245	6	ADA80370	Ada80370	Human PRO
724	27	62.8	168	3	AAW57768	Aaw57768	Arabidops	797	27	62.8	245	6	ADA75612	Ada75612	Human PRO
725	27	62.8	170	1	AAW93257	Aaw93257	Fusion pr	798	27	62.8	245	6	ADA46837	Ada46837	Human PRO
726	27	62.8	172	1	AAW93262	Aaw93262	Peptide S	799	27	62.8	245	6	ADB25133	Adb25133	Human PRO
727	27	62.8	180	6	AAE33454	Aae33454	Rat RT1B	800	27	62.8	245	6	ADA93309	Ada93309	Human PRO
728	27	62.8	180	6	AAE33454	Aae33454	Peptide S	801	27	62.8	245	6	ADB26659	Adb26659	Human PRO
729	27	62.8	183	4	AAU48492	Aau48492	Propionib	802	27	62.8	245	6	ADB30946	Adb30946	Human PRO
730	27	62.8	183	6	ABM45011	Abm45011	Propionib	803	27	62.8	245	6	ADA60874	Ada60874	Homo sapi
731	27	62.8	184	6	AAQ29812	Aaq29812	Maize roo	804	27	62.8	245	6	ADB24021	Adb24021	Human PRO
732	27	62.8	185	2	AAV06797	Aav06797	Betalaph	805	27	62.8	245	6	ADA96350	Ada96350	Human PRO
733	27	62.8	185	6	AAE33447	Aae33447	Rat RT1B	806	27	62.8	245	6	ADA80922	Ada80922	Human PRO
734	27	62.8	186	9	ABE42119	Abel42119	L. pneumo	807	27	62.8	245	6	ADA95798	Ada95798	Human PRO
735	27	62.8	189	3	AAE51920	Aae51920	Gene 41 h	808	27	62.8	245	6	ADB26107	Adb26107	Human PRO
736	27	62.8	190	9	ABE38965	Abel38965	L. pneumo	809	27	62.8	245	6	ADB21592	Adb21592	Novel hum
737	27	62.8	194	8	ADP07862	Adp07862	Human sec	810	27	62.8	245	7	ADA77371	Ada77371	Human PRO
738	27	62.8	197	3	AAE16552	Aae16552	Arabidops	811	27	62.8	245	7	ADB18111	Adb18111	Human PRO
739	27	62.8	205	8	ADH71866	Adh71866	Human pro	812	27	62.8	245	7	ADA86794	Ada86794	Novel hum
740	27	62.8	206	2	AAV08897	Aav08897	Varicella	813	27	62.8	245	7	ADA87897	Ada87897	Novel hum
741	27	62.8	211	5	AAW48252	Aaw48252	Human CIR	814	27	62.8	245	7	ADA46285	Ada46285	Novel hum
742	27	62.8	212	6	ABU22130	Abu22130	Protein e	815	27	62.8	245	7	ADB28315	Adb28315	Human PRO
743	27	62.8	226	3	AAW90759	Aaw90759	M. janna	816	27	62.8	245	7	ADB28867	Adb28867	Human PRO
744	27	62.8	227	4	ABW71050	Abw71050	Fructophil	817	27	62.8	245	7	ADA76819	Ada76819	Human PRO
745	27	62.8	230	9	ADW26691	Adw26691	Fructo-ol	818	27	62.8	245	7	ADA88449	Ada88449	Novel hum
746	27	62.8	232	3	AAE21295	Aae21295	Arabidops	819	27	62.8	245	7	ADA97454	Ada97454	Human PRO
747	27	62.8	232	3	AAQ47204	Aaq47204	Arabidops	820	27	62.8	245	7	ADB27211	Adb27211	Human PRO
748	27	62.8	232	5	ABE90189	Abel90189	Human pol	821	27	62.8	245	7	ADB22144	Adb22144	Novel hum
749	27	62.8	238	8	AD43146	Ad43146	IPT-like	822	27	62.8	245	7	ADA66835	Ada66835	Human PRO
750	27	62.8	239	7	ABO64619	Abol64619	Klebsiell	823	27	62.8	245	7	ADB22696	Adb22696	Human PRO
751	27	62.8	240	3	AAE21294	Aae21294	Arabidops	824	27	62.8	245	7	ADB23469	Adb23469	Human PRO
752	27	62.8	240	3	AAQ47203	Aaq47203	Arabidops	825	27	62.8	245	7	ADA92191	Ada92191	Novel hum
753	27	62.8	244	4	AAU19788	Aau19788	Human nov	826	27	62.8	245	7	ADB15254	Adb15254	Human PRO
754	27	62.8	244	5	ABP48008	Abp48008	Human pol	827	27	62.8	245	7	ADB38506	Adb38506	Novel hum



828	27	62.8	245	7	ADB37954	Novel	hum	901	27	62.8	245	7	ADG23005	Novel	hum
829	27	62.8	245	7	ADB66426	Novel	hum	902	27	62.8	245	7	ADF97340	Human	PRO
830	27	62.8	245	7	ADB89506	Human	PRO	903	27	62.8	245	7	ADG80404	Human	PRO
831	27	62.8	245	7	ADB90238	Human	PRO	904	27	62.8	245	7	ADG79852	Human	PRO
832	27	62.8	245	7	ADB39339	Novel	hum	905	27	62.8	245	7	ADH55144	Novel	hum
833	27	62.8	245	7	ADB46962	Novel	hum	906	27	62.8	245	7	ADH55696	Novel	hum
834	27	62.8	245	7	ADB86569	Human	PRO	907	27	62.8	245	7	ADI63915	Novel	hum
835	27	62.8	245	7	ADB77174	Novel	hum	908	27	62.8	245	7	ADI63363	Novel	hum
836	27	62.8	245	7	ADB34331	Human	PRO	909	27	62.8	245	7	ADH81777	Novel	hum
837	27	62.8	245	7	ADB35435	Human	PRO	910	27	62.8	245	7	ADH81225	Novel	hum
838	27	62.8	245	7	ADB33779	Human	PRO	911	27	62.8	245	7	ADM82394	Novel	hum
839	27	62.8	245	7	ADB334883	Human	PRO	912	27	62.8	245	7	ADM82394	Novel	hum
840	27	62.8	245	7	ADB35987	Human	PRO	913	27	62.8	245	7	ADN15793	Novel	hum
841	27	62.8	245	7	ADB46382	Novel	hum	914	27	62.8	245	7	ADN16422	Novel	hum
842	27	62.8	245	7	ADC50255	Novel	hum	915	27	62.8	245	7	ADN15241	Novel	hum
843	27	62.8	245	7	ADC71802	Novel	hum	916	27	62.8	245	7	ADN14689	Novel	hum
844	27	62.8	245	7	ADC59781	Novel	hum	917	27	62.8	245	7	ADI64864	Novel	hum
845	27	62.8	245	7	ADC52788	Novel	hum	918	27	62.8	245	7	ADC80951	Novel	hum
846	27	62.8	245	7	ADC57142	Novel	hum	919	27	62.8	245	7	ADD76399	Human	PRO
847	27	62.8	245	7	ADC60333	Novel	hum	920	27	62.8	245	7	ADD87763	Human	PRO
848	27	62.8	245	7	ADC50808	Novel	hum	921	27	62.8	245	7	ADD86167	Human	PRO
849	27	62.8	245	7	ADC65335	Human	PRO	922	27	62.8	245	7	ADH75615	Human	PRO
850	27	62.8	245	7	ADC54433	Novel	hum	923	27	62.8	245	7	ADH23191	Human	PRO
851	27	62.8	245	7	ADC33394	Novel	hum	924	27	62.8	245	7	ADH23743	Human	PRO
852	27	62.8	245	7	ADC58917	Novel	hum	925	27	62.8	245	7	ADH24386	Human	PRO
853	27	62.8	245	7	ADC55795	Novel	hum	926	27	62.8	245	7	ADH87211	Human	PRO
854	27	62.8	245	7	ADC58365	Novel	hum	927	27	62.8	245	7	ADH89077	Human	PRO
855	27	62.8	245	7	ADD03039	Novel	hum	928	27	62.8	245	7	ADH18216	Human	PRO
856	27	62.8	245	7	ADC90031	Novel	hum	929	27	62.8	245	7	ADH88525	Human	PRO
857	27	62.8	245	7	ADC69450	Human	PRO	930	27	62.8	245	7	ADH94545	Human	PRO
858	27	62.8	245	7	ADC48339	Human	PRO	931	27	62.8	245	7	ADH90956	Human	PRO
859	27	62.8	245	7	ADD09868	Human	PRO	932	27	62.8	245	7	ADH95097	Human	PRO
860	27	62.8	245	7	ADD04443	Novel	hum	933	27	62.8	245	7	ADH93207	Human	PRO
861	27	62.8	245	7	ADC80399	Novel	hum	934	27	62.8	245	7	ADH34788	Human	PRO
862	27	62.8	245	7	ADD10906	Human	PRO	935	27	62.8	245	7	ADH92103	Novel	hum
863	27	62.8	245	7	ADC47787	Human	PRO	936	27	62.8	245	7	ADH90404	Human	PRO
864	27	62.8	245	7	ADC79847	Novel	hum	937	27	62.8	245	7	ADH91551	Novel	hum
865	27	62.8	245	7	ADD09316	Human	PRO	938	27	62.8	245	7	ADG02130	Human	PRO
866	27	62.8	245	7	ADD41029	Novel	hum	939	27	62.8	245	7	ADG21916	Novel	hum
867	27	62.8	245	7	ADD52168	Human	PRO	940	27	62.8	245	7	ADG19986	Human	PRO
868	27	62.8	245	7	ADD52908	Human	PRO	941	27	62.8	245	7	ADG97892	Human	PRO
869	27	62.8	245	7	ADD53460	Novel	hum	942	27	62.8	245	7	ADG24109	Novel	hum
870	27	62.8	245	7	ADD51616	Human	PRO	943	27	62.8	245	7	ADH98463	Human	PRO
871	27	62.8	245	7	ADD02415	Human	PRO	944	27	62.8	245	7	ADG03294	Human	PRO
872	27	62.8	245	7	ADD01849	Human	PRO	945	27	62.8	245	7	ADG16600	Human	PRO
873	27	62.8	245	7	ADD54031	Novel	hum	946	27	62.8	245	7	ADG05059	Human	PRO
874	27	62.8	245	7	ADD92348	Human	PRO	947	27	62.8	245	7	ADG19326	Human	PRO
875	27	62.8	245	7	ADD931244	Human	PRO	948	27	62.8	245	7	ADG13163	Human	PRO
876	27	62.8	245	7	ADE03858	Human	PRO	949	27	62.8	245	7	ADG08220	Novel	hum
877	27	62.8	245	7	ADE32155	Novel	hum	950	27	62.8	245	7	ADG15390	Human	PRO
878	27	62.8	245	7	ADE32087	Human	PRO	951	27	62.8	245	7	ADG15390	Human	PRO
879	27	62.8	245	7	ADD79311	Human	PRO	952	27	62.8	245	7	ADG05973	Human	PRO
880	27	62.8	245	7	ADE41847	Human	PRO	953	27	62.8	245	7	ADG23557	Novel	hum
881	27	62.8	245	7	ADE17664	Human	PRO	954	27	62.8	245	7	ADG03846	Human	PRO
882	27	62.8	245	7	ADD91796	Human	PRO	955	27	62.8	245	7	ADG24747	Novel	hum
883	27	62.8	245	7	ADE33259	Novel	hum	956	27	62.8	245	7	ADG07044	Novel	hum
884	27	62.8	245	7	ADE33811	Novel	hum	957	27	62.8	245	7	ADG07596	Novel	hum
885	27	62.8	245	7	ADD79863	Human	PRO	958	27	62.8	245	7	ADG55091	Novel	hum
886	27	62.8	245	7	ADD92900	Human	PRO	959	27	62.8	245	7	ADG60755	Novel	hum
887	27	62.8	245	7	ADE19320	Human	PRO	960	27	62.8	245	7	ADG1859	Novel	hum
888	27	62.8	245	7	ADE18768	Human	PRO	961	27	62.8	245	7	ADG2060	Human	PRO
889	27	62.8	245	7	ADE42964	Human	PRO	962	27	62.8	245	7	ADG57299	Novel	hum
890	27	62.8	245	7	ADD95753	Human	PRO	963	27	62.8	245	7	ADG56747	Novel	hum
891	27	62.8	245	7	ADE22639	Human	PRO	964	27	62.8	245	7	ADG55643	Novel	hum
892	27	62.8	245	7	ADD78757	Human	PRO	965	27	62.8	245	7	ADG58403	Novel	hum
893	27	62.8	245	7	ADE32707	Novel	hum	966	27	62.8	245	7	ADG70769	Novel	hum
894	27	62.8	245	7	ADE42399	Human	PRO	967	27	62.8	245	7	ADG57851	Novel	hum
895	27	62.8	245	7	ADD80415	Human	PRO	968	27	62.8	245	7	ADG53435	Novel	hum
896	27	62.8	245	7	ADD89443	Human	PRO	969	27	62.8	245	7	ADG71321	Novel	hum
897	27	62.8	245	7	ADE40727	Human	PRO	970	27	62.8	245	7	ADG81508	Human	PRO
898	27	62.8	245	7	ADE04526	Human	PRO	971	27	62.8	245	7	ADH30470	Human	PRO
899	27	62.8	245	7	ADE92655	Human	PRO	972	27	62.8	245	7	ADH11837	Novel	hum
900	27	62.8	245	7	ADG21364	Novel	hum	973	27	62.8	245	7	ADG52259	Novel	hum

974 27 62.8 245 8 ADG53987 Novel hum  
975 27 62.8 245 8 ADG80956 Human PRO  
976 27 62.8 245 8 ADG56195 Novel hum  
977 27 62.8 245 8 ADH12461 Novel hum  
978 27 62.8 245 8 ADG611307 Novel hum  
979 27 62.8 245 8 ADH28394 Human PRO  
980 27 62.8 245 8 ADG54539 Novel hum  
981 27 62.8 245 8 ADG59579 Novel hum  
982 27 62.8 245 8 ADI181003 Human PRO  
983 27 62.8 245 8 ADG09746 Novel hum  
984 27 62.8 245 8 ADI15217 Novel hum  
985 27 62.8 245 8 ADG09094 Novel hum  
986 27 62.8 245 8 ADI14549 Novel hum  
987 27 62.8 245 8 ADI18144 Novel hum  
988 27 62.8 245 8 ADJ63425 Novel hum  
989 27 62.8 245 8 ADJ77320 Human PRO  
990 27 62.8 245 8 ADJ65442 Human PRO  
991 27 62.8 245 8 ADM27578 Human PRO  
992 27 62.8 245 8 ADM42302 Human PRO  
993 27 62.8 245 8 ADM28164 Human PRO  
994 27 62.8 245 8 ADI95646 Human PRO  
995 27 62.8 245 8 ADI96198 Novel hum  
996 27 62.8 245 8 ADS32150 Novel hum  
997 27 62.8 245 8 ADT03134 Human PRO  
998 27 62.8 245 9 ADZ03185 Human sec  
999 27 62.8 245 9 AEB13931 Cancer ce  
1000 27 62.8 246 8 ADX80244 Plant ful

## ALIGNMENTS

RESULT 1  
ABB08365  
ID ABB08365 standard; protein; 9 AA.  
XX ABB08365;  
XX  
XX 07-MAY-2002 (first entry)  
XX  
XX The natural epitope of human cancer antigen eIF3.  
XX Human; melanoma antigen eukaryotic initiation factor 3; eIF3;  
KW ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;  
KW anti-cancer; vaccine.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Domain 1 /note= "HLA-2 binding residue"  
FT Domain 2 /note= "HLA-2 binding residue"  
FT Domain 3..8 /note= "T-cell receptor (TCR) binding domain"  
FT Domain 9 /note= "HLA-2 binding residue"  
FT  
XX WO200192307-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 30-MAY-2001; 2001WO-US017456.  
XX  
XX 31-MAY-2000; 2000US-0209391P.  
PR 17-AUG-2000; 2000US-0226258P.  
PR 20-DEC-2000; 2000US-0257008P.  
XX  
XX (GENZ ) GENZYME CORP.  
PA Nicolette CA;  
XX  
XX WPI; 2002-139606/18.  
XX

DR N-PSDB; ABA97216.  
XX  
PT New therapeutic compounds useful against human ovarian cancer, for  
PT modulating immune response in a subject, and for generating antibodies  
XX that specifically recognize and bind to these molecules.  
PS Claim 10; Page 59; 68pp; English.  
XX  
CC The invention relates to novel therapeutic compounds, that are designed  
CC to enhance binding to MHC molecules and to enhance immunoregulatory  
CC properties relative to their natural counterparts. The activity of the  
CC compounds of the invention may be described as cytostatic and  
CC immunomodulatory. The compounds are useful against human ovarian cancer,  
CC for modulating immune response in a subject, and for generating  
CC antibodies that specifically recognize and bind to these molecules.  
CC Compositions comprising the compounds are useful as components of anti-  
CC cancer vaccines and to expand immune effector cells that are specific for  
CC cells characterized by expression of antigen eIF3 (melanoma antigen  
CC eukaryotic initiation factor). The peptides or polypeptides conjugated to  
CC a detectable agent may be used in diagnostic procedures, such as in the  
CC detection and purification of antibodies, and as immunogens for  
CC production of antibodies. The polynucleotides can be used as primers for  
CC detecting genes or gene transcripts expressed in APC to confirm  
CC transduction of the polynucleotides into host cells. The current sequence  
CC represents the natural epitope of human cancer antigen eIF3 (corresponds  
XX to residues 242-250 of ABB08360)  
XX Sequence 9 AA;  
Query Match 100.0%; Score 43; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLQLMLDRV 9  
Db 1 NLQLMLDRV 9  
RESULT 2  
ABR82217  
ID ABR82217 standard; peptide; 9 AA.  
XX ABR82217;  
XX  
XX 13-OCT-2003 (first entry)  
XX  
XX Human antigen eIF3 epitope (residues 242-250).  
XX Eukaryotic translation initiation factor 3; eIF3; neoplasia; cancer;  
KW cytostatic; gene therapy; human; antigen; epitope.  
XX Homo sapiens.  
XX WO2003050543-A1.  
XX 19-JUN-2003.  
XX  
XX 05-DEC-2001; 2001WO-US047997.  
XX  
XX 05-DEC-2001; 2001WO-US047997.  
XX (GENZ ) GENZYME CORP.  
XX Nicolette CA;  
XX  
XX WPI; 2003-532936/50.  
XX  
XX Aiding in the diagnosis of a neoplastic condition, useful for treating  
PT cancer and related malignancies comprises determining the amount of  
PT expression of an eIF3 protein in a test sample isolated from the cell or  
PT tissue.  
XX  
XX Claim 6; Page 30; 77pp; English.

XX The invention relates to aiding in the diagnosis of a neoplastic  
 CC condition or susceptibility to a neoplastic condition of an animal cell  
 CC or tissue. The method involves determining the amount of expression of an  
 CC eukaryotic translation initiation factor 3 (eIF3) protein in a test  
 CC sample isolated from the cell or tissue, and diagnosing a neoplastic  
 CC condition or susceptibility to a neoplastic condition based on the amount  
 CC of expression of the eIF3 protein. The methods, compounds and kits are  
 CC useful in therapeutics, diagnostic and screening methods for human cancer  
 CC and related malignancies, e.g. ovarian, breast, lung, colon, prostate,  
 CC pancreatic or gastrointestinal cancer, or melanoma. The present sequence  
 CC represents the human antigen eIF3 epitope  
 XX

SQ Sequence 9 AA;  
 Query Match 100.0%; Score 43; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLQLMDRV 9  
 DB 1 NLQLMDRV 9  
 |||||

RESULT 3  
 AAB56775  
 ID AAB56775 standard; protein; 256 AA.  
 AC AAB56775;  
 XX 13-MAR-2001 (first entry)  
 XX Human prostate cancer antigen protein sequence SEQ ID NO:1353.  
 DE Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease.  
 XX Homo sapiens.  
 OS WO200055174-A1.  
 PN 21-SEP-2000.  
 PD 08-MAR-2000; 2000WO-US005988.  
 XX 12-MAR-1999; 99US-0124270P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX Rosen CA, Ruben SM;  
 PI WPI; 2000-587513/55.  
 DR N-PSDB; AAB15978.  
 XX Prostate cancer associated gene sequences, referred to as prostate cancer  
 PT antigens, useful for treatment, prevention, and diagnosis of disorders  
 PT such as prostate cancer.  
 XX Claim 11; Page 1777-1778; 2338pp; English.  
 PS AAB15566 to AAB16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytostatic,  
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic

CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAB16506 to AAB16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention  
 XX Sequence 256 AA;  
 SQ  
 Query Match 100.0%; Score 43; DB 3; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLQLMDRV 9  
 DB 146 NLQLMDRV 154  
 |||||

RESULT 4  
 ADE29060  
 ID ADE29060 standard; protein; 302 AA.  
 XX ADE29060;  
 AC ADE29060;  
 XX 29-JAN-2004 (first entry)  
 XX Human EIF3S3 selected interacting domain protein - SEQ ID 46.  
 DE anti-HIV; SID; selected interacting domain; HIV; gene therapy; siRNA;  
 KW silencing RNA; HIV-1 integrase; LSGDF; MCM7; HB01; Snurportin; VBPI;  
 KW Transportin-SR; EIF3S3; human.  
 XX Homo sapiens.  
 OS WO2003046176-A2.  
 PN 05-JUN-2003.  
 PD 26-NOV-2002; 2002WO-BP013868.  
 XX 26-NOV-2001; 2001US-0333346P.  
 PR 31-MAY-2002; 2002US-0385132P.  
 XX (HYBR-) HYBRIGENICS.  
 PA Legrain P, Rain J, Benarous R, Emiliani S, Berlioz-Torrent C;  
 PI Blot G;  
 XX WPI; 2003-505199/47.  
 DR N-PSDB; ADE29037.  
 XX New complex between two interacting proteins, useful for screening a  
 PT molecules that inhibit human immunodeficiency virus or for preparing a  
 PT medicament for treating HIV-1.  
 XX Claim 9; SEQ ID NO 46; 102pp; English.  
 PS The invention relates to a novel complex between two interacting proteins  
 CC listed within the specification. The complex of the invention  
 CC demonstrates anti-HIV activity whilst the SID (selected interacting  
 CC domains) and polypeptides may be useful for screening molecules that  
 CC inhibit human immunodeficiency virus (HIV), as well as during gene  
 CC therapy procedures. The siRNAs (silencing RNAs) targeted against cellular  
 CC proteins interacting with HIV-1 integrase, LSGDF, MCM7, HB01, Snurportin,  
 CC VBPI, Transportin-SR and EIF3S3, are useful in preparing a medicament for  
 CC treating HIV-1. The current sequence is that of the human SID protein of  
 CC the invention.  
 XX Sequence 302 AA;  
 SQ  
 Query Match 100.0%; Score 43; DB 7; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RESULT 7  
ABR82212  
ID ABR82212 standard; protein; 352 AA.

XX AC ABR82212;  
XX 13-OCT-2003 (first entry)  
DT Human antigen eukaryotic translation initiation factor 3 (eIF3).  
XX  
XX  
DE  
XX  
XX  
KW Eukaryotic translation initiation factor 3; eIF3; neoplasia; cancer;  
KW cytosolic; gene therapy; human; antigen.  
XX

OS Homo sapiens.  
XX  
PN WO2003050543-A1.  
XX  
XX 19-JUN-2003.  
PD  
XX  
XX 05-DEC-2001; 2001WO-US047997.  
PF  
XX  
XX 05-DEC-2001; 2001WO-US047997.  
PR  
XX

PA (GENZ ) GENZYME CORP.

XX Nicolette CA;  
PI  
XX  
XX WPI; 2003-532936/50.  
DR  
XX N-PSDB; ACC85029.  
XX

PT Aiding in the diagnosis of a neoplastic condition, useful for treating  
PT cancer and related malignancies comprises determining the amount of  
PT expression of an eIF3 protein in a test sample isolated from the cell or  
PT tissue.  
XX

PS Claim 6; Page 71-72; 77pp; English.

XX The invention relates to aiding in the diagnosis of a neoplastic  
CC condition or susceptibility to a neoplastic condition of an animal cell  
CC or tissue. The method involves determining the amount of expression of an  
CC eukaryotic translation initiation factor 3 (eIF3) protein in a test  
CC sample isolated from the cell or tissue, and diagnosing a neoplastic  
CC condition or susceptibility to a neoplastic condition based on the amount  
CC of expression of the eIF3 protein. The methods, compounds and kits are  
CC useful in therapeutics, diagnostic and screening methods for human cancer  
CC and related malignancies, e.g. ovarian, breast, lung, colon, prostate,  
CC pancreatic or gastrointestinal cancer, or melanoma. The present sequence  
CC represents the human antigen eIF3  
XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 43; DB 7; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
DB 242 NLQLMDRV 250

RESULT 8  
ADJ68541  
ID ADJ68541 standard; protein; 352 AA.  
XX  
XX ADJ68541;  
XX

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID347.  
XX  
XX mitochondrial; human; screening assay; diabetes mellitus;  
KW

KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX

OS Homo sapiens.

XX WO2003087768-A2.

XX 23-OCT-2003.

XX 04-APR-2003; 2003WO-US010870.

XX 12-APR-2002; 2002US-0372843P.

XX 17-JUN-2002; 2002US-0389987P.

XX 20-SEP-2002; 2002US-0412418P.

XX (MITO-) MITOKOR.

XX (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;

XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX

PS Claim 1; SEQ ID NO 347; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, neurotropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 43; DB 7; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
DB 242 NLQLMDRV 250

RESULT 9  
ABM81006  
ID ABM81006 standard; protein; 352 AA.  
XX  
XX AC ABM81006;  
XX

DT 18-NOV-2004 (first entry)

XX Tumour-associated antigenic target (TAT) polypeptide PRO81700, SEQ:2599.  
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
KW chromosome identification; chromosome mapping; gene mapping;  
KW gene therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2004030615-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 29-SEP-2003; 2003WO-US028547.  
XX  
PR 02-OCT-2002; 2002US-0414971P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Wu TD, Zhang Z, Zhou Y;  
XX  
XX WPI; 2004-347921/32.  
DR N-PSDB; ACN38836.  
XX  
XX New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a  
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.  
XX  
PS Claim 12; SEQ ID NO 2599; 7273pp; English.  
XX  
XX The invention relates to human tumour-associated antigenic target (TAT)  
CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
CC overexpressed in cancer tissues compared to normal tissues, and may thus  
CC serve as effective targets for the diagnosis and treatment of cancer in  
CC mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
CC TAT polypeptide; and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention  
XX  
XX Sequence 352 AA;  
SQ  
Query Match 100.0%; Score 43; DB 8; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLQLLMDRV 9  
Db 242 NLQLLMDRV 250  
RESULT 10  
ADS34462  
ID ADS34462 standard; protein; 352 AA.  
XX  
AC ADS34462;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE POSH protein associated protein #26.  
XX  
KW cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant;

KW antiviral; neuroleptic; central nervous system; POSH polypeptide;  
KW POSH-associated protein; POSH-AP; HERPUD1; Ubiquitin ligase;  
KW antiviral agent; anti-apoptotic agent; anti-cancer agent;  
KW secretory pathway trafficking inhibitor;  
KW neurological disorder progression disorder; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; schizophrenia;  
KW Niemann-Pick's disease.  
XX  
OS Homo sapiens.  
XX  
PN WO2004078130-A2.  
XX  
PD 16-SEP-2004.  
XX  
PF 02-MAR-2004; 2004WO-US006308.  
XX  
PR 03-MAR-2003; 2003US-0451437P.  
PR 05-MAR-2003; 2003US-0452284P.  
PR 19-MAR-2003; 2003US-0455760P.  
PR 20-MAR-2003; 2003US-0456640P.  
PR 03-APR-2003; 2003US-0460525P.  
PR 04-APR-2003; 2003US-0460792P.  
PR 21-APR-2003; 2003US-0464285P.  
PR 09-MAY-2003; 2003US-0469462P.  
PR 15-MAY-2003; 2003US-0471378P.  
PR 20-MAY-2003; 2003US-0472327P.  
PR 30-MAY-2003; 2003US-0474706P.  
PR 03-JUN-2003; 2003US-0475825P.  
PR 17-JUN-2003; 2003US-0479317P.  
PR 19-JUN-2003; 2003US-0480215P.  
PR 19-JUN-2003; 2003US-0480376P.  
PR 08-AUG-2003; 2003US-0493860P.  
PR 28-AUG-2003; 2003US-0498634P.  
PR 16-SEP-2003; 2003US-0503931P.  
PR 10-NOV-2003; 2003WO-US035712.  
PR 05-FEB-2004; 2004WO-US003600.  
PR 02-MAR-2004; 2004US-0549896P.  
XX  
XX (PROT-) PROTEOLOGICS INC.  
XX  
XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;  
PI Greener T;  
XX  
XX WPI; 2004-662346/64.  
XX  
XX Isolated, purified or recombinant complex, useful for identifying an  
PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and  
PT POSH-associated protein (POSH-AP).  
XX  
PS Disclosure; SEQ ID NO 236; 374pp; English.  
XX  
XX The invention relates to an isolated, purified or recombinant complex (I)  
CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)  
CC or HERPUD1 and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are  
CC useful for identifying an agent that modulates an activity of a POSH  
CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-  
CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking  
CC of a protein through the secretory pathway, an agent that inhibits the  
CC progression of a neurological disorder, an agent that modulates a POSH  
CC function, an agent that modulates a HERPUD1 function. The methods can be  
CC used for treating a viral infection, for inhibiting an activity of a POSH  
CC -AP in a cell, for treating a POSH-associated disease in a subject. The  
CC POSH-associated disease is viral infection, POSH-associated cancer or  
CC POSH-associated neurological disorder. The methods are useful for  
CC treating or preventing POSH-associated neurological disorder in a subject  
CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,  
CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a  
CC protein of the invention.  
XX  
XX Sequence 352 AA;  
SQ  
Query Match 100.0%; Score 43; DB 8; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
|||||  
Db 242 NLQLMDRV 250

RESULT 11  
ADW08703  
ID ADW08703 standard; protein; 352 AA.  
XX  
AC ADW08703;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Human protein which is down-regulated in HCV-infected tissue - SEQ ID 40.  
XX  
KW gene targeting; hepatitis C virus infection; protein deactivation;  
KW protein activation.  
XX  
OS Homo sapiens.  
XX  
PN EP1493750-A2.  
XX  
PD 05-JAN-2005.  
XX  
PF 28-JUN-2004; 2004EP-00015098.  
XX  
PR 30-JUN-2003; 2003GB-00015248.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
XX  
PI Berndt P, Kilby PM, Rugman P;  
XX  
DR WPI; 2005-050476/06.  
XX  
PT New targets for an antiviral compound having at least one down- and up-  
PT regulated hepatitis C virus (HCV) polypeptide, useful in predicting  
PT outcomes, treating or preventing HCV infections.  
XX  
PS Claim 1; SEQ ID NO 40; 346pp; English.  
XX  
CC The invention comprises the amino acid sequences of protein targets for  
CC anti-hepatitis C virus (anti-HCV) drugs. The human protein targets of the  
CC invention are either up-regulated or down-regulated in HCV-infected  
CC tissue. The proteins of the invention are useful in the preparation of a  
CC medicament for the treatment or prevention of HCV infection. The present  
CC amino acid sequence represents a human protein of the invention which is  
CC down-regulated in HCV-infected tissue.  
XX  
SQ Sequence 352 AA;

Query Match 100.0%; Score 43; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
|||||  
Db 242 NLQLMDRV 250

RESULT 12  
ADW06453  
ID ADW06453 standard; protein; 352 AA.  
XX  
AC ADW06453;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1018.  
XX  
KW cytosstatic; cyclin-dependent kinase; cdk; biomarker.  
XX

OS Homo sapiens.  
XX  
PN WO2005012875-A2.  
XX  
PD 10-FEB-2005.  
XX  
PF 29-JUL-2004; 2004WO-US024424.  
XX  
PR 29-JUL-2003; 2003US-0490890P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;  
XX  
DR WPI; 2005-163068/17.  
DR N-PSDB; ADX06452.  
XX  
PT Biomarkers useful for predicting or determining the response of a mammal  
PT to a cancer treatment comprising administration of a modulator of cyclin-  
PT dependent kinase activity.  
XX  
PS Claim 5; SEQ ID NO 1018; 141pp; English.  
XX  
CC This invention describes a novel method of predicting or determining  
CC whether a mammal will respond or is responding to an anti-cancer agent  
CC that modulates cyclin-dependent kinase (cdk) activity. The method  
CC comprises measuring the level of one or more biomarkers selected from  
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID  
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the  
CC invention is utilized in a kit for determining or predicting whether  
CC patient would be susceptible or resistant to treatment by an agent  
CC modulating cdk activity. The invention also describes a method for  
CC utilizing individualized genetic profiles for treating diseases and  
CC disorders based on patient's response and molecular level, specialized  
CC microarrays comprising the biomarkers described, antibodies directed  
CC against the biomarkers and a cell culture model to identify biomarkers.  
CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-  
CC oxazolyl)methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-  
CC tartaric acid salt. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences. This  
CC sequence represents a biomarker used in the method of the invention.  
XX  
SQ Sequence 352 AA;

Query Match 100.0%; Score 43; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
|||||  
Db 242 NLQLMDRV 250

RESULT 13  
ADC31312  
ID ADC31312 standard; protein; 368 AA.  
XX  
AC ADC31312;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human novel polypeptide sequence, SEQ ID NO:1394.  
XX  
KW Human; diagnostic; drug screening; forensics; gene mapping;  
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;  
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;  
KW ulcers; osteoporosis; autoimmune disease; cancer;  
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;  
KW neuroprotective; antianemic; anticoagulant; thrombolytic; vulnery;  
KW antitumor; osteopathic; immunosuppressive; antiinflammatory; cytostatic;  
KW gene therapy; chromosome 8p22.  
XX

OS Homo sapiens.  
XX WO2003029271-A2.  
XX 10-APR-2003.  
XX 24-SEP-2002; 2002WO-US030474.  
XX 24-SEP-2001; 2001US-0324631P.  
XX (HYSE-) HYSEQ INC.  
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;  
XX Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;  
XX Haley-Vicente D, Drmanac RT;  
XX WPI; 2003-371981/35.  
XX N-PSDB; ADC30341.  
XX New polynucleotide and polypeptide useful for diagnosing, preventing or  
XX treating conditions such as neurodegenerative diseases, anemias, platelet  
XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
XX cancer.  
XX Claim 20; SEQ ID NO 1394; 1185pp; English.  
XX The invention relates to 971 novel human cDNA sequences (ADC29919-  
XX ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The  
XX invention also relates to nucleic acid sequences over 99% identical with  
XX the novel human cDNAs. The invention additionally encompasses expression  
XX vectors and host cells comprising a nucleic acid of the invention; the  
XX recombinant production of a polypeptide of the invention; an antibody  
XX against a polypeptide of the invention; a method of detecting  
XX polynucleotides or polypeptides of the invention; and methods of  
XX identifying a compound which binds to a polypeptide of the invention. The  
XX invention further discloses methods of preventing, treating or  
XX ameliorating a medical condition; kits comprising polynucleotide probes  
XX and/or monoclonal antibodies for carrying out the methods of the  
XX invention; methods for the identification of compounds that modulate the  
XX expression or activity of the polynucleotide and/or polypeptide; and 767  
XX contig sequences corresponding to the cDNA sequences of the invention  
XX (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628  
XX -ADC33394). The nucleic acids and polypeptides of the invention are  
XX useful in diagnostics, drug screening, forensics, gene mapping, in the  
XX identification of mutations responsible for genetic disorders or other  
XX traits, for assessing biodiversity, and in producing many other types of  
XX data and products dependent on DNA and amino acid sequences. They are  
XX also used for treating diseases such as Parkinson's disease, Alzheimer's  
XX disease and other neurodegenerative diseases, anaemia, platelet  
XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
XX cancer. The nucleic acids may also be used as hybridisation probes or  
XX primers, and in the recombinant production of a protein. The polypeptides  
XX are also useful in generating antibodies, as molecular weight markers,  
XX and as food supplements. The present sequence represents a specifically  
XX claimed human polypeptide sequence of the invention. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 368 AA;  
SQ  
Query Match 100.0%; Score 43; DB 7; Length 368;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 NLQLMDRV 9  
Db 258 NLQLMDRV 266  
|||||||  
RESULT 14  
AAG57646  
ID AAG57646 standard; protein; 260 AA.

XX AAG57646;  
XX AC 18-OCT-2000 (first entry)  
XX DT Arabidopsis thaliana protein fragment SEQ ID NO: 74312.  
XX DE Arabidopsis thaliana  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX PN EPI033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-00301439.  
XX PR 25-FEB-1999; 99US-0121825P.  
XX PR 05-MAR-1999; 99US-0123180P.  
XX PR 09-MAR-1999; 99US-0123548P.  
XX PR 23-MAR-1999; 99US-0125788P.  
XX PR 25-MAR-1999; 99US-0126264P.  
XX PR 29-MAR-1999; 99US-0126785P.  
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Query Match 83.7%; Score 36; DB 3; Length 260;  
Best Local Similarity 87.5%; Pred. NO. 46;  
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QY 2 LQLMDRV 9  
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DB 95 LQLMDRI 102

RESULT 15  
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ID AAG57645 standard; protein; 311 AA.  
XX  
AC AAG57645;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74311.  
XX

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

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PR 29-OCT-1999; 99US-0162142P.

Query Match 83.7%; Score 36; DB 3; Length 311;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9
Db 146 LQLLMDRI 153

RESULT 16
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ID ADT56346 standard; protein; 311 AA.
XX
AC ADT56346;
XX
DT 13-JAN-2005 (first entry)
XX
DE Plant polypeptide, SEQ ID 6423.
XX
KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
XX
OS Viridiplantae.
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XX US2004216190-A1.
XX 28-OCT-2004.
XX 18-DEC-2003; 2003US-00739930.
XX 28-APR-2003; 2003US-00424599.
XX 28-APR-2003; 2003US-00425115.
XX (KOVA/) KOVALIC D K.
XX Kovalic DK;
XX WPI; 2004-757369/74.
XX New recombinant DNA constructs useful in the field of biochemistry and
genetics, and in particular for producing transgenic plants with improved
biological characteristics.
XX Claim 2; SEQ ID NO 6423; 14pp; English.
XX The invention relates a recombinant DNA construct comprising a
polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
(SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
Arabidopsis, wheat and rape but the specification does not indicate which
sequences is derived from which organism. Also included is a method of
producing a plant having an improved property, comprising transforming a
plant with a recombinant DNA construct comprising a promoter region
functional in a plant cell operably joined to a polynucleotide encoding a
polypeptide associated with the property, and growing the transformed
plant. The property is selected from improving plant cold tolerance, for
manipulating growth rate in plant cells by modification of the cell cycle
pathway, for improving plant drought tolerance, for providing increased
resistance to plant disease, for galactomannan production, for production
of plant growth regulators, for improving plant heat tolerance, for
improving plant tolerance to herbicides, for increasing the rate of
homologous recombination in plants, for lignin production, for improving
plant tolerance to extreme osmotic conditions, for improving plant
tolerance to pathogens or pests, for yield improvement by modification of
photosynthesis, for modifying seed oil yield and/or content, for
modifying seed protein yield and/or content, for yield improvement by
modification of carbohydrate, nitrogen or phosphorus use and/or uptake
and for yield improvement by providing improved plant growth and
development under at least one stress condition. The polynucleotide may
also encode a plant transcription factor. The methods and compositions of
the present invention are useful in the field of biochemistry and
genetics, in particular for producing transgenic plants with improved
biological characteristics such as increased yield, improved nitrogen
flow, increasing plant tolerance to cold or heat, improving plant
tolerance to extreme osmotic and drought conditions, and improving plant
tolerance to plant pests or pathogens. They can also be used in physical
arrays of molecules, plant breeding markers, computer-based storage and
analysis systems. The present sequence is one of the 5544 plant protein
sequences of the invention. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=20040216190.
XX
SQ Sequence 311 AA;
Query Match 83.7%; Score 36; DB 8; Length 311;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9
Db 146 LQLLMDRI 153

RESULT 17
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ID AAG57644 standard; protein; 334 AA.  
XX AAG57644;  
AC AAG57644;  
XX 18-OCT-2000 (first entry)  
DT XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74310.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
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PR 05-MAR-1999; 99US-0123180P.  
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PR 29-MAR-1999; 99US-0126785P.  
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PR 06-APR-1999; 99US-0128234P.  
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PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144336P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.

PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154479P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155559P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158023P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161933P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 83.7%; Score 36; DB 3; Length 334;  
Best Local Similarity 87.5%; Pred. No. 60;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMDRV 9  
|||||:  
Db 169 LQLMDRI 176

RESULT 18  
AAB92665  
ID AAB92665 standard; protein; 133 AA.  
XX AC AAB92665;  
XX DT 26-JUN-2001 (first entry)  
XX DE Human protein sequence SEQ ID NO:11024.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX OS Homo sapiens.  
XX PN EP1074617-A2.  
XX PD 07-FEB-2001.  
XX XX 28-JUL-2000; 2000EP-00116126.  
XX PR 29-JUL-1999; 99JP-00248036.  
PR 27-AUG-1999; 99JP-00300253.  
PR 11-JAN-2000; 2000JP-00118776.  
PR 02-MAY-2000; 2000JP-00183767.  
PR 09-JUN-2000; 2000JP-00241899.  
XX PA (HELI-) HELIX RES INST.  
XX XX Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.  
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.  
XX PS Claim 8; SEQ ID NO 11024; 2537pp + Sequence Listing; English.  
XX CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention  
XX SQ Sequence 133 AA;  
Query Match 81.4%; Score 35; DB 4; Length 133;  
Best Local Similarity 87.5%; Pred. No. 36;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLQLMDR 8  
|||||:  
Db 23 NLQLVDR 30  
RESULT 19  
ADP55533  
ID ADP55533 standard; protein; 133 AA.  
XX AC ADP55533;  
XX DT 18-NOV-2004 (first entry)  
XX XX

```
DE Human PRO protein sequence SEQ ID NO:1509.
XX
KW human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; anti-allergic; antianaemic; antiarthritic;
KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW virucide; gene therapy.
XX
OS Homo sapiens.
XX
XX WO2004039956-A2.
XX
XX 13-MAY-2004.
XX
XX 28-OCT-2003; 2003WO-US034381.
XX
XX 29-OCT-2002; 2002US-0422472P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
XX Wood WI, Wu TD;
XX
XX WPI; 2004-376182/35.
XX
XX N-PSDB; ADP55532.
XX
XX New PRO polynucleotides and polypeptides, useful in diagnosing
XX and treating an immune related disease, e.g. systemic lupus
XX erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
XX stimulating an immune response.
XX
XX Claim 1; SEQ ID NO 1509; 3009pp; English.
XX
XX The present invention describes an isolated PRO nucleic acid (I). Also
XX described: (1) a vector comprising (I); (2) a host cell comprising the
XX vector of (1); (3) a process for producing a PRO polypeptides; (4) an
XX isolated PRO polypeptide; (5) a chimeric molecule comprising the
XX polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
XX antibody which specifically binds to a polypeptide of (4); (7) a
XX composition of matter comprising a polypeptide of (4), an agonist or
XX antagonist of the polypeptide or an antibody that binds to the
XX polypeptide in combination with a carrier; (8) an article of manufacture
XX comprising a container, a label on the container and a composition of
XX matter of (7); (9) a method of treating an immune related disease in a
XX mammal; (10) a method for determining the presence of a PRO polypeptide
XX in a sample suspected of having the polypeptide; (11) a method of
XX diagnosing an immune related disease or an inflammatory immune response
XX in a mammal; (12) a method of identifying a compound that inhibits or
XX mimics the activity of or expression of a gene encoding a PRO polypeptide
XX ; and (13) a method of stimulating the immune response in a mammal. The
XX PRO sequences have anti-allergic, antianaemic, antiarthritic,
XX antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,
XX antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
XX haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
XX nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
XX virucide activities, and can be used in gene therapy. The nucleic acid
XX (I) and the encoded polypeptides, compositions, kits and methods are
XX useful in diagnosing and treating an immune related disease and in
XX stimulating an immune response. The present sequence represents a human
XX PRO protein from the present invention.
XX
XX Sequence 133 AA;
XX
XX Query Match 81.4%; Score 35; DB 8; Length 133;
XX Best Local Similarity 87.5%; Pred. No. 36;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 NQLQLMDR 8
XX |||||:|
XX 23 NQLQLVDR 30
XX
XX RESULT 21
XX AAY28922
XX ID AAY28922 standard; protein; 180 AA.
XX
XX AAY28922;
XX
XX 21-SEP-1999 (first entry)
XX
XX Human regulatory protein HRGP-8.
XX
XX Regulatory protein; HRGP; human; cell proliferation; immune response;
```

KW cancer; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma;  
 KW tetracarcinoma; Addison's disease; adult respiratory distress syndrome;  
 KW allergy; anemia; asthma; atherosclerosis; bronchitis; cholecystitis;  
 KW Crohn's disease; ulcerative colitis; atopic dermatitis; dermatomyositis;  
 KW diabetes mellitus; emphysema; atrophic gastritis; glomerulonephritis;  
 KW gout; Grave's disease; hyperinsinophilia; irritable bowel syndrome; AIDS;  
 KW lupus erythematosus; multiple sclerosis; myasthenia gravis; infarction;  
 KW osteoarthritis; osteoporosis; pancreatitis; polymyositis; hemodialysis;  
 KW arthritis; scleroderma; Sjogren's syndrome; and autoimmune thyroiditis;  
 KW infection; trauma.

XX Homo sapiens.

OS  
 XX WO9933870-A2.

PN  
 XX 08-JUL-1999.

XX  
 XX 22-DEC-1998; 98WO-US027471.

PF  
 XX 31-DEC-1997; 97US-00001403.

PR  
 XX (INCY-) INCYTE PHARM INC.

PA  
 XX Lal P, Bandman O, Hillman JL, Au-Young J, Tang YT, Yue H;

PI  
 PI Shah P, Guegler KJ, Corley NC;

PT  
 DR WPI; 1999-430229/36.

DR  
 DR N-PSDB; AAX89292.

XX  
 XX New human regulatory proteins, useful for diagnosing, preventing and  
 PT treating disorders associated with expression of regulatory proteins.

XX  
 XX Claim 1; Page 77; 89pp; English.

XX The invention provides novel human regulatory proteins (AAX28915-926),  
 CC designated HRGP, and their polynucleotides (AAX89285-296). The proteins of  
 CC can be produced using standard recombinant technology. The expression of  
 CC HRGP is closely associated with cell proliferation and the polypeptides  
 CC and polynucleotides are useful in the diagnosis, treatment and prevention  
 CC of diseases associated with cell proliferation, particularly immune  
 CC responses and cancer. The protein or agonists may be administered to  
 CC treat or prevent a cancer such as adenocarcinoma, leukemia, lymphoma,  
 CC melanoma, myeloma, sarcoma, and tetracarcinoma. Such cancers include, but  
 CC are not limited to, cancers of the adrenal gland, bladder, bone, brain,  
 CC cervix, breast, gall bladder, ganglia, ovary and pancreas. Where HRGP is  
 CC promoting leukocyte activity or proliferation, antagonists which decrease  
 CC the activity of HRGP are administered. Such responses may be associated  
 CC with disorders such as Addison's disease, adult respiratory distress  
 CC syndrome, AIDS, allergies, anemia, asthma, atherosclerosis, bronchitis,  
 CC cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis,  
 CC dermatomyositis, diabetes mellitus, emphysema, atrophic gastritis, gout,  
 CC glomerulonephritis, Grave's disease, hyperinsinophilia, irritable bowel  
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,  
 CC myocardial or pericardial infarction, osteoarthritis, osteoporosis,  
 CC pancreatitis, polymyositis, rheumatoid arthritis, scleroderma, Sjogren's  
 CC syndrome, and autoimmune thyroiditis, complications of cancer,  
 CC hemodialysis, extracorporeal circulation; viral, bacterial, fungal,  
 CC parasitic, protozoan, and helminthic infections; and trauma. The HRGP  
 CC polynucleotide may be used for diagnosis of these conditions, and as a  
 CC source of primers and probes

XX  
 SQ Sequence 180 AA;

Query Match 81.4%; Score 35; DB 2; Length 180;  
 Best Local Similarity 87.5%; Pred. No. 49;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDR 8

Db 23 NLQLLVDR 30

RESULT 22

XX

AC ADD22442;

XX

AC ADD22442;

XX

AC ADD22442;

XX

ABB89507  
 ID ABB89507 standard; protein; 180 AA.

XX  
 AC ABB89507;

XX  
 DT 24-MAY-2002 (first entry)

XX  
 DE Human polypeptide SEQ ID NO 1883.

XX  
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

XX  
 KW anti-allergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;

XX  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;

XX  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;

XX  
 KW neurological disease; infection; human; secreted protein.

XX  
 OS Homo sapiens.

XX  
 PN WO200190304-A2.

XX  
 XX 29-NOV-2001.

XX  
 XX 18-MAY-2001; 2001WO-US016450.

XX  
 XX 19-MAY-2000; 2000US-0205515P.

XX  
 XX (HUMA-) HUMAN GENOME SCI INC.

XX  
 PA Birse CE, Rosen CA;

XX  
 PI WPI; 2002-122018/16.

XX  
 DR N-PSDB; ABB89916.

XX  
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and

XX  
 PT prevention of neural, immune system, muscular, reproductive,

XX  
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative

XX  
 PT disorders.

XX  
 PS Claim 11; SEQ ID NO 1883; 2081pp + Sequence Listing; English.

XX  
 CC The invention relates to novel genes (ABB89449-ABB89453) and proteins

XX  
 CC (ABB89404-ABB89444) useful for preventing, treating or ameliorating

XX  
 CC medical conditions e.g. by protein or gene therapy. The genes are

XX  
 CC isolated from a range of human tissues disclosed in the specification.

XX  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in

XX  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

XX  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,

XX  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

XX  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic

XX  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

XX  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

XX  
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing

XX  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)

XX  
 CC infectious diseases such as viral, bacterial, fungal and parasitic

XX  
 CC infections. Note: The sequence data for this patent did not form part of

XX  
 CC the printed specification, but was obtained in electronic format directly

XX  
 CC from WIPO at ffp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 180 AA;

XX  
 Query Match 81.4%; Score 35; DB 5; Length 180;

XX  
 Best Local Similarity 87.5%; Pred. No. 49;

XX  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX  
 QY 1 NLQLLMDR 8

XX  
 Db 23 NLQLLVDR 30

XX  
 RESULT 23

XX  
 ID ADD22442

XX  
 ID ADD22442 standard; protein; 180 AA.

XX  
 XX

XX  
 AC ADD22442;

XX 15-JAN-2004 (first entry)  
 XX HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 92.  
 DE tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;  
 KW colon; mouth; lung; prostatic; gynecological; human.  
 KW Homo sapiens.  
 OS  
 XX JP2003111595-A.  
 PN  
 XX 15-APR-2003.  
 PD  
 XX 24-JUN-2002; 2002JP-00183603.  
 PF  
 XX 25-JUN-2001; 2001JP-00191974.  
 PR  
 XX (ITOY/) ITO Y.  
 PA  
 XX WPI; 2003-611129/58.  
 DR  
 XX Novel tumor antigenic peptide or polypeptide useful for inducing  
 PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,  
 PT prostatic or gynecological cancer.  
 PT  
 XX Claim 2; SEQ ID NO 92; 98pp; Japanese.  
 PS  
 XX The invention relates to a novel tumour antigenic peptide or polypeptide  
 CC comprising a sequence selected from 99 sequences fully defined in the  
 CC specification. The tumour antigenic peptide or polypeptide comprises a  
 CC sequence selected from 99 sequences fully defined in the specification,  
 CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-  
 CC Pro-leu-Ser-Gln-Glu-Thr-Phe, and the polypeptide preferably has a  
 CC sequence comprising 393 amino acids fully defined in the specification.  
 CC The invention further provides a cancer vaccine comprising a tumour  
 CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour  
 CC antigenic peptide, polypeptide, its encoding polynucleotide, a  
 CC hybridising polynucleotide, a recombinant vector containing the  
 CC polynucleotide, a host transformed with the vector or an antibody are  
 CC useful for screening for compounds that interact with the tumour  
 CC antigenic peptide, the polypeptide or its encoding polynucleotide and  
 CC increases the expression of the tumour antigenic peptide, the polypeptide  
 CC or polynucleotide. The tumour antigenic peptide or the polypeptide is  
 CC useful for inducing cytotoxic T cells. The tumour antigenic peptide  
 CC vaccine is useful for treating cancer such as colon, mouth, lung,  
 CC prostatic or gynecological cancer. The invention also provides a  
 CC pharmaceutical composition useful for treating cancer. The tumour  
 CC antigenic peptide or the polypeptide is useful as an antigen to create  
 CC antibodies. This sequence represents one of the tumour antigenic  
 CC polypeptides of the invention.  
 XX  
 SQ Sequence 180 AA;  
 Query Match 81.4%; Score 35; DB 7; Length 180;  
 Best Local Similarity 87.5%; Pred. No. 49;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLQLLMDR 8  
 Db 23 NLQLLVDR 30  
 |||||:  
 |||||:  
 RESULT 24  
 ADI15876  
 ID ADI15876 standard; protein; 180 AA.  
 XX  
 AC ADI15876;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Human PP 78.  
 DE  
 XX tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;  
 KW cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;  
 KW stomach cancer; buccal cancer; renal cancer; lung cancer;  
 KW gynecological cancer; prostate cancer.  
 XX Homo sapiens.  
 OS  
 XX WO2003008450-A1.  
 PN  
 XX 30-JAN-2003.  
 PD  
 XX 11-JUN-2002; 2002WO-JP005799.  
 PF  
 XX 12-JUN-2001; 2001JP-00177058.  
 PR  
 XX 21-AUG-2001; 2001JP-00250728.  
 PR  
 XX (ITOH/) ITOH K.  
 PA  
 XX Itoh K, Shichijo S;  
 PI  
 XX WPI; 2003-267996/26.  
 DR  
 XX N-PSDB; ADI15951.  
 DR  
 XX Tumor antigen peptides recognized by human leukocyte antigen (HLA)-A2 or  
 PT HLA-A26 restricted cytotoxic T-cells for treatment and prevention of  
 PT cancer including preparation of cancer vaccines.  
 PT  
 XX Claim 2; SEQ ID NO 220; 323pp; Japanese.  
 PS  
 XX The invention relates to a tumour antigen peptide recognised by human  
 CC leukocyte antigen (HLA)-A2 or HLA-A26 restricted cytotoxic T-cells (CTL)  
 CC and/or capable of inducing CTL. The tumour antigen peptide is useful for  
 CC the treatment, prevention, diagnosis and vaccine production for cancers  
 CC including colorectal, stomach, buccal, renal, lung, gynecological and  
 CC prostatic cancer. The present sequence represents the amino acid sequence  
 CC of a human protein.  
 CC  
 XX Sequence 180 AA;  
 SQ  
 Query Match 81.4%; Score 35; DB 7; Length 180;  
 Best Local Similarity 87.5%; Pred. No. 49;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLQLLMDR 8  
 Db 23 NLQLLVDR 30  
 |||||:  
 |||||:  
 RESULT 25  
 ADI15933  
 ID ADI15933 standard; protein; 180 AA.  
 XX  
 AC ADI15933;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Human PP 76.  
 DE  
 XX tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;  
 KW cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;  
 KW stomach cancer; buccal cancer; renal cancer; lung cancer;  
 KW gynecological cancer; prostate cancer.  
 XX Homo sapiens.  
 OS  
 XX WO2003008450-A1.  
 PN  
 XX 30-JAN-2003.  
 PD  
 XX 11-JUN-2002; 2002WO-JP005799.  
 PF  
 XX 12-JUN-2001; 2001JP-00177058.  
 PR  
 XX 21-AUG-2001; 2001JP-00250728.  
 PR

KW tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;  
 KW cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;  
 KW stomach cancer; buccal cancer; renal cancer; lung cancer;  
 KW gynecological cancer; prostate cancer.  
 XX Homo sapiens.  
 OS  
 XX WO2003008450-A1.  
 PN  
 XX 30-JAN-2003.  
 PD  
 XX 11-JUN-2002; 2002WO-JP005799.  
 PF  
 XX 12-JUN-2001; 2001JP-00177058.  
 PR  
 XX 21-AUG-2001; 2001JP-00250728.  
 PR  
 XX (ITOH/) ITOH K.  
 PA  
 XX Itoh K, Shichijo S;  
 PI  
 XX WPI; 2003-267996/26.  
 DR  
 XX N-PSDB; ADI15951.  
 DR  
 XX Tumor antigen peptides recognized by human leukocyte antigen (HLA)-A2 or  
 PT HLA-A26 restricted cytotoxic T-cells for treatment and prevention of  
 PT cancer including preparation of cancer vaccines.  
 PT  
 XX Claim 2; SEQ ID NO 220; 323pp; Japanese.  
 PS  
 XX The invention relates to a tumour antigen peptide recognised by human  
 CC leukocyte antigen (HLA)-A2 or HLA-A26 restricted cytotoxic T-cells (CTL)  
 CC and/or capable of inducing CTL. The tumour antigen peptide is useful for  
 CC the treatment, prevention, diagnosis and vaccine production for cancers  
 CC including colorectal, stomach, buccal, renal, lung, gynecological and  
 CC prostatic cancer. The present sequence represents the amino acid sequence  
 CC of a human protein.  
 CC  
 XX Sequence 180 AA;  
 SQ  
 Query Match 81.4%; Score 35; DB 7; Length 180;  
 Best Local Similarity 87.5%; Pred. No. 49;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLQLLMDR 8  
 Db 23 NLQLLVDR 30  
 |||||:  
 |||||:  
 RESULT 25  
 ADI15933  
 ID ADI15933 standard; protein; 180 AA.  
 XX  
 AC ADI15933;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Human PP 76.  
 DE  
 XX tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;  
 KW cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;  
 KW stomach cancer; buccal cancer; renal cancer; lung cancer;  
 KW gynecological cancer; prostate cancer.  
 XX Homo sapiens.  
 OS  
 XX WO2003008450-A1.  
 PN  
 XX 30-JAN-2003.  
 PD  
 XX 11-JUN-2002; 2002WO-JP005799.  
 PF  
 XX 12-JUN-2001; 2001JP-00177058.  
 PR  
 XX 21-AUG-2001; 2001JP-00250728.  
 PR



XX PA (ITOH/) ITOH K.  
 XX PI Itoh K, Shichiho S;  
 XX XX  
 XX WPI; 2003-267996/26.  
 DR N-PSDB; ADI16002.  
 XX XX  
 PT Tumor antigen peptides recognized by human leukocyte antigen (HLA)-A2 or  
 PT HLA-A26 restricted cytotoxic T-cells for treatment and prevention of  
 PT cancer including preparation of cancer vaccines.  
 XX XX  
 PS Claim 2; SEQ ID NO 277; 323pp; Japanese.  
 XX XX  
 CC The invention relates to a tumour antigen peptide recognised by human  
 CC leukocyte antigen (HLA)-A2 or HLA-A26 restricted cytotoxic T-cells (CTL)  
 CC and/or capable of inducing CTL. The tumour antigen peptide is useful for  
 CC the treatment, prevention, diagnosis and vaccine production for cancers  
 CC including colorectal, stomach, buccal, renal, lung, gynecological and  
 CC prostate cancer. The present sequence represents the amino acid sequence  
 CC of a human protein.  
 XX XX  
 SQ Sequence 180 AA;

Query Match 81.4%; Score 35; DB 7; Length 180;  
 Best Local Similarity 87.5%; Pred. No. 49;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
 DB 23 NLQLVDR 30  
 |||||:|

## RESULT 26

ADJ81699  
 ID ADJ81699 standard; protein; 180 AA.

AC ADJ81699;

DT 06-MAY-2004 (first entry)

DE Tumour antigen peptide-related human protein SeqID12.

XX tumour antigen peptide; cytotoxic T cell; HLA-A constraint property;  
 KW HLA-A3 super type; cytostatic; vaccine; gene therapy; cancer;  
 KW prostatic cancer; colon cancer; stomach cancer; cervical carcinoma;  
 KW breast cancer; lung cancer; oesophageal cancer; bladder cancer; melanoma;  
 KW cancer recognition; HLA-A restricted sexual -cell cytotoxic T cell;  
 KW human.

XX Homo sapiens.

XX JP2004000216-A.

XX 08-JAN-2004.

XX 28-APR-2003; 2003JP-00124482.

XX 26-APR-2002; 2002JP-00126764.

XX (ITOT/) ITO T.

XX WPI; 2004-085221/09.

DR N-PSDB; ADJ81705.

XX Novel tumor antigen peptide inducing and/or activating cytotoxic T cells,  
 PT useful as a vaccine for cancer.

XX Claim 2; SEQ ID NO 12; 77pp; Japanese.

XX This invention relates to a novel tumour antigen peptide inducing a  
 CC cytotoxic T cell to the HLA-A constraint property which belongs to one or  
 CC more HLA-A3 super type and which attains and is recognised by cytotoxic T

CC cells. The invention may be useful for the development of compounds with  
 CC a cytostatic activity or a vaccine. In addition, the sequences disclosed  
 CC may be useful for gene therapy. The invention is useful for treating  
 CC cancer such as prostatic cancer, colon cancer, stomach cancer, cervical  
 CC carcinoma, breast cancer, lung cancer, oesophageal cancer, bladder cancer  
 CC or melanoma. In addition, the invention may be useful for screening  
 CC compounds which increases recognition by HLA-A restricted sexual-cell  
 CC cytotoxic T cells. The invention is useful for fundamental research of  
 CC the molecule related to recognition of the cancer by cytotoxic T cells.  
 CC The invention or compositions developed through its use may be  
 CC efficiently useful in treating cancer and screening compounds which  
 CC increases recognition by HLA-A restricted sexual -cell cytotoxic T cells.  
 CC The present sequence is that of a human protein which was used during the  
 CC derivation of the novel tumour antigen peptides of the invention.

SQ Sequence 180 AA;

Query Match 81.4%; Score 35; DB 8; Length 180;  
 Best Local Similarity 87.5%; Pred. No. 49;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
 DB 23 NLQLVDR 30  
 |||||:|

## RESULT 27

ADP55282

ID ADP55282 standard; protein; 180 AA.

XX ADP55282;

XX 18-NOV-2004 (first entry)

DE Human PRO protein sequence SEQ ID NO:1258.

XX human; PRO; immune related disease; inflammatory immune response;  
 KW immune response stimulation; anti-allergic; antianaemic; antiarthritic;  
 KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;  
 KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;  
 KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
 KW virucide; gene therapy.

XX Homo sapiens.

XX WO2004039956-A2.

XX 13-MAY-2004.

XX 28-OCT-2003; 2003WO-US034381.

XX 29-OCT-2002; 2002US-0422472P.

XX (GETH ) GENENTECH INC.

XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;

PI Wood WI, Wu TD;

DR WPI; 2004-376182/35.

DR N-PSDB; ADP55281.

XX New PRO polynucleotides and polypeptides, useful in diagnosing  
 PT and treating an immune related disease, e.g. systemic lupus  
 PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
 PT stimulating an immune response.

XX Claim 1; SEQ ID NO 1258; 3009pp; English.

XX The present invention describes an isolated PRO nucleic acid (I). Also  
 CC described: (1) a vector comprising (I); (2) a host cell comprising the  
 CC vector of (1); (3) a process for producing a PRO polypeptide; (4) an  
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the

CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
 CC antibody which specifically binds to a polypeptide of (4); (7) a  
 CC composition of matter comprising a polypeptide of (4), an agonist or  
 CC antagonist of the polypeptide or an antibody that binds to the  
 CC polypeptide in combination with a carrier; (8) an article of manufacture  
 CC comprising a container, a label on the container and a composition of  
 CC matter of (7); (9) a method of treating an immune related disease in a  
 CC mammal; (10) a method for determining the presence of a PRO polypeptide  
 CC in a sample suspected of having the polypeptide; (11) a method of  
 CC diagnosing an immune related disease or an inflammatory immune response  
 CC in mammal; (12) a method of identifying a compound that inhibits or  
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide  
 CC ; and (13) a method of stimulating the immune response in a mammal. The  
 CC PRO sequences have anti-allergic, antianaemic, antiarthritic,  
 CC antiasthmatic, antidiabetic, antianaemic, antiinflammatory, antipsoriatic,  
 CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,  
 CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,  
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
 CC virucide activities, and can be used in gene therapy. The nucleic acid  
 CC (I) and the encoded polypeptides, compositions, kits and methods are  
 CC useful in diagnosing and treating an immune related disease and in  
 CC stimulating an immune response. The present sequence represents a human  
 CC PRO protein from the present invention.

XX Sequence 180 AA;  
 SQ

Query Match 81.4%; Score 35; DB 8; Length 180;  
 Best Local Similarity 87.5%; Pred. No. 49;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDR 8  
 |||||:  
 Db 23 NLQLLVDR 30

## RESULT 28

ADS11897  
 ID ADS11897 standard; protein; 236 AA.

XX ADS11897;

XX 16-DEC-2004 (first entry)

XX Human therapeutic contig protein - SEQ ID 2134.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnary;  
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
 KW aplastic anaemia; cancer; wound healing; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..236  
 FT /label= Unknown, OTHER  
 FT /note= "OTHER = In-frame STOP codon"

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;  
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
 XX WPI; 2004-668857/65.  
 DR N-PSDB; ADS11299.

PT New polynucleotide, useful in preparing a composition for diagnosing or

PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
 PT aplastic anemia or cancer for promoting wound healing.  
 XX  
 PS Example 2; SEQ ID NO 2134; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded  
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
 CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may  
 CC be useful in preparing a composition for diagnosing or treating  
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
 CC disorders, such as aplastic anemia or cancer, as well as for promoting  
 CC wound healing. The molecules may also be utilised during gene therapy  
 CC procedures. The current sequence is that of a human therapeutic contig  
 CC protein of the invention.

XX Sequence 236 AA;

Query Match 81.4%; Score 35; DB 8; Length 236;  
 Best Local Similarity 87.5%; Pred. No. 66;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDR 8  
 |||||:  
 Db 79 NLQLLVDR 86

## RESULT 29

AAB56651

ID AAB56651 standard; protein; 239 AA.

XX AAB56651;

DT 13-MAR-2001 (first entry)

XX Human prostate cancer antigen protein sequence SEQ ID NO:1229.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease.

XX Homo sapiens.

XX WO200055174-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005988.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (ROSE/) ROSEN C A.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587513/55.

XX N-PSDB; AAF15854.

XX Prostate cancer associated gene sequences, referred to as prostate cancer  
 PT antigens, useful for treatment, prevention, and diagnosis of disorders  
 FT such as prostate cancer.

XX Claim 11; Page 1651-1652; 2338pp; English.

XX AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytostatic,  
 CC cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,  
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen

CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic  
 CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention

XX SQ Sequence 239 AA;

Query Match 81.4%; Score 35; DB 3; Length 239;  
 Best Local Similarity 87.5%; Pred. No. 67;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
 |||||:  
 Db 82 NLQLVDR 89

RESULT 30  
 ADE55015  
 ID ADE55015 standard; protein; 1809 AA.  
 XX AC ADE55015;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P49816, SEQ ID NO 820.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WQ2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P49816.

XX PT New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat

XX or human polynucleotides or a polynucleotide which represents a fragment,

XX derivative or allelic variation of the nucleic acid sequence. Also

XX claimed are a vector comprising the novel polynucleotide, a host cell

XX comprising the vector, a method for identifying a nucleotide sequence

XX which is differentially regulated in an animal subjected to pain and a

XX kit to perform the method, an array, a method for identifying an agent

XX that increases or decreases the expression of the polynucleotide sequence

XX that is differentially expressed in neuronal tissue of a first animal

XX subjected to pain, a method for identifying a compound which regulates

XX the expression of a polynucleotide sequence which is differentially

XX expressed in an animal subjected to pain, a method for identifying a

CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1809 AA;

Query Match 81.4%; Score 35; DB 7; Length 1809;  
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
 |||||:  
 Db 444 NLQLMER 451

RESULT 31

ADE55009

ID ADE55009 standard; protein; 1809 AA.

XX AC ADE55009;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P49816, SEQ ID NO 814.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WQ2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P49816.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat

XX or human polynucleotides or a polynucleotide which represents a fragment,

XX derivative or allelic variation of the nucleic acid sequence. Also

XX claimed are a vector comprising the novel polynucleotide, a host cell

XX comprising the vector, a method for identifying a nucleotide sequence

XX which is differentially regulated in an animal subjected to pain and a

XX kit to perform the method, an array, a method for identifying an agent

XX that increases or decreases the expression of the polynucleotide sequence

XX that is differentially expressed in neuronal tissue of a first animal

XX subjected to pain, a method for identifying a compound which regulates

XX the expression of a polynucleotide sequence which is differentially

expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 1809 AA;

Query Match 81.4%; Score 35; DB 7; Length 1809;  
Best Local Similarity 87.5%; Pred. No. 5.9e+02;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMR 8  
|||:|  
Db 444 NLQLLMR 451

RESULT 32

ADE55006  
ID ADE55006 standard; protein; 1809 AA.

XX ADE55006;

DT 29-JAN-2004 (first entry)

DE Rat Protein P49816, SEQ ID NO 811.

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

FN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P49816.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

PS The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a rat protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1809 AA;

QY Query Match 81.4%; Score 35; DB 7; Length 1809;

Best Local Similarity 87.5%; Pred. No. 5.9e+02;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMR 8

Db 444 NLQLLMR 451

RESULT 33

ADE55012

ID ADE55012 standard; protein; 1809 AA.

AC ADE55012;

XX 29-JAN-2004 (first entry)

DE Rat Protein P49816, SEQ ID NO 817.

Rat; pain; neuronal tissue; Gene therapy; spinal segmental nerve injury;

chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

Rattus norvegicus.

WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.

01-NOV-2001; 2001US-0346382P.

26-NOV-2001; 2001US-0333347P.

(GEO ) GEN HOSPITAL CORP.

(FARB ) BAYER AG.

Woolf C, D'urso D, Befort K, Costigan M;

WPI; 2003-268312/26.

GENBANK; P49816.

New composition comprising two or more isolated polypeptides, useful for

preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat

or human polynucleotides or a polynucleotide which represents a fragment,

derivative or allelic variation of the nucleic acid sequence. Also

claimed are a vector comprising the novel polynucleotide, a host cell

comprising the vector, a method for identifying a nucleotide sequence

which is differentially regulated in an animal subjected to pain and a

kit to perform the method, an array, a method for identifying an agent

CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1809 AA;

Query Match 81.4%; Score 35; DB 7; Length 1809;  
 Best Local Similarity 87.5%; Pred. No. 5.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 1;

QY 1 NLQLMDR 8  
 DB 444 NLQLMER 451  
 |||||:|

RESULT 34

ADX97164  
 ID ADX97164 standard; protein; 372 AA.

AC ADX97164;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 59828.

XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW Galactonnanan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU//) LIU J.

XX (ZHOU//) ZHOU Y.

XX (KOVA//) KOVALIC D K.

XX (SCRE//) SCREEN S E.

XX (TAB//) TABASKA J E.

XX (CAOY//) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.

XX Claim 1; SEQ ID NO 59828; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.

XX SQ Sequence 372 AA;

Query Match 79.1%; Score 34; DB 8; Length 372;

Best Local Similarity 77.8%; Pred. No. 1.7e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9

DB 357 NAKLLMDRV 365  
 | : |||||

RESULT 35

ABB59885  
 ID ABB59885 standard; protein; 1116 AA.

XX ABB59885;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 6447.

XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEXE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL03988.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.

XX Disclosure; SEQ ID NO 6447; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 1116 AA;

Query Match 79.1%; Score 34; DB 4; Length 1116;  
Best Local Similarity 66.7%; Pred. No. 5.6e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQQLMDRV 9  
Db 630 NLQALLDRI 638  
|||:|:

RESULT 36  
ADM26506  
ID ADM26506 standard; protein; 509 AA.  
XX  
AC ADM26506;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
DE Hyperthermophile Methanopyrus kandleri protein #1112.  
XX  
XX hyperthermophile; protein stability enhancement;  
KW protein activity enhancement.  
KW  
XX Methanopyrus kandleri.  
OS  
XX  
XX WO2003076575-A2.  
XX  
XX 18-SEP-2003.  
XX  
XX 04-MAR-2003; 2003WO-US006664.  
XX  
XX 04-MAR-2002; 2002US-0361742P.  
PR 14-MAY-2002; 2002US-0380423P.  
PR 16-SEP-2002; 2002US-0410974P.  
XX  
XX (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALY/) MALYKH A.  
XX  
XX Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;  
PI  
XX  
XX WPI; 2003-748383/70.  
DR  
DR N-PSDB; ADM27081.  
XX  
XX New isolated nucleic acids encoding any of about 1700 Methanopyrus  
PT kandleri proteins, and the encoded proteins, useful as a medicaments or  
PT as diagnostic agents.  
PT  
XX  
XX Claim 31; SEQ ID NO 1112; 1023pp; English.  
PS  
XX  
XX The invention comprises the amino acid sequence of proteins from the  
CC hyperthermophile Methanopyrus kandleri, the invention also comprises the  
CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri  
CC proteins of the invention are useful for enhancing the stability and/or  
CC activity of other proteins. The Methanopyrus kandleri genome is useful in  
CC a variety of diagnostic and analytical methods. The present amino acid  
CC sequence represents a Methanopyrus kandleri protein of the invention.

XX SQ Sequence 509 AA;

Query Match 76.7%; Score 33; DB 7; Length 509;  
Best Local Similarity 77.8%; Pred. No. 3.9e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQQLMDRV 9  
Db 112 NLQFLURDRV 120  
|||:|:

RESULT 37  
AAE39967  
ID AAE39967 standard; protein; 874 AA.  
XX  
AC AAE39967;  
XX  
XX 15-JAN-2004 (first entry)  
XX  
DE Vigna unguiculata starch synthase isoform V protein.  
XX  
KW Starch synthase isoform V protein; starch biosynthesis; transgenic plant;  
transgenic; enzyme.  
XX  
OS Vigna unguiculata.  
XX  
XX US2003097688-A1.  
PN  
XX 22-MAY-2003.  
PD  
XX 05-JUN-2002; 2002US-00163214.  
PF  
XX 08-JUN-2001; 2001US-0297099P.  
PR  
XX (ALLE/) ALLEN S M.  
PA (BROG/) BROGLIE K E.  
PA (BUTL/) BUTLER K H.  
PA (THOR/) THORPE C J.  
XX  
XX Allen SM, Broglie KE, Butler KH, Thorpe CJ;  
PI  
XX WPI; 2003-765535/72.  
DR  
XX Novel isolated starch synthase isoform V polypeptide having starch in  
PT synthase activity, useful for altering starch biosynthesis pathway in  
PT plants.  
XX  
XX Example 3; Fig 1; 40pp; English.  
PS  
XX The invention relates to novel starch synthase isoform V proteins having  
CC starch synthase activity and polynucleotides encoding them. Sequences of  
CC the invention are useful for transforming a cell. They are useful for  
CC producing a plant. They are useful for altering starch biosynthesis  
CC pathway in plants. The present sequence is Vigna unguiculata starch  
CC synthase isoform V protein  
XX  
XX SQ Sequence 874 AA;

Query Match 76.7%; Score 33; DB 7; Length 874;  
Best Local Similarity 75.0%; Pred. No. 7e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQQLMDR 8  
Db 195 NLQALLDK 202  
|||:|:

RESULT 38  
ABP63841  
ID ABP63841 standard; protein; 125 AA.  
XX  
XX ABP63841;  
AC



KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
XX US2003233675-A1.  
XX  
XX 18-DEC-2003.  
XX  
XX 20-FEB-2003; 2003US-00369493.  
XX  
XX 21-FEB-2002; 2002US-0360039P.  
XX  
XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
XX for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 11994; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
XX promoter functional in a plant cell, where the promoter is positioned to  
XX provide for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source. The invention also relates to a transformed plant  
XX comprising the recombinant DNA construct and a method of producing a  
XX transformed plant having an improved property. The plant is a crop plant  
XX such as maize or soybean. The method of producing a transformed plant  
XX having an improved property comprises transforming a plant with the  
XX recombinant DNA construct and growing the transformed plant, where the  
XX polynucleotide or polypeptide is useful for improving plant properties.  
XX The recombinant DNA construct is useful for producing plants with  
XX improved plant properties, e.g. improved cold, heat or drought tolerance,  
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
XX increased resistance to plant disease, better growth rate by modification  
XX of the cell cycle pathway with plant growth regulators, increased rate of  
XX homologous recombination, modified seed oil or protein yield and/or  
XX content, improved yield by modification of carbohydrate, nitrogen or  
XX phosphorus use and/or uptake, by modification of photosynthesis or by  
XX providing improved plant growth and development under at least one stress  
XX condition, improved lignin production or improved galactomannan  
XX production. This sequence represents a bacterial polypeptide used in the  
XX scope of the invention. Note: The sequence data for this patent did not  
XX form part of the printed specification but was obtained in electronic  
XX format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 203 AA;  
  
Query Match 74.4%; Score 32; DB 8; Length 203;  
Best Local Similarity 87.5%; Pred. No. 2.3e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 LQLMDRV 9  
Db 125 LQLMDRV 132  
| | | | |  
  
RESULT 41  
AAU44957  
ID AAU44957 standard; protein; 228 AA.

XX AAU44957;  
AC  
XX 27-FEB-2002 (first entry)  
DT  
XX  
XX Propionibacterium acnes immunogenic protein #5853.  
DE  
XX  
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertonosis; osteomyelitis;  
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
KW dermatological; osteopathic; neuroprotectant.  
XX  
OS Propionibacterium acnes.  
XX  
XX WO200181581-A2.  
XX  
XX 01-NOV-2001.  
XX  
XX 20-APR-2001; 2001WO-US012865.  
XX  
XX 21-APR-2000; 2000US-0199047P.  
XX  
XX 02-JUN-2000; 2000US-0208841P.  
XX  
XX 07-JUL-2000; 2000US-0216747P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;  
XX  
XX WPI; 2001-616774/71.  
XX  
XX N-PSDB; AAS59524.  
XX  
XX Propionibacterium acnes polypeptides and nucleic acids useful for  
XX vaccinating against and diagnosing infections, especially useful for  
XX treating acne vulgaris.  
XX  
XX Example 1; SEQ ID NO 6152; 1069pp; English.  
XX  
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
XX polypeptides. The proteins and their associated DNA sequences are used in  
XX the treatment, prevention and diagnosis of medical conditions caused by  
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
XX pustulosis, hypertonosis and osteomyelitis), uveitis and endophthalmitis.  
XX P. acnes is also involved in infections of bone, joints and the central  
XX nervous system, however it is particularly involved in the inflammatory  
XX lesions associated with acne vulgaris. A method for detecting the  
XX presence or absence of P. acnes in a patient comprises contacting a  
XX sample with a binding agent that binds to the proteins of the invention  
XX and determining the amount of bound protein in the sample. The  
XX polypeptides may be used as antigens in the production of antibodies  
XX specific for P. acnes proteins. These antibodies can be used to  
XX downregulate expression and activity of P. acnes polypeptides and  
XX therefore treat P. acnes infections. The antibodies may also be used as  
XX diagnostic agents for determining P. acnes presence, for example, by  
XX enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
XX this patent did not form part of the printed specification, but was  
XX obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 228 AA;  
  
Query Match 74.4%; Score 32; DB 4; Length 228;  
Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NLQLMDR 8  
Db 125 NLQLMDR 132  
| | | | |  
  
RESULT 42  
ABM41476  
ID ABM41476 standard; protein; 228 AA.



XX AC ABM41476;  
XX DT 20-OCT-2003 (first entry)  
XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #6152.  
XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
KW immunostimulant; immune response; vaccine.  
XX OS Propionibacterium acnes.  
XX PN WC2003033515-AL.  
XX PD 24-APR-2003.  
XX PF 11-OCT-2002; 2002WO-US032727.  
XX PR 15-OCT-2001; 2001US-00978825.  
XX PA (CORI-) CORIXA CORP.  
XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;  
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
PI Barth B, Vallieue-Douglas J;  
XX WIPI; 2003-381789/36.  
XX N-PSDB; ACP64453.  
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the  
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
PT or for stimulating an immune response specific for a P. acnes protein.  
XX Example 1; SEQ ID NO 6152; 1481pp; English.  
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)  
CC encoding a Propionibacterium acnes protein. The invention also relates to  
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
CC immunogenic fragments of P. acnes polypeptides. The invention  
CC additionally encompasses expression vectors and host cells comprising a  
CC polynucleotide of the invention, antibodies against polypeptides of the  
CC invention; fusion proteins comprising a polypeptide of the invention; a  
CC method for stimulating an immune response specific for a P. acnes  
CC polypeptide and an isolated T cell population comprising T cells prepared  
CC via this method; a vaccine composition (comprising P. acnes polypeptides,  
CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
CC antigen-presenting cells that express the polypeptide); a method and kit  
CC for detecting or determining the presence or absence of P. acnes in a  
CC patient; and a method for inhibiting the development of P. acnes in a  
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion  
CC proteins, T cell populations or antigen-presenting cells that express the  
CC polypeptides are useful for diagnosing, preventing or treating acne  
CC vulgaris, or for stimulating an immune response specific for a P. acnes  
CC protein. The polynucleotides can also be used as probes or primers for  
CC nucleic acid hybridisation. The vaccine composition is useful for the  
CC stimulation of an immune response against P. acnes, or for treating acne,  
CC and the kit is useful for performing a diagnostic assay. The present  
CC sequence represents a polypeptide predicted to be encoded by an ORF (open  
CC reading frame) contained within the P. acnes polynucleotides of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 228 AA;

Query Match 74.4%; Score 32; DB 6; Length 228;  
Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLQLLMWR 8  
DB 125 NLQLLEDQ 132

RESULT 43  
ADR94245  
ID ADR94245 standard; protein; 250 AA.  
XX AC ADR94245;  
XX DT 16-DEC-2004 (first entry)  
XX DE Novel S. pneumoniae protein sequence, SEQ ID 2880.  
XX KW Meningitis; bacteraemia; pneumonia; otitis media; vaccine;  
KW bacterial infection.  
XX OS Streptococcus pneumoniae.  
XX PN US6800744-B1.  
XX PD 05-OCT-2004.  
XX PF 30-JUN-1998; 98US-00107433.  
XX PR 02-JUL-1997; 97US-0051553P.  
XX PR 12-MAY-1998; 98US-0085131P.  
XX PA (GENO-) GENOME THERAPEUTICS CORP.  
XX PI Doucette-Stamm LA, Bush D;  
XX WIPI; 2004-697205/68.  
XX N-PSDB; ADR91642.  
XX New isolated nucleic acid encoding a Streptococcus pneumoniae  
PT polypeptide, useful for diagnosing, preventing and/or treating  
PT pathological conditions resulting from the bacterial infection.  
XX Disclosure; SEQ ID NO 2880; 151pp; English.  
XX The invention relates to an isolated nucleic acid comprising a sequence  
CC encoding a Streptococcus pneumoniae ADR91366polypeptide, or its  
CC fragments, with any of 9 fully defined sequences (appearing as ADR94308,  
CC ADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682,  
CC ADR96079) or any of the fully defined sequences appearing as ADR91705,  
CC ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or  
CC ADR93476 or at least 20 or 30 consecutive nucleotides of the nucleotide  
CC sequences, or at least 40, 60 or 300 consecutive nucleotides, which is  
CC hybridisable under high stringency conditions to the nucleotide sequence.  
CC The nucleic acids and proteins are chosen from 5206 disclosed sequences.  
CC Also included are a recombinant expression vector comprising the isolated  
CC nucleic acid cited above operably linked to a transcription regulatory  
CC element, a cell comprising the recombinant expression vector and a probe  
CC comprising at least 20 consecutive nucleotides of the nucleotide  
CC sequences as cited above. The methods and compositions of the present  
CC invention are useful for the diagnosis, prevention and/or treatment of  
CC pathological conditions resulting from bacterial infection by  
CC Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and  
CC otitis media. The present sequence is one of the 2603 disclosed S.  
CC pneumoniae protein sequences. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=6800744B1.  
XX SQ Sequence 250 AA;

Query Match 74.4%; Score 32; DB 8; Length 250;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLQLLMWRV 9  
DB 196 NLPLLDRI 204

RESULT 44  
AEA58115  
ID AEA58115 standard; protein; 250 AA.  
XX AC AEA58115;  
XX DT 25-AUG-2005 (first entry)  
XX DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:2880.  
XX KW bacterial infection; Streptococcus pneumoniae infection; antibacterial;  
XX KW vaccine.  
XX OS Streptococcus pneumoniae.  
XX PN US2005136404-A1.  
XX PD 23-JUN-2005.  
XX PF 10-JUL-2003; 2003US-00617320.  
XX PR 02-JUL-1997; 97US-0051553P.  
XX PR 12-MAY-1998; 98US-0085131P.  
XX PR 30-JUN-1998; 98US-00107433.  
XX PA (DOUC/) DOUCETTE-STAMM L A.  
XX PA (BUSH/) BUSH D.  
XX PI Doucette-Stamm LA, Bush D;  
XX WPI: 2005-477576/48.  
XX N-PSDB; AEA55512.  
XX New isolated nucleic acid molecules and encoded polypeptides useful for  
PT diagnosing, preventing or treating bacterial infections, particularly  
PT Streptococcus pneumoniae infection.  
XX Claim 5; SEQ ID NO 2880; 144pp; English.  
XX The invention relates to an isolated nucleic acid molecule for detecting,  
CC preventing or treating pathological conditions resulting from bacterial  
CC infection. The isolated nucleic acid comprises: (a) any of the 2603  
CC nucleotide sequences of AEA55236 to AEA57838; (b) a nucleotide sequence  
CC encoding a Streptococcus pneumoniae polypeptide comprising any of the  
CC 2603 amino acid sequences of AEA57839 to AEA60441; or (c) a nucleotide  
CC sequence of at least 8 nucleotides in length, where the sequence is  
CC hybridizable to a nucleic acid having any of the nucleotide sequences in  
CC (a). Also described: (1) a recombinant expression vector comprising the  
CC above nucleic acid operably linked to a transcription regulatory element;  
CC (2) a cell comprising the recombinant expression vector; (3) producing an  
CC S. pneumoniae polypeptide; (4) a probe comprising a nucleotide sequence  
CC consisting of at least 8 nucleotides of any of AEA55236 to AEA57838; (5)  
CC treating a subject for S. pneumoniae infection; (6) a recombinant or  
CC substantially pure preparation of an S. pneumoniae polypeptide or its  
CC fragment, where the polypeptide is selected from AEA57839 to AEA60441;  
CC (7) a vaccine composition for preventing or treating an S. pneumoniae  
CC infection, comprising an amount of the above nucleic acid or polypeptide;  
CC (8) detecting the presence of a Streptococcus nucleic acid in a sample;  
CC (9) a computer readable medium having recorded the nucleotide sequences  
CC of AEA55236 to AEA57838; (10) a computer based system for identifying  
CC fragments of the Streptococcus genome of commercial importance. The  
CC composition and methods are useful for diagnosing, preventing or treating  
CC bacterial infections, particularly S. pneumoniae infection. The present  
CC sequence represents a S. pneumoniae ORF amino acid sequence from the  
CC present invention. Note - The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from the USPTO web site.  
XX SQ Sequence 250 AA;  
Query Match 74.4%; Score 32; DB 9; Length 250;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Result 45  
ABP28324  
ID ABP28324 standard; protein; 269 AA.  
XX AC ABP28324;  
XX DT 02-JUL-2002 (first entry)  
XX DE Streptococcus polypeptide SEQ ID NO 5824.  
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX OS Streptococcus pyogenes.  
XX PN WO200234771-A2.  
XX PD 02-MAY-2002.  
XX PF 29-OCT-2001; 2001WO-GB004789.  
XX PR 27-OCT-2000; 2000GB-00026333.  
XX PR 24-NOV-2000; 2000GB-00028727.  
XX PR 07-MAR-2001; 2001GB-00005640.  
XX PA (CHIR-) CHIRON SPA.  
XX PA (GENO-) INST GENOMIC RES.  
XX PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;  
XX PI Tettelin H;  
XX WPI: 2002-352536/38.  
XX N-PSDB; ABN68955.  
XX New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX Claim 1; Page 3745; 4525pp; English.  
XX The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX SQ Sequence 269 AA;  
Query Match 74.4%; Score 32; DB 5; Length 269;  
Best Local Similarity 85.7%; Pred. No. 3.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Result 46  
QLLMDRV 9  
ID QLLMDRV 9  
XX AC QLLMDRV 9;  
XX DT 02-JUL-2002 (first entry)  
XX DE Streptococcus polypeptide SEQ ID NO 5824.  
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX OS Streptococcus pyogenes.  
XX PN WO200234771-A2.  
XX PD 02-MAY-2002.  
XX PF 29-OCT-2001; 2001WO-GB004789.  
XX PR 27-OCT-2000; 2000GB-00026333.  
XX PR 24-NOV-2000; 2000GB-00028727.  
XX PR 07-MAR-2001; 2001GB-00005640.  
XX PA (CHIR-) CHIRON SPA.  
XX PA (GENO-) INST GENOMIC RES.  
XX PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;  
XX PI Tettelin H;  
XX WPI: 2002-352536/38.  
XX N-PSDB; ABN68955.  
XX New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX Claim 1; Page 3745; 4525pp; English.  
XX The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX SQ Sequence 269 AA;  
Query Match 74.4%; Score 32; DB 5; Length 269;  
Best Local Similarity 85.7%; Pred. No. 3.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Result 47  
QLLMDRV 9  
ID QLLMDRV 9  
XX AC QLLMDRV 9;  
XX DT 02-JUL-2002 (first entry)  
XX DE Streptococcus polypeptide SEQ ID NO 5824.  
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX OS Streptococcus pyogenes.  
XX PN WO200234771-A2.  
XX PD 02-MAY-2002.  
XX PF 29-OCT-2001; 2001WO-GB004789.  
XX PR 27-OCT-2000; 2000GB-00026333.  
XX PR 24-NOV-2000; 2000GB-00028727.  
XX PR 07-MAR-2001; 2001GB-00005640.  
XX PA (CHIR-) CHIRON SPA.  
XX PA (GENO-) INST GENOMIC RES.  
XX PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;  
XX PI Tettelin H;  
XX WPI: 2002-352536/38.  
XX N-PSDB; ABN68955.  
XX New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX Claim 1; Page 3745; 4525pp; English.  
XX The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX SQ Sequence 269 AA;  
Query Match 74.4%; Score 32; DB 5; Length 269;  
Best Local Similarity 85.7%; Pred. No. 3.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 55 QLLMDRI 61

RESULT 46  
ADK46631  
ID ADK46631 standard; protein; 283 AA.  
XX  
AC ADK46631;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Streptococcus pneumoniae protein, Seq ID No 3146.  
XX  
KW Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.  
XX  
OS Streptococcus pneumoniae.  
XX  
PN US6699703-B1.  
XX  
PD 02-MAR-2004.  
XX  
PF 26-MAY-2000; 2000US-00583110.  
XX  
PR 02-JUL-1997; 97US-0051553P.  
PR 12-MAY-1998; 98US-0085131P.  
PR 30-JUN-1998; 98US-00107433.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Houseweart CE;  
XX  
DR WPI; 2004-212399/20.  
DR N-PSDB; ADK43970.  
XX  
PT New nucleic acid molecules and polypeptides useful for diagnosing,  
PT preventing and treating pathological conditions resulting from bacterial  
PT infection, e.g. Streptococcus pneumoniae infection, and in drug  
PT screening.  
XX  
PS Disclosure; SEQ ID NO 3146; 301pp; English.  
XX  
CC The invention relates to isolated Streptococcus pneumoniae nucleic acids  
CC and polypeptides. The nucleic acids and proteins are useful for  
CC diagnosing, preventing and treating pathological conditions resulting  
CC from bacterial infection, such as S. pneumoniae infection. These may also  
CC be used for drug screening procedures. The present sequence represents a  
CC Streptococcus pneumoniae polypeptide of the invention. Note: The sequence  
CC data for this patent did not appear in the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 283 AA;

Query Match 74.4%; Score 32; DB 8; Length 283;  
Best Local Similarity 66.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
Db 172 NLPLLDRI 180

RESULT 47  
AEB91419  
ID AEB91419 standard; protein; 572 AA.  
XX  
AC AEB91419;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:129.  
XX  
KW algorithm; adhesin; pharmaceutical; vaccine; drug screening;

KW bordetella pertussis infection; antibacterial; pneumonia;  
KW antiinflammatory; respiratory-gen.; gastric ulcer; antitumor;  
KW gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.  
XX  
OS Mycoplasma pneumoniae.  
XX  
PN WO2005076010-A2.  
XX  
PD 18-AUG-2005.  
XX  
PF 07-FEB-2005; 2005WO-IN000037.  
XX  
PR 06-FEB-2004; 2004IN-DE000173.  
PR 20-JUL-2004; 2004US-0589227P.  
XX  
PA (COUL ) COUNCIL SCI & IND RES SOUTH AFRICA.  
XX  
PI Sachdeva G, Kumar K, Jain P, Brahmachari SK, Ramachandran S;  
XX  
DR WPI; 2005-597835/61.  
XX  
CC Computational method for identifying adhesin and adhesin like molecules,  
CC comprises computing sequence-based attributes of protein sequences using  
CC neural network software and training an artificial neural network.  
XX  
PS Claim 16; SEQ ID NO 129; 402pp; English.  
XX  
CC The present invention relates to a computational method (M1) for  
CC identifying adhesin and adhesin-like proteins, by computing the sequence-  
CC based attributes of protein sequences using five attribute modules of a  
CC neural network software, training an artificial neural network (ANN) for  
CC each of the computed five attributes, and identifying the adhesin and  
CC adhesin-like proteins having probability of being an adhesin (Pad) as  
CC equal or greater than 0.51. Also claimed is a set of 274 annotated genes  
CC encoding adhesin and adhesin-like proteins, having 274 fully defined 162-  
CC 1151 base pair (SEQ ID NO: 385-638) sequences; a set of 105 hypothetical  
CC genes encoding adhesin and adhesin-like proteins, having 105 fully  
CC defined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 279 annotated  
CC adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base  
CC pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-  
CC like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO:  
CC 280-384) sequences; and a fully connected multilayer feed forward ANN (I)  
CC based on (M1). (M1) is useful for identifying adhesin and adhesin-like  
CC proteins, of therapeutic potential, and identifying and short-listing  
CC proteins for further testing in development of new vaccine formulations  
CC to eliminate diseases caused by various pathogenic organisms. (M1) is  
CC useful for identifying putative adhesins that are important in drug  
CC discovery and preventing therapeutics for whooping cough, pneumonia,  
CC gastric ulcer and urinary tract infections. (M1) identifies adhesins from  
CC distantly related organisms, and from bacteria belonging to a wide  
CC phylogenetic spectrum. (M1) is capable of predicting adhesive nature of  
CC unique proteins. The present sequence is a microbial pathogen adhesin  
CC protein sequence.  
XX  
SQ Sequence 572 AA;

Query Match 74.4%; Score 32; DB 9; Length 572;  
Best Local Similarity 66.7%; Pred. No. 7.1e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
Db 428 NNQLLDRI 436

RESULT 48  
ABP28470  
ID ABP28470 standard; protein; 621 AA.  
XX  
AC ABP28470;  
XX  
DT 02-JUL-2002 (first entry)  
XX

DE Streptococcus polypeptide SEQ ID NO 6116.  
 XX  
 KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 XX  
 OS Streptococcus agalactiae.  
 XX  
 PN WO200234771-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 29-OCT-2001; 2001WO-GB004789.  
 XX  
 PR 27-OCT-2000; 2000GB-00026333.  
 PR 24-NOV-2000; 2000GB-00028727.  
 PR 07-MAR-2001; 2001GB-00005640.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Telford J, Masignani V, Margarit Y Rosl, Grandi G, Fraser C;  
 PI Tettelin H;  
 XX  
 DR WPI; 2002-352536/38.  
 DR N-PSDB; ABN69101.  
 XX  
 PS New Streptococcus protein for the treatment or prevention of infection or  
 PT disease caused by Streptococcus bacteria, such as meningitis, and for  
 PT detecting a compound that binds to the protein.  
 XX  
 PS Claim 1; Page 3774; 4525pp; English.  
 XX  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins  
 XX  
 SQ Sequence 621 AA;  
 Query Match 74.4%; Score 32; DB 5; Length 621;  
 Best Local Similarity 55.6%; Pred. No. 7.7e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NLQLMDRV 9  
 Db 155 NLQMISDRI 163  
 RESULT 49  
 AEB91420  
 ID AEB91420 standard; protein; 1244 AA.  
 XX  
 AC AEB91420;  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:130.  
 XX  
 KW algorithm; adhesin; pharmaceutical; vaccine; drug screening;

KW bordetella pertussis infection; antibacterial; pneumonia;  
 KW antiinflammatory; respiratory-gen.; gastric ulcer; antitumor;  
 XX gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.  
 XX OS Mycoplasma pneumoniae.  
 XX  
 PN WO2005076010-A2.  
 XX  
 PD 18-AUG-2005.  
 XX  
 PF 07-FEB-2005; 2005WO-IN000037.  
 XX  
 PR 06-FEB-2004; 2004IN-DE000173.  
 PR 20-JUL-2004; 2004US-0589227P.  
 XX  
 PA (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.  
 XX  
 PI Sachdeva G, Kumar K, Jain P, Brahmachari SK, Ramachandran S;  
 PI WPI; 2005-597835/61.  
 DR  
 XX  
 PT Computational method for identifying adhesin and adhesin like molecules,  
 PT comprises computing sequence-based attributes of protein sequences using  
 PT neural network software and training an artificial neural network.  
 XX  
 PS Claim 16; SEQ ID NO 130; 402pp; English.  
 XX  
 CC The present invention relates to a computational method (M1) for  
 CC identifying adhesin and adhesin-like proteins, by computing the sequence-  
 CC based attributes of protein sequences using five attribute modules of a  
 CC neural network software, training an artificial neural network (ANN) for  
 CC each of the computed five attributes, and identifying the adhesin and  
 CC adhesin-like proteins having probability of being an adhesin (Pad) as  
 CC equal or greater than 0.51. Also claimed is a set of 274 annotated genes  
 CC encoding adhesin and adhesin-like proteins, having 274 fully defined 162-  
 CC 11151 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical  
 CC genes encoding adhesin and adhesin-like proteins, having 105 fully  
 CC defined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 279 annotated  
 CC adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base  
 CC pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-  
 CC like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO:  
 CC 280-384) sequences; and a fully connected multilayer feed forward ANN (I)  
 CC based on (M1). (M1) is useful for identifying adhesin and adhesin-like  
 CC proteins, of therapeutic potential, and identifying and short-listing  
 CC proteins for further testing in development of new vaccine formulations  
 CC to eliminate diseases caused by various pathogenic organisms. (M1) is  
 CC useful for identifying putative adhesins that are important in drug  
 CC discovery and preventing therapeutics for whooping cough, pneumonia,  
 CC gastric ulcer and urinary tract infections. (M1) identifies adhesins from  
 CC distantly related organisms, and from bacteria belonging to a wide  
 CC phylogenetic spectrum. (M1) is capable of predicting adhesive nature of  
 CC unique proteins. The present sequence is a microbial pathogen adhesin  
 CC protein sequence.  
 XX  
 SQ Sequence 1244 AA;  
 Query Match 74.4%; Score 32; DB 9; Length 1244;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NLQLMDRV 9  
 Db 1082 NNQLLDRI 1090  
 RESULT 50  
 AAO26550  
 ID AAO26550 standard; protein; 2697 AA.  
 XX  
 AC AAO26550;  
 XX  
 DT 06-MAR-2003 (first entry)  
 XX

DE Cochliobolus ORF protein sequence SEQ ID No 5.  
 XX Fungicide; antiinflammatory; cytostatic; library; plant; fungal; avian;  
 XX mammalian DNA; Cochliobolus; anti-fungal; fungicide; pathogenic;  
 KW endocrine; gastrointestinal; cardiovascular disorder; cancer; secretory.  
 XX  
 XX Cochliobolus sp.  
 OS  
 XX US2002142324-A1.  
 PN  
 XX  
 XX 03-OCT-2002.  
 PD  
 XX  
 XX 24-SEP-2001; 2001US-00961527.  
 PF  
 XX  
 XX 22-SEP-2000; 2000US-0234650P.  
 PR  
 XX 22-SEP-2000; 2000US-0234673P.  
 PR  
 XX (WANG/) WANG X.  
 PA (TURG/) TURGEON B G.  
 PA (YODE/) YODER O.  
 PA (WUJ/) WU J.  
 XX  
 XX Wang X, Turgeon BG, Yoder O, Wu J;  
 PI  
 XX WPI; 2003-102510/09.  
 DR  
 XX N-PSDB; AALS4019.  
 DR  
 XX  
 XX Preparing library of modified DNA fragments involves generating a library  
 PT of DNA fragments having a double strand break and inserting detectable  
 PT polynucleotide into the break to yield library of modified DNA fragments.  
 PT  
 XX  
 PS Claim 13; Page 39-45; 65pp; English.  
 XX  
 XX The invention relates to a novel method for preparing a library of  
 CC modified DNA fragments. The novel method comprises contacting a library  
 CC of DNA fragments in a vector with an agent to cause at least one double  
 CC strand break in at least one fragment to yield a library of DNA fragments  
 CC having at least one double strand break, and inserting a detectable  
 CC polynucleotide or gene into the break to yield a library of modified DNA  
 CC fragments. The novel method is useful for preparing a cDNA or genomic  
 CC library of modified DNA fragments, where the DNA is plant, fungal, avian  
 CC or mammalian DNA. The library is useful for identifying the function of a  
 CC gene, by contacting cells (plant, bacterial, fungal, avian or mammalian  
 CC cells) with the library to yield a population of cells containing at  
 CC least one recombinant cell, in which homologous recombination has  
 CC occurred between the genome of the cell and the modified DNA in at least  
 CC one member of the library and identifying the recombinant cell by a  
 CC change in phenotype. The isolated Cochliobolus polypeptide of the  
 CC invention is useful for identifying an agent having anti-fungal activity.  
 CC The anti-fungal agent of the invention is useful as a fungicide to  
 CC suppress the growth of pathogenic fungi. The inhibitors of the isolated  
 CC Cochliobolus polypeptide may specifically inhibit fungal pathogenicity or  
 CC growth and are also useful as a therapeutic in disorders associated with  
 CC protein processing and maturation including endocrine, gastrointestinal,  
 CC and cardiovascular disorders, in inflammation and in cancers,  
 CC particularly those involving secretory and gastrointestinal tissues. This  
 CC sequence represents a protein of an ORF region of the Cochliobolus DNA  
 CC sequence of the invention  
 XX  
 SQ Sequence 2697 AA;

Query Match 74.4%; Score 32; DB 6; Length 2697;  
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LQLMDRV 9  
 |||||  
 Db 605 LQFLMDRI 612

Search completed: May 9, 2006, 02:16:31  
 Job time : 128.4 secs

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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:17:29 ; Search time 16.4 Seconds  
(without alignments)  
52.802 Million cell updates/sec

Title: US-09-870-216C-11

Perfect score: 43

Sequence: 1 NIQLLMDRV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80:\*

1: piri:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	83.7	311	2	G86324
2	35	81.4	1809	2	S57329
3	34	79.1	1116	2	T13854
4	32	74.4	283	2	E98065
5	32	74.4	305	2	F69306
6	32	74.4	572	2	S73730
7	32	74.4	1244	2	S73731
8	31	72.1	258	2	B72697
9	31	72.1	270	2	D69791
10	31	72.1	291	2	AE2416
11	31	72.1	445	1	S74826
12	31	72.1	467	2	C84420
13	31	72.1	519	2	E84811
14	31	72.1	582	2	A90192
15	31	72.1	651	2	JN0657
16	31	72.1	652	2	AD0546
17	31	72.1	672	2	A72076
18	31	72.1	672	2	B86548
19	31	72.1	841	2	JQ0647
20	31	72.1	861	2	E97473
21	31	72.1	861	2	A12691
22	31	72.1	1504	2	A33602
23	30	69.8	129	2	T09329
24	30	69.8	144	2	F91130
25	30	69.8	144	2	F85975
26	30	69.8	217	2	T44404
27	30	69.8	218	2	AE1147
28	30	69.8	219	2	AE1506
29	30	69.8	227	2	A75304

hypothetical prote  
protein F2D10.16 [  
DNA-directed DNA p  
hypothetical prote  
bis(5'-nucleosyl)-  
hypothetical prote  
gene R protein - A  
probable o-sialogl  
protein M88.4 [imp  
GTP-binding protei  
aspartate-tRNA lig  
fatty acid elongas  
importin alpha-lik  
conserved hypotet  
hypothetical prote  
aspartyl-tRNA synt  
RNA polymerase sig  
hypothetical prote  
probable mmpL1 pro  
ABC transporter AT  
probable dna repai  
starch synthase ho  
hypothetical prote  
hypothetical prote  
DNA polymerase III  
type I site-specif  
carboxypeptidase Y  
tuberos sclerosis  
hypothetical prote  
hypothetical prote  
conserved hypotet  
hypothetical prote  
probable transcrip  
hypothetical prote  
dethiobiotin synth  
DNA polymerase III  
nematode resistanc  
hypothetical prote  
hypothetical prote  
HD-hydrolase domai  
hypothetical expor  
sialoglycoproteina  
hypothetical prote  
DltD protein for D  
DltD protein for D  
hypothetical prote  
lysostaphin (EC 3.  
conserved hypotet  
steroid 17alpha-mo  
transcription term  
oligo-1,6-glucosid  
probable chemotaxi  
hypothetical prote  
hypothetical prote  
5-aminolevulinate  
5-aminolevulinate  
5-aminolevulinate  
two-component sens  
conserved hypotet  
MG307 homolog H08  
hypothetical prote  
GTPase regulator a  
replication factor  
replication factor  
exonuclease RaxA [  
first chain of maj  
kinesin-like prote  
hypothetical prote  
sodium channel mRNA

103	29	67.4	1687	2	T43144	vitellogenin II pr	176	28	65.1	614	2	T16268	hypothetical prote
104	29	67.4	1757	2	T14318	ubiquitin-protein	177	28	65.1	620	2	H85431	ATPase-like protei
105	29	67.4	1819	2	D97033	uncharacterized pr	178	28	65.1	671	2	P82960	hypothetical prote
106	29	67.4	2009	2	A25019	sodium channel pro	179	28	65.1	682	2	T04846	protein kinase hom
107	29	67.4	2028	2	T52022	1-phosphatidylinos	180	28	65.1	682	2	T06106	hypothetical prote
108	29	67.4	2051	2	F96529	probable Phosphati	181	28	65.1	787	2	H90543	conserved hypotet
109	29	67.4	2429	1	SJHUA	spectrin alpha cha	182	28	65.1	799	2	S18209	fibroblast growth
110	29	67.4	4367	1	B54802	dynein heavy chain	183	28	65.1	890	2	F84548	hypothetical prote
111	28	65.1	155	2	I45913	interleukin-2 prec	184	28	65.1	917	2	JC7799	PAIS-1 protein -
112	28	65.1	155	2	S38662	interleukin-2 - go	185	28	65.1	940	2	D86852	exonuclease ABC s
113	28	65.1	155	2	S11488	interleukin-2 prec	186	28	65.1	953	2	D71645	exonuclease ABC c
114	28	65.1	156	2	A70057	conserved hypotet	187	28	65.1	955	2	F97861	exonuclease ABC s
115	28	65.1	158	2	D90391	conserved hypotet	188	28	65.1	992	2	T08772	hypothetical prote
116	28	65.1	177	2	S25492	gene 28 protein -	189	28	65.1	1026	2	G87346	hypothetical prote
117	28	65.1	179	2	T39848	protein transport	190	28	65.1	1055	2	C82600	multidrug-efflux t
118	28	65.1	184	2	T21126	ADP-ribosylation f	191	28	65.1	1186	1	DNBBEG	DNA-binding protei
119	28	65.1	187	2	T27416	hypothetical prote	192	28	65.1	1238	1	JC5573	copper-transportin
120	28	65.1	189	1	A38285	interleukin-11 pre	193	28	65.1	1297	2	S25714	son-of-sevenless-2
121	28	65.1	199	1	B38285	interleukin-11 pre	194	28	65.1	1484	2	C97196	probable membrane
122	28	65.1	205	2	E97991	Tns252, relaxase,	195	28	65.1	3848	2	T17414	TipC protein - gli
123	28	65.1	227	2	B90429	nitroreductase, bl	196	28	65.1	5147	1	IJFFTM	cadherin-related t
124	28	65.1	227	2	G81805	phosphoglycerate m	197	28	65.1	5281	2	S41309	cyclosporin synthe
125	28	65.1	227	2	A96924	uncharacterized me	198	27	62.8	97	2	T37433	guanylate kinase-r
126	28	65.1	229	2	B83281	histidine transpor	199	27	62.8	100	2	S38868	neuropeptide HC81
127	28	65.1	240	2	T38050	hypothetical prote	200	27	62.8	120	2	S08496	hypothetical prote
128	28	65.1	273	2	JN0522	tcpD protein - Vib	201	27	62.8	127	2	B87383	hypothetical prote
129	28	65.1	278	2	D82275	toxin co-regulated	202	27	62.8	130	2	B83992	hypothetical prote
130	28	65.1	279	2	G83041	probable N-hydroxy	203	27	62.8	131	2	AG2694	hypothetical prote
131	28	65.1	284	2	C90602	hypothetical prote	204	27	62.8	137	2	E97476	hypothetical prote
132	28	65.1	295	2	E70133	ATP-binding protei	205	27	62.8	138	2	AD0176	conserved hypotet
133	28	65.1	296	2	H69933	5'-3' exonuclease	206	27	62.8	143	2	AE2491	hypothetical prote
134	28	65.1	309	1	E64762	probable 2,6-dioxo	207	27	62.8	146	2	S51810	trypsin inhibitor
135	28	65.1	309	2	D90679	hypothetical prote	208	27	62.8	146	2	S51811	trypsin inhibitor
136	28	65.1	309	2	H85529	hypothetical prote	209	27	62.8	151	1	I36854	guanylate kinase-r
137	28	65.1	315	2	T47486	hypothetical prote	210	27	62.8	151	2	JQ1794	guanylate kinase-r
138	28	65.1	325	2	AG2053	hypothetical prote	211	27	62.8	151	2	E42523	guanylate kinase-r
139	28	65.1	326	2	H84261	hypothetical prote	212	27	62.8	153	2	T20538	hypothetical prote
140	28	65.1	330	2	T29675	hypothetical prote	213	27	62.8	154	2	AB2509	hypothetical prote
141	28	65.1	341	2	AD3252	uroporphyrinogen d	214	27	62.8	157	2	AC1713	hypothetical prote
142	28	65.1	347	2	C83928	transcription regu	215	27	62.8	157	2	AE1342	hypothetical prote
143	28	65.1	353	1	B26952	electron transfer	216	27	62.8	163	2	T28380	ORF MSV219 hypotet
144	28	65.1	353	2	F95317	FixB electron tran	217	27	62.8	179	2	B69302	conserved hypotet
145	28	65.1	360	2	T26037	hypothetical prote	218	27	62.8	180	2	AD0134	probable prophage
146	28	65.1	360	2	S32695	Wnt-2 protein - Ca	219	27	62.8	188	2	A72628	hypothetical prote
147	28	65.1	363	2	T17543	probable D-lactate	220	27	62.8	193	2	B84435	conserved hypotet
148	28	65.1	374	2	H75002	methyl-accepting c	221	27	62.8	214	2	H83120	probable two-compo
149	28	65.1	384	2	D69548	conserved hypotet	222	27	62.8	224	2	A98193	DNA repair protein
150	28	65.1	392	2	A75593	alcohol dehydrogen	223	27	62.8	224	2	B86040	DNA repair protein
151	28	65.1	394	2	T19116	hypothetical prote	224	27	62.8	238	2	T23352	hypothetical prote
152	28	65.1	408	2	T47498	hypothetical prote	225	27	62.8	247	2	H64330	proliferating-cell
153	28	65.1	417	2	S34433	site-specific DNA-	226	27	62.8	247	2	S66972	probable membrane
154	28	65.1	419	2	H81667	transcription term	227	27	62.8	256	2	S04363	class II histocomp
155	28	65.1	438	2	A83544	probable transport	228	27	62.8	256	2	S02855	class II histocomp
156	28	65.1	450	2	C86466	hypothetical prote	229	27	62.8	256	2	T28695	hypothetical prote
157	28	65.1	452	2	S74653	sensory transducti	230	27	62.8	261	2	AC1773	formate dehydrogen
158	28	65.1	464	2	G85666	transcription term	231	27	62.8	262	2	C83566	hypothetical prote
159	28	65.1	464	2	D72058	transcription term	232	27	62.8	263	2	T10369	late expression fa
160	28	65.1	464	2	F81509	probable transcrip	233	27	62.8	273	2	JN0850	hypothetical 28.3K
161	28	65.1	485	2	F85512	aminoacyl-histidin	234	27	62.8	276	2	AF2307	protease IV [imp
162	28	65.1	485	2	H90661	X-His dipeptidase	235	27	62.8	276	2	D98219	ABC transporter AT
163	28	65.1	485	2	JU0300	hypothetical prote	236	27	62.8	276	2	AF3067	hypothetical prote
164	28	65.1	490	2	F89933	hypothetical prote	237	27	62.8	281	2	H86159	hypothetical prote
165	28	65.1	501	2	T13766	hypothetical prote	238	27	62.8	282	2	T07303	cell division inhi
166	28	65.1	503	2	T47496	hypothetical prote	239	27	62.8	297	2	H72076	hypothetical prote
167	28	65.1	506	2	AB2064	hypothetical prote	240	27	62.8	309	2	D95905	conserved hypotet
168	28	65.1	532	2	G70536	probable cpsY prot	241	27	62.8	316	2	A41626	protein farnesyltr
169	28	65.1	534	2	F82615	methyltransferase	242	27	62.8	318	2	D96774	unknown protein F1
170	28	65.1	544	2	E97051	site-specific DNA	243	27	62.8	326	2	A84277	hypothetical prote
171	28	65.1	548	2	S13579	oligo-1,6-glucosid	244	27	62.8	330	2	AC1095	B. subtilis DNA po
172	28	65.1	560	2	C71155	hypothetical prote	245	27	62.8	330	2	AF1458	B. subtilis DNA po
173	28	65.1	603	2	JC4666	lymphocyte specifi	246	27	62.8	336	2	B87475	DNA polymerase III
174	28	65.1	612	2	F82429	protein-export mem	247	27	62.8	344	2	C72395	transcription regu
175	28	65.1	614	2	S43427	intermediate filam	248	27	62.8	351	2	B72315	conserved hypotet



249	27	62.8	352	2	B69089	anthranilate phosph	322	27	62.8	660	2	AB0893	RNA polymerase sig
250	27	62.8	355	2	S50372	hypothetical prote	323	27	62.8	672	2	T06560	photomorphogenesis
251	27	62.8	360	2	S78016	hypothetical prote	324	27	62.8	673	2	T40817	zinc finger protei
252	27	62.8	371	2	A75085	hypothetical prote	325	27	62.8	675	2	T01112	photomorphogenesis
253	27	62.8	372	2	D70753	probable oxidoredu	326	27	62.8	683	2	S34961	synaptic vesicle p
254	27	62.8	374	2	G89875	hypothetical prote	327	27	62.8	691	2	T44543	probable bacteriop
255	27	62.8	378	2	G97301	hypothetical prote	328	27	62.8	692	2	A81593	hypothetical prote
256	27	62.8	383	2	B87680	uncharacterized co	329	27	62.8	692	2	D86547	hypothetical prote
257	27	62.8	396	2	H83914	alkaline xylanase	330	27	62.8	696	2	S75626	hypothetical prote
258	27	62.8	396	2	JD0003	xylanase (EC 3.2.1	331	27	62.8	713	2	T19501	hypothetical prote
259	27	62.8	396	2	T05503	hypothetical prote	332	27	62.8	715	2	T19500	hypothetical prote
260	27	62.8	401	2	C89777	capsular polysacch	333	27	62.8	724	2	I50531	hypothetical prote
261	27	62.8	406	2	A35401	cytochrome P450 10	334	27	62.8	724	2	A42953	transmembrane tran
262	27	62.8	414	2	G84311	hypothetical prote	335	27	62.8	754	2	T12453	nitrous oxide redu
263	27	62.8	418	2	T45807	translation initia	336	27	62.8	755	1	LQBYPK	hypothetical prote
264	27	62.8	420	2	B90991	probable tagatose	337	27	62.8	768	2	A56234	DNA ligase (ATP) (
265	27	62.8	420	2	F64976	probable tagatose	338	27	62.8	779	2	T44659	ral guanine nucleo
266	27	62.8	420	2	D85836	probable tagatose	339	27	62.8	783	2	B96802	nitrous oxide redu
267	27	62.8	431	2	T06019	hypothetical prote	340	27	62.8	807	2	E85631	hypothetical prote
268	27	62.8	435	2	B87592	hypothetical prote	341	27	62.8	808	2	G90968	hypothetical prote
269	27	62.8	451	2	B70805	hypothetical prote	342	27	62.8	868	1	VGBE31	host specificity p
270	27	62.8	456	2	A12789	manganese transpor	343	27	62.8	872	2	T10582	glycoprotein B - h
271	27	62.8	461	2	H97568	manganese transpor	344	27	62.8	887	2	B96598	hypothetical prote
272	27	62.8	464	2	A28569	alpha-methyl dopa-h	345	27	62.8	893	2	A84591	hypothetical prote
273	27	62.8	466	2	T32610	hypothetical prote	346	27	62.8	930	2	B72537	26S proteasome reg
274	27	62.8	467	2	F82840	phosphomannomutase	347	27	62.8	948	2	S73549	hypothetical prote
275	27	62.8	473	2	T38801	hypothetical prote	348	27	62.8	977	2	D85741	exonuclease ABC c
276	27	62.8	475	2	S54989	reverse transcript	349	27	62.8	1060	2	H86686	hypothetical prote
277	27	62.8	475	2	S54993	reverse transcript	350	27	62.8	1102	2	S44772	DNA-directed DNA p
278	27	62.8	475	2	S54994	reverse transcript	351	27	62.8	1102	2	S44772	C2984.4 protein -
279	27	62.8	479	2	F86356	reverse transcript	352	27	62.8	1103	2	T04617	hypothetical prote
280	27	62.8	489	2	F97119	Ti6E15.2 protein -	353	27	62.8	1157	2	A90769	probable host spec
281	27	62.8	489	2	C71410	nicotinic acid pho	354	27	62.8	1159	2	A90899	probable host spec
282	27	62.8	495	2	A38650	hypothetical prote	355	27	62.8	1159	2	G85816	hypothetical prote
283	27	62.8	501	2	A96695	myosin heavy chain	356	27	62.8	1170	2	A53612	laminin Blk chain
284	27	62.8	512	2	A96695	hypothetical prote	357	27	62.8	1201	2	T00444	hypothetical prote
285	27	62.8	512	2	AG0842	multidrug resistan	358	27	62.8	1234	2	C84465	hypothetical prote
286	27	62.8	512	2	F91072	multidrug resistan	359	27	62.8	1242	2	S78061	DNA-directed RNA p
287	27	62.8	518	2	G65048	hypothetical prote	360	27	62.8	1244	2	S76102	hypothetical prote
288	27	62.8	524	1	T25507	hypothetical prote	361	27	62.8	1279	2	T41389	rna binding protei
289	27	62.8	524	1	S60406	hypothetical prote	362	27	62.8	1309	2	H96650	protein T3P18.3 li
290	27	62.8	524	2	T04564	cytochrome P450 ho	363	27	62.8	1312	1	BWBIDL	RAD50 protein - ye
291	27	62.8	527	2	S03974	cytochrome P450 ho	364	27	62.8	1350	2	T42697	hypothetical prote
292	27	62.8	531	2	S03974	amine oxidase (fla	365	27	62.8	1364	1	AJFFPP	hypothetical prote
293	27	62.8	532	2	AH3538	probable membrane	366	27	62.8	1411	2	S44770	C2984.3 proteinin
294	27	62.8	533	2	T40153	ubiquinone biosynt	367	27	62.8	1412	2	A26122	alpha-2-macroglobu
295	27	62.8	533	2	A96958	hypothetical prote	368	27	62.8	1483	2	T19751	hypothetical prote
296	27	62.8	551	2	A96958	dnak protein (heat	369	27	62.8	1483	2	T49451	kinesin-like prote
297	27	62.8	554	2	T22433	hypothetical prote	370	27	62.8	1742	2	AB1960	two-component sens
298	27	62.8	560	2	T46189	calcium-dependent	371	27	62.8	1749	2	S03124	vitellogenin A2 pr
299	27	62.8	562	2	S75308	DNA ligase (EC 6.5	372	27	62.8	1807	2	A59252	vitellin heavy chain
300	27	62.8	564	2	AH1696	alpha-acetolactate	373	27	62.8	1976	2	A47297	myosin heavy chain
301	27	62.8	565	2	AF1325	alpha-acetolactate	374	27	62.8	1992	2	A84652	hypothetical prote
302	27	62.8	585	2	D69762	hypothetical prote	375	27	62.8	2420	2	E98274	hypothetical prote
303	27	62.8	585	2	C70181	protein-export mem	376	27	62.8	2866	2	A64556	toxin-like oucer m
304	27	62.8	587	2	A12247	GTP cyclohydrolase	377	27	62.8	2893	2	T18489	hypothetical prote
305	27	62.8	598	2	T40659	probable peroxisom	378	27	62.8	4981	2	T15789	hypothetical prote
306	27	62.8	613	1	RNECS	transcription init	379	27	62.8	7829	2	H69301	hypothetical prote
307	27	62.8	613	2	F91122	RNA polymerase sig	380	27	60.5	62	2	S43286	conserved hypotet
308	27	62.8	613	2	E85967	RNA polymerase sig	381	27	60.5	64	2	AF2574	MURF4 protein - Tr
309	27	62.8	613	1	RNEBST	ferrous iron trans	382	27	60.5	72	2	T43995	hypothetical prote
310	27	62.8	615	1	AH2028	transcription init	383	27	60.5	105	2	T44182	hypothetical prote
311	27	62.8	615	2	G64571	hypothetical prote	384	27	60.5	106	2	T17991	hypothetical prote
312	27	62.8	623	2	C71865	conserved hypotet	385	27	60.5	122	2	AB3353	transcription regu
313	27	62.8	624	2	T44840	hypothetical prote	386	27	60.5	128	2	F69902	conserved hypotet
314	27	62.8	631	2	T26232	probable drdgluco	387	27	60.5	129	2	T05752	hypothetical prote
315	27	62.8	642	2	B90767	hypothetical prote	388	27	60.5	130	2	D89812	conserved hypotet
316	27	62.8	642	2	G90970	probable terminase	389	27	60.5	131	2	D89812	hypothetical prote
317	27	62.8	642	2	B49849	terminase large ch	390	27	60.5	146	2	AB2575	hypothetical prote
318	27	62.8	646	2	AB0901	ATP-dependent RNA	391	27	60.5	150	2	AD2256	hypothetical prote
319	27	62.8	654	2	A85717	hypothetical prote	392	27	60.5	152	2	E72487	hypothetical prote
320	27	62.8	655	2	T39064	RNA binding protei	393	27	60.5	165	2	S28020	peptidylprolyl iso
321	27	62.8	659	2	S30893	nrtc protein - Syn	394	27	60.5	169	2	AE3257	shikimate kinase (
										171	2	TL7389	vrJ protein - Dic
										172	1	DWECHD	3-hydroxydecanoyl-

395	26	60.5	172	2	AF0626	D-3-hydroxydecanoyl	468	26	60.5	364	2	AD0566	hypothetical ATP-b
396	26	60.5	172	2	F90758	3-hydroxydecanoyl-	469	26	60.5	367	2	F95159	prephenate dehydro
397	26	60.5	172	2	D85622	3-hydroxydecanoyl-	470	26	60.5	368	1	S74797	GTP-binding protei
398	26	60.5	173	2	AE2857	conserved hypothet	471	26	60.5	369	2	F95904	hypothetical prote
399	26	60.5	173	2	C97634	hypothetical prote	472	26	60.5	370	2	S64479	probable membrane
400	26	60.5	175	2	H72538	hypothetical prote	473	26	60.5	380	2	S62523	sepin homolog - f
401	26	60.5	186	2	AD0355	probable exported	474	26	60.5	381	2	S18543	hypothetical prote
402	26	60.5	189	2	H90414	conserved hypothet	475	26	60.5	382	1	PECH	pepsin A (EC 3.4.2
403	26	60.5	191	2	C87438	hypothetical prote	476	26	60.5	383	2	H50482	conserved hypothet
404	26	60.5	193	1	G69347	conserved hypothet	477	26	60.5	383	2	A86182	hypothetical prote
405	26	60.5	196	2	B82038	hypothetical prote	478	26	60.5	385	2	H70937	hypothetical prote
406	26	60.5	197	2	D90396	conserved hypothet	479	26	60.5	386	2	T28375	ORF MSV214 SCG gen
407	26	60.5	200	2	A82933	hypothetical prote	480	26	60.5	386	2	T08353	hypothetical prote
408	26	60.5	202	2	D82235	conserved hypothet	481	26	60.5	389	2	C82130	conserved hypothet
409	26	60.5	205	2	S74960	hypothetical prote	482	26	60.5	390	2	T30020	hypothetical prote
410	26	60.5	205	2	AH3407	hypothetical cytos	483	26	60.5	398	2	A82820	porin O precursor
411	26	60.5	210	2	D89825	hypothetical prote	484	26	60.5	399	2	C96751	probable GTP-bindi
412	26	60.5	222	2	C82789	hypothetical prote	485	26	60.5	399	2	T06251	GTP binding protei
413	26	60.5	223	2	F83598	5'-phosphoribosylg	486	26	60.5	406	2	E81300	probable glucose-6
414	26	60.5	224	2	H65164	cell division prot	487	26	60.5	407	2	I38062	transcription fact
415	26	60.5	226	2	H82861	DNA repair protein	488	26	60.5	412	2	F70852	hypothetical prote
416	26	60.5	227	2	B70438	conjugal transfer	489	26	60.5	420	2	H86331	F69.9 protein - A
417	26	60.5	231	2	C97552	hypothetical prote	490	26	60.5	422	2	G72227	hypothetical prote
418	26	60.5	231	2	AD2772	hypothetical prote	491	26	60.5	425	1	KEXL2A	keratin, 64K type
419	26	60.5	237	2	E55210	heti protein - Ana	492	26	60.5	425	2	F83590	probable oxidoredu
420	26	60.5	239	2	T15829	hypothetical prote	493	26	60.5	425	2	T15959	hypothetical prote
421	26	60.5	240	2	S71878	glutathione transf	494	26	60.5	426	2	H83897	imidazoloneproton
422	26	60.5	247	2	C96594	unknown protein, 7	495	26	60.5	427	2	S64570	probable succinate
423	26	60.5	249	2	S74547	hypothetical prote	496	26	60.5	427	2	A55496	apexin precursor -
424	26	60.5	252	2	A49232	outer membrane pro	497	26	60.5	428	2	A89950	glutamate-1-semial
425	26	60.5	257	2	D71240	probable NH(3)-dep	498	26	60.5	429	2	T37765	pumilio-like prote
426	26	60.5	260	2	G84553	hypothetical prote	499	26	60.5	429	2	T48051	hypothetical prote
427	26	60.5	264	2	S29144	hypothetical prote	500	26	60.5	434	1	B70511	cycochrome P450 Rv
428	26	60.5	268	2	T46902	hypothetical prote	501	26	60.5	436	2	T39118	probable alpha-gal
429	26	60.5	271	2	AF2209	rRNA (adenine-N6,N	502	26	60.5	436	2	A13456	dihydropyrimidine
430	26	60.5	272	2	H95954	probable Sir2-like	503	26	60.5	440	2	E83994	xylose isomerase x
431	26	60.5	276	2	B95996	hypothetical prote	504	26	60.5	446	2	S26965	NADH oxidase - Ent
432	26	60.5	279	2	B82974	probable permease	505	26	60.5	448	2	T15542	hypothetical prote
433	26	60.5	281	2	A84981	prolipoprotein dia	506	26	60.5	457	2	S18239	glycerol-3-phospha
434	26	60.5	282	2	T13218	hypothetical prote	507	26	60.5	457	2	AF2975	aminotransferase,
435	26	60.5	283	2	H86547	hypothetical prote	508	26	60.5	457	2	E98307	probable aminotran
436	26	60.5	283	2	G72075	hypothetical prote	509	26	60.5	460	2	T23667	hypothetical prote
437	26	60.5	290	2	I58425	arylamine N-acetyl	510	26	60.5	468	2	S65951	[phosphorylase] ph
438	26	60.5	290	2	C82454	hypothetical prote	511	26	60.5	472	2	D87321	succinylglutamic s
439	26	60.5	292	2	T04514	xyloglucan endo-1,	512	26	60.5	472	2	A13367	multidrug resistan
440	26	60.5	292	2	T33987	hypothetical prote	513	26	60.5	475	2	D86450	hypothetical prote
441	26	60.5	292	2	H69999	ABC transporter (A	514	26	60.5	476	2	B96547	probable protein k
442	26	60.5	292	2	S18883	ribonucleoprotein	515	26	60.5	479	2	T30997	hypothetical prote
443	26	60.5	301	2	AD1169	ABC transporter (A	516	26	60.5	493	2	AB0451	conserved hypothet
444	26	60.5	301	2	AF1526	Similar to ABC tra	517	26	60.5	495	2	T31203	hypothetical prote
445	26	60.5	303	2	A69542	conserved hypothet	518	26	60.5	496	2	A54770	N-acetylglucosamin
446	26	60.5	303	2	E89964	hypothetical prote	519	26	60.5	508	2	B81212	fatty acid efflux
447	26	60.5	304	2	D71290	probable ATP-bindi	520	26	60.5	509	2	AG0365	probable membrane
448	26	60.5	309	2	S70793	vsb2 protein - My	521	26	60.5	510	2	E97307	probable cardiolip
449	26	60.5	311	2	C84101	hypothetical prote	522	26	60.5	510	2	T45952	hypothetical prote
450	26	60.5	312	2	A75514	peptidase-related	523	26	60.5	512	2	D32302	probable aspartate
451	26	60.5	314	2	F90577	lipoprotein vsaE [	524	26	60.5	514	1	HQVULB	cycochrome-c3 hydr
452	26	60.5	319	2	B86433	hypothetical prote	525	26	60.5	514	2	AC1014	maltoe transport
453	26	60.5	319	2	S77714	RNA-binding protei	526	26	60.5	514	2	S05332	inner membrane pro
454	26	60.5	321	2	T47138	hypothetical prote	527	26	60.5	514	2	S20604	inner membrane pro
455	26	60.5	322	2	C70344	hypothetical prote	528	26	60.5	516	2	T44002	conserved herpesvi
456	26	60.5	324	2	H87540	alcohol dehydrogen	529	26	60.5	516	2	R81789	multidrug resistan
457	26	60.5	324	2	S12111	ribonucleoprotein,	530	26	60.5	520	1	A42209	D-steroidspecific a
458	26	60.5	330	2	S08500	QUTG protein - Eme	531	26	60.5	524	2	JS0746	cycochrome P450 1A
459	26	60.5	342	2	AD2273	GTP-binding protei	532	26	60.5	524	2	JOX0189	cycochrome P450 1A
460	26	60.5	342	2	S72529	1,3-beta-glucanase	533	26	60.5	525	2	AD0324	probable solute-bi
461	26	60.5	345	2	T08563	dnat-related prote	534	26	60.5	526	2	E75045	2-isopropylmalate
462	26	60.5	347	2	T07108	glucan endo-1,3-be	535	26	60.5	533	2	T09935	hypothetical prote
463	26	60.5	348	2	T08814	1,3-beta-glucanase	536	26	60.5	534	2	T52649	beta-1,2-xylosyltr
464	26	60.5	352	2	T49396	hypothetical prote	537	26	60.5	536	2	B81319	hypothetical prote
465	26	60.5	354	2	C82038	nitrogen regulatio	538	26	60.5	538	2	T46863	L-aspartate oxidas
466	26	60.5	359	2	C86493	Pmp 4 [imported] -	539	26	60.5	539	2	AH2502	hypothetical prote
467	26	60.5	361	1	F69254	probable hexosyltr	540	26	60.5	543	2	AB0460	ubiquinone biosynt

541	26	60.5	544	2	S52081	diphosphate-fructo	614	26	60.5	812	2	A46417	NIP1 protein - yea
542	26	60.5	545	2	S59143	NADH2 dehydrogenas	615	26	60.5	827	2	B95969	probable H+/K+-exc
543	26	60.5	546	2	D84546	probable importin	616	26	60.5	829	2	S72366	DNA topoisomerase
544	26	60.5	547	2	A71544	probable di-phospho	617	26	60.5	829	2	AH2282	hypothetical prote
545	26	60.5	548	2	B81698	pyrophosphate-fruc	618	26	60.5	830	2	T18860	hypothetical prote
546	26	60.5	549	2	T05867	probable growth re	619	26	60.5	831	2	JX0359	DNA-directed DNA p
547	26	60.5	550	2	JC7562	glioblastoma RING	620	26	60.5	832	2	A33530	DNA-directed DNA p
548	26	60.5	551	2	S71751	dolichyl-phosphate	621	26	60.5	846	2	JC7720	acetyltransferase
549	26	60.5	552	2	T22184	hypothetical prote	622	26	60.5	849	2	B86306	similar to tuftelli
550	26	60.5	553	2	A89956	hypothetical prote	623	26	60.5	857	2	C97707	clpB protein (mpo
551	26	60.5	554	2	B95134	hypothetical prote	624	26	60.5	858	2	D71711	endopeptidase clp
552	26	60.5	555	2	H98002	dihydrolipoamide d	625	26	60.5	865	1	VGBEBB	glycoprotein B pre
553	26	60.5	556	2	F86863	hypothetical prote	626	26	60.5	868	2	G64119	DNA topoisomerase
554	26	60.5	557	2	F64110	hypothetical prote	627	26	60.5	868	2	G71691	hypothetical prote
555	26	60.5	558	2	A97119	single-stranded-DN	628	26	60.5	869	2	F64132	membrane alanyl am
556	26	60.5	559	2	T12886	probable membrane	629	26	60.5	876	2	AH1964	aconitate hydratase
557	26	60.5	560	2	T47620	conserved hypotHet	630	26	60.5	891	2	B97759	hypothetical prote
558	26	60.5	561	2	F81417	histon acetyltrans	631	26	60.5	902	2	D71079	hypothetical prote
559	26	60.5	562	1	EDBEMC	MCP-domain signal	632	26	60.5	913	1	VGBEPS	glycoprotein gII p
560	26	60.5	563	1	C64215	immediate-early ph	633	26	60.5	919	1	VGBEQH	glycoprotein B pre
561	26	60.5	564	2	B84546	GTP-binding membra	634	26	60.5	929	2	T29162	hypothetical prote
562	26	60.5	565	2	T45093	probable splicing	635	26	60.5	948	2	B81883	excinuclease ABC c
563	26	60.5	566	2	AC2508	hypothetical prote	636	26	60.5	948	2	A56602	excinuclease ABC c
564	26	60.5	567	2	S69564	hypothetical prote	637	26	60.5	949	2	A81138	glycoprotein B hom
565	26	60.5	568	2	T18445	hypothetical prote	638	26	60.5	950	1	FWBR1	excinuclease ABC c
566	26	60.5	569	1	EDBESM	hypothetical prote	639	26	60.5	952	2	T03158	Caz+-transporting
567	26	60.5	570	1	A11180	immediate-early pr	640	26	60.5	975	2	T42576	tegument protein 6
568	26	60.5	571	2	T26148	amidasase homolog 1	641	26	60.5	979	2	JH0109	probable envelope
569	26	60.5	572	2	E96028	hypothetical prote	642	26	60.5	980	1	VGBR2H	glycoprotein 14 pr
570	26	60.5	573	2	A97866	probable 4-hydroxy	643	26	60.5	980	1	VGBEC6	glycoprotein B pre
571	26	60.5	574	1	RNR57P	RNA polymerase sig	644	26	60.5	1002	2	S62035	glycoprotein B pre
572	26	60.5	575	1	A82479	transcription init	645	26	60.5	1003	2	AH2335	isoleucine-tRNA li
573	26	60.5	576	2	G64605	threonyl-tRNA synt	646	26	60.5	1034	2	S36758	toxin secretion AB
574	26	60.5	577	2	D71909	iron(III) transport	647	26	60.5	1051	2	C95367	mgII protein - mou
575	26	60.5	578	2	G86863	ferrous iron trans	648	26	60.5	1089	2	C70522	conserved hypotHet
576	26	60.5	579	2	S54123	threonine-tRNA lig	649	26	60.5	1091	2	T18666	lodestar mmpL8 pro
577	26	60.5	580	2	T28924	neurofilament prot	650	26	60.5	1092	2	S42798	fibronectin-bindin
578	26	60.5	581	2	T01999	hypothetical prote	651	26	60.5	1099	2	S48053	protein tyrosine k
579	26	60.5	582	2	A90506	hypothetical prote	652	26	60.5	1100	2	S43677	protein tyrosine k
580	26	60.5	583	2	D96739	ser/thr protein ki	653	26	60.5	1112	2	D96753	Similar to disease
581	26	60.5	584	2	T28391	hypothetical prote	654	26	60.5	1124	2	A55747	I-JAK protein-tyro
582	26	60.5	585	2	A83624	ORF MSV230 hypotHe	655	26	60.5	1125	2	T30298	dynein heavy chain
583	26	60.5	586	2	F96032	probable chemotaxi	656	26	60.5	1132	2	T00259	hypothetical prote
584	26	60.5	587	2	B98988	hypothetical prote	657	26	60.5	1134	2	T04890	hypothetical prote
585	26	60.5	588	2	S75963	translation elonga	658	26	60.5	1135	1	A29813	132K ninaC protein
586	26	60.5	589	2	AC2348	translation elonga	659	26	60.5	1136	1	USBS81	paraportal crystal
587	26	60.5	590	1	S04429	translation elonga	660	26	60.5	1155	2	AC3675	chromosome segrega
588	26	60.5	591	2	T07447	DNA-directed RNA p	661	26	60.5	1156	2	T07756	phycochrome B - so
589	26	60.5	592	2	S61502	flagellar biosynth	662	26	60.5	1160	2	T13713	betas3 protein - fr
590	26	60.5	593	2	S04390	translation elonga	663	26	60.5	1165	2	A97457	structural mainten
591	26	60.5	594	2	E75536	translation elonga	664	26	60.5	1166	2	T15628	hypothetical prote
592	26	60.5	595	2	S40710	hypothetical prote	665	26	60.5	1219	2	T06608	disease resistance
593	26	60.5	596	2	S70834	transcription init	666	26	60.5	1225	2	A56514	chromokinesin - ch
594	26	60.5	597	2	S58251	probable membrane	667	26	60.5	1231	2	A54803	microtubule-associ
595	26	60.5	598	2	B83222	regulatory protein	668	26	60.5	1232	2	B39432	ATP-dependent deox
596	26	60.5	599	2	T75540	glycogen operon pr	669	26	60.5	1236	2	T50904	Mg protoporphyrin
597	26	60.5	600	2	T02457	hypothetical prote	670	26	60.5	1250	2	T00454	hypothetical prote
598	26	60.5	601	2	A70764	probable glgX prot	671	26	60.5	1259	2	I58401	protein-tyrosine k
599	26	60.5	602	2	B97747	oligopeptidase B (	672	26	60.5	1400	2	T33758	hypothetical prote
600	26	60.5	603	2	B70333	hypothetical prote	673	26	60.5	1456	2	G86466	hypothetical prote
601	26	60.5	604	2	S35532	hnRNA-binding prot	674	26	60.5	1462	1	A69809	probable multifunc
602	26	60.5	605	2	T50143	pumilio family pro	675	26	60.5	1501	1	B29813	174K ninaC protein
603	26	60.5	606	2	S61568	probable membrane	676	26	60.5	1520	2	B82274	conserved hypotHet
604	26	60.5	607	2	D72338	(p)ppGpp synthetas	677	26	60.5	1578	2	S76238	hypothetical prote
605	26	60.5	608	2	J50198	genome polyprotein	678	26	60.5	1802	2	G71616	hypothetical prote
606	26	60.5	609	2	S73756	probable lipoprotei	679	26	60.5	1957	2	S68453	sodium channel pro
607	26	60.5	610	2	D84847	probable receptor-	680	26	60.5	2016	2	A38195	sodium channel pro
608	26	60.5	611	1	ISHUT1	DNA topoisomerase	681	26	60.5	2019	2	A33996	sodium channel pro
609	26	60.5	612	2	AF2279	hypothetical prote	682	26	60.5	2098	2	T13166	rough deal protein
610	26	60.5	613	2	A49546	DNA topoisomerase	683	26	60.5	2109	1	ZLVN	genome polyprotein
611	26	60.5	614	2	JU0144	DNA topoisomerase	684	26	60.5	2225	2	T26063	hypothetical prote
612	26	60.5	615	2	A82882	cell division prot	685	26	60.5	2326	2	T29140	hypothetical prote
613	26	60.5	616	2	T23780	hypothetical prote	686	26	60.5	2672	2	A48126	translation activa

687	26	60.5	2958	2	S64921	probable membrane	760	25	58.1	203	2	F97987	conserved hypothet
688	26	60.5	3125	1	GNVSPPP	genome polyprotein	761	25	58.1	203	2	C95120	hypothetical prote
689	26	60.5	3140	1	GNVSRA	genome polyprotein	762	25	58.1	203	2	G97989	hypothetical prote
690	26	60.5	3140	1	S47508	genome polyprotein	763	25	58.1	204	2	S78299	conserved hypothet
691	26	60.5	3141	1	GNVSPD	genome polyprotein	764	25	58.1	204	2	A82389	hypothetical prote
692	26	60.5	3227	2	T37964	probable ubiquitin	765	25	58.1	204	2	E65183	hypothetical prote
693	26	60.5	3433	1	S28381	utrophin - human	766	25	58.1	205	2	T33628	hypothetical prote
694	26	60.5	4563	1	LFRUB	apolipoprotein B-1	767	25	58.1	207	2	T31239	traE protein homol
695	25.5	59.3	412	2	E95077	GTP-binding protei	768	25	58.1	212	2	AG0344	probable phosphori
696	25.5	59.3	412	2	E97945	conserved hypothet	769	25	58.1	212	2	AH1944	phosphoglycerate m
697	25	58.1	54	2	D26506	complement C2 (EC	770	25	58.1	212	2	C86852	hypothetical prote
698	25	58.1	59	2	D81133	hypothetical prote	771	25	58.1	214	1	A8BYD	AD88 protein - yea
699	25	58.1	65	2	B75298	hypothetical prote	772	25	58.1	216	2	D70374	phosphoribosylglyc
700	25	58.1	65	2	T14397	hypothetical prote	773	25	58.1	216	2	F90397	hypothetical prote
701	25	58.1	75	2	T30318	probable cold-indu	774	25	58.1	217	2	T45187	hypothetical prote
702	25	58.1	78	2	G00530	steroid hormone re	775	25	58.1	219	1	A41316	flagellin A precu
703	25	58.1	82	2	A49036	hypothetical prote	776	25	58.1	220	2	D64678	NADH2 dehydrogenas
704	25	58.1	88	2	H90303	MHC alpha chain -	777	25	58.1	222	2	H83528	phosphoribosylamin
705	25	58.1	97	2	A46114	orf18 protein - eq	778	25	58.1	222	2	T47768	hypothetical prote
706	25	58.1	103	2	F64910	hypothetical prote	779	25	58.1	224	2	T51638	probable transcrip
707	25	58.1	108	2	F85691	unknown protein en	780	25	58.1	226	2	A49159	prolactin - golden
708	25	58.1	108	2	A99822	hypothetical prote	781	25	58.1	226	2	A53273	MHC class II histo
709	25	58.1	111	2	A98095	type III secretion	782	25	58.1	226	2	S51642	transcription fact
710	25	58.1	111	2	E85940	type III secretion	783	25	58.1	227	2	H71811	hypothetical prote
711	25	58.1	113	2	G82871	ribonuclease p pro	784	25	58.1	228	2	B85720	hypothetical prote
712	25	58.1	113	2	C90279	conserved hypothet	785	25	58.1	228	2	E90897	hypothetical prote
713	25	58.1	117	2	T39528	very hypothetical	786	25	58.1	228	2	G64908	probable transcrip
714	25	58.1	117	2	A83312	conserved hypothet	787	25	58.1	230	2	S48263	hypothetical prote
715	25	58.1	118	2	A99787	conserved hypothet	788	25	58.1	233	2	C82360	cell division ATP-
716	25	58.1	119	2	H97183	stage V sporulatio	789	25	58.1	238	1	S06739	probable adenylate
717	25	58.1	123	2	E81851	ribosomal-binding	790	25	58.1	239	2	A80772	probable exported
718	25	58.1	123	2	B81091	ribosome-binding f	791	25	58.1	243	2	E87413	hemolysin A (impor
719	25	58.1	125	2	S11703	E1 protein - Esche	792	25	58.1	243	2	T26432	hypothetical prote
720	25	58.1	126	2	S47103	urease (EC 3.5.1.5	793	25	58.1	245	2	D71554	hypothetical prote
721	25	58.1	136	2	T17640	hypothetical prote	794	25	58.1	245	2	B69841	probable adenylate
722	25	58.1	141	2	AD3572	hypothetical cytos	795	25	58.1	251	2	T39441	very hypothetical
723	25	58.1	144	2	H95037	PTS system, IIA co	796	25	58.1	251	2	H97257	spore coat protein
724	25	58.1	144	2	C97908	hypothetical prote	797	25	58.1	252	2	B88637	protein W09G12.4 [
725	25	58.1	147	2	B86699	hypothetical prote	798	25	58.1	253	2	B38957	interleukin 12A pr
726	25	58.1	152	2	B89839	conserved hypothet	799	25	58.1	258	2	C86541	CT105 hypothetical
727	25	58.1	157	2	E97424	hypothetical 18.7K	800	25	58.1	258	2	G83069	probable oxidoredu
728	25	58.1	157	2	AD2642	conserved hypothet	801	25	58.1	258	2	D72082	hypothetical prote
729	25	58.1	158	2	A12718	conserved hypothet	802	25	58.1	260	2	A80438	hypothetical prote
730	25	58.1	158	2	E97500	hypothetical prote	803	25	58.1	261	2	AH1397	formate dehydrogen
731	25	58.1	162	2	T36151	protein T21E12.3 [	804	25	58.1	262	2	D95147	choline kinase [im
732	25	58.1	163	2	T36151	probable asnc-fami	805	25	58.1	263	2	F83227	hypothetical prote
733	25	58.1	168	2	H86798	prophage pi3 prote	806	25	58.1	268	2	D70023	lipoic acid synthet
734	25	58.1	170	2	S76918	hypothetical prote	807	25	58.1	268	2	B30819	interferon-regulat
735	25	58.1	172	2	D82194	3-hydroxydecanoyl-	808	25	58.1	269	2	F71323	conserved hypothet
736	25	58.1	172	2	AH0174	3-hydroxydecanoyl-	809	25	58.1	270	2	JC4350	thiostrepton - Str
737	25	58.1	172	2	F87416	hypothetical prote	810	25	58.1	270	2	G71061	hypothetical prote
738	25	58.1	174	2	E90414	conserved hypothet	811	25	58.1	280	2	G81421	probable flagellar
739	25	58.1	174	2	D86239	protein T10024.23	812	25	58.1	280	2	I64007	hypothetical prote
740	25	58.1	177	2	G64116	3-hydroxydecanoyl-	813	25	58.1	286	2	C86019	probable aldolase
741	25	58.1	179	2	S21380	flagellar motor sw	814	25	58.1	286	2	C91173	probable aldolase
742	25	58.1	179	2	AE2645	flagellar motor sw	815	25	58.1	286	2	I80309	sepa protein - Bac
743	25	58.1	180	2	D87754	protein C43E11.9 [	816	25	58.1	288	2	T32138	hypothetical prote
744	25	58.1	182	2	A54869	ADP-ribosylation f	817	25	58.1	289	2	B98015	choline kinase [im
745	25	58.1	182	2	B54869	ADP-ribosylation f	818	25	58.1	291	2	E71491	probable geranyl t
746	25	58.1	183	2	AE1223	transcription regu	819	25	58.1	292	2	F69372	conserved hypothet
747	25	58.1	192	2	T17331	hypothetical prote	820	25	58.1	292	2	G93722	osmoprotection pro
748	25	58.1	193	2	A82758	hypothetical prote	821	25	58.1	296	2	I52860	smooth muscle myos
749	25	58.1	194	2	G90202	ATP synthase subun	822	25	58.1	296	2	C49539	xyloglucan endo-1,
750	25	58.1	195	1	B69441	conserved hypothet	823	25	58.1	296	2	F90067	hypothetical prote
751	25	58.1	195	2	T08812	probable succinate	824	25	58.1	299	2	T47917	probable transcrip
752	25	58.1	195	2	T22032	hypothetical prote	825	25	58.1	299	2	D95382	probable transcrip
753	25	58.1	195	2	E72590	probable capsular	826	25	58.1	300	2	A32837	transcription acti
754	25	58.1	195	2	E97427	flagellar motor sw	827	25	58.1	300	2	C84079	lipoic acid synthet
755	25	58.1	195	2	T02799	glutaredoxin-relat	828	25	58.1	308	2	T24912	hypothetical prote
756	25	58.1	196	2	B75124	probable imidazole	829	25	58.1	308	2	S13584	nosR protein - Pse
757	25	58.1	197	2	H75314	adenylate kinase -	830	25	58.1	310	2	A89849	HPr kinase/phospha
758	25	58.1	201	2	AH2587	Recombination prot	831	25	58.1	311	2	S49845	H+-transporting tw
759	25	58.1	201	2	H97369	recombination prot	832	25	58.1	311	2	T11568	probable HPr kinase

833	25	58.1	311	2	B89905	hypothetical prote	906	25	58.1	383	2	T29851	hypothetical prote
834	25	58.1	311	2	H84746	hypothetical prote	907	25	58.1	384	2	D75683	inner membrane pro
835	25	58.1	312	2	T16257	hypothetical prote	908	25	58.1	386	2	D71851	tetracycline resis
836	25	58.1	312	2	T47497	hypothetical prote	909	25	58.1	389	2	T04612	tyrosine transamin
837	25	58.1	312	2	S50430	hypothetical prote	910	25	58.1	395	2	T23402	hypothetical prote
838	25	58.1	313	2	T28312	ORF MSV151 probabl	911	25	58.1	395	2	A69512	conserved hypochet
839	25	58.1	313	2	T35935	transcription regu	912	25	58.1	395	2	H84113	hypothetical prote
840	25	58.1	314	1	PWBYG	H+-transporting tw	913	25	58.1	396	1	S33310	endopeptidase I -
841	25	58.1	314	2	T27383	hypothetical prote	914	25	58.1	396	2	E90562	elongation factor
842	25	58.1	315	1	A28626	Shigella toxin cha	915	25	58.1	396	2	T45399	iron-sulfur cofact
843	25	58.1	315	1	XUBPH9	Shiga-like toxin c	916	25	58.1	397	2	AE1272	acetate kinase hom
844	25	58.1	315	2	S36979	H+-transporting tw	917	25	58.1	397	2	AG1634	acetate kinase hom
845	25	58.1	315	2	JN0725	Shiga-like toxin I	918	25	58.1	399	1	S57699	flavonemoglobin -
846	25	58.1	315	2	P91000	Shiga toxin I subu	919	25	58.1	400	2	T44805	malonyl-CoA transa
847	25	58.1	315	2	H85845	Shiga toxin I subu	920	25	58.1	405	1	WZBBE2	DNA polymerase pro
848	25	58.1	315	2	A53887	Shiga-like toxin I	921	25	58.1	405	2	S42875	dihydrolipoamide S
849	25	58.1	316	1	PWVCG	H+-transporting tw	922	25	58.1	405	2	C83443	beta-ketoacyl-ACP
850	25	58.1	318	2	E87650	hypothetical prote	923	25	58.1	405	2	T33872	hypothetical prote
851	25	58.1	318	2	E95218	iron-compound ABC	924	25	58.1	406	2	I70160	pyruvate dehydrog
852	25	58.1	318	2	C98082	hypothetical prote	925	25	58.1	406	2	T42561	DNA polymerase pro
853	25	58.1	319	2	D87087	hypothetical prote	926	25	58.1	407	1	A55305	pyruvate dehydrog
854	25	58.1	322	2	AF3047	conserved hypochet	927	25	58.1	407	2	I70159	pyruvate dehydrog
855	25	58.1	324	2	T04576	hypothetical prote	928	25	58.1	407	2	A56607	arrestin homolog -
856	25	58.1	325	2	A28214	phosphotriesterase	929	25	58.1	409	2	T30586	glycosyltransferas
857	25	58.1	326	2	T32067	hypothetical prote	930	25	58.1	409	2	T38296	nitrogen permease
858	25	58.1	327	2	AE3340	cblB protein [impo	931	25	58.1	410	2	F87122	probable aminotran
859	25	58.1	327	2	E98238	hypothetical prote	932	25	58.1	411	2	F84135	multidrug-efflux t
860	25	58.1	330	2	I65768	smooth muscle myos	933	25	58.1	412	2	S07537	myosin heavy chain
861	25	58.1	330	2	C89848	peptide chain rele	934	25	58.1	412	2	E90032	imidazolonepropion
862	25	58.1	332	2	F81743	conserved hypochet	935	25	58.1	412	2	S23759	transposase - leuc
863	25	58.1	332	2	B81383	probable lipoprote	936	25	58.1	413	2	T31051	transposase homolo
864	25	58.1	333	2	T25818	hypothetical prote	937	25	58.1	417	2	A44529	succinate-CoA liga
865	25	58.1	334	2	B69361	signal-transducin	938	25	58.1	417	2	S64245	hypothetical prote
866	25	58.1	334	2	F71480	probable flagellar	939	25	58.1	423	2	T72376	hypothetical prote
867	25	58.1	334	2	F82489	response regulator	940	25	58.1	423	2	AC3553	4-aminobutyrate tr
868	25	58.1	334	2	T19127	hypothetical prote	941	25	58.1	424	1	S07792	site-specific DNA-
869	25	58.1	341	2	S23907	translation elonga	942	25	58.1	425	2	T46698	hypothetical prote
870	25	58.1	342	2	AE3391	alcohol dehydrogen	943	25	58.1	428	2	AF1984	hypothetical prote
871	25	58.1	342	2	B86678	protein H06H21.2 [	944	25	58.1	430	2	AE1296	adenylosuccinate 1
872	25	58.1	342	2	AB2416	two-component sens	945	25	58.1	430	2	AC1668	adenylosuccinate 1
873	25	58.1	345	2	T33223	hypothetical prote	946	25	58.1	430	2	B99106	hypothetical prote
874	25	58.1	348	2	C26720	CAMP-regulated D2	947	25	58.1	430	2	A72485	probable Leu/Ile/V
875	25	58.1	354	2	B69035	sensory transducti	948	25	58.1	435	1	EFUC1A	translation elonga
876	25	58.1	355	2	AE3008	monooxygenase [imp	949	25	58.1	435	2	AF2582	heat shock chapero
877	25	58.1	355	2	H98275	mtaG protein (AF18	950	25	58.1	435	2	D97364	halu protein (AE00
878	25	58.1	357	2	AC3663	hypothetical prote	951	25	58.1	435	2	S43507	translation elonga
879	25	58.1	358	2	C86190	hypothetical prote	952	25	58.1	435	2	H90162	hypothetical prote
880	25	58.1	359	2	AC0921	conserved hypochet	953	25	58.1	435	2	F96939	TPR repeats contai
881	25	58.1	363	2	AC3466	maltose/maltodextr	954	25	58.1	436	2	D70693	probable ugps lipo
882	25	58.1	363	2	T33731	hypothetical prote	955	25	58.1	436	2	D86378	protein F21J9.8 [i
883	25	58.1	363	2	T30964	hypothetical prote	956	25	58.1	440	2	D69596	branched-chain ami
884	25	58.1	364	1	PWSPG	H+-transporting tw	957	25	58.1	441	2	AE1015	probable DNA-damag
885	25	58.1	365	2	A43720	parathion hydrolas	958	25	58.1	442	2	S57710	unusual floral org
886	25	58.1	367	2	T23290	hypothetical prote	959	25	58.1	443	2	D97610	cell division prot
887	25	58.1	369	2	S13721	Wnt-1 protein prec	960	25	58.1	443	2	AE2832	cell division prot
888	25	58.1	369	2	G17510	probable translati	961	25	58.1	445	2	F82166	mukf protein Vc171
889	25	58.1	369	2	T08266	conserved hypochet	962	25	58.1	446	2	D86046	escN [imported] -
890	25	58.1	370	2	G87621	3-dehydroquinat s	963	25	58.1	446	2	H91199	type III secretion
891	25	58.1	370	2	SI5013	wnt-1 protein - ze	964	25	58.1	449	2	S67819	GumC protein - Xan
892	25	58.1	371	2	H71634	hypothetical prote	965	25	58.1	450	2	C75033	adenylosuccinate 1
893	25	58.1	372	2	G97844	hypothetical prote	966	25	58.1	451	2	S43425	tubulin alpha chai
894	25	58.1	373	2	AC3338	hypothetical prote	967	25	58.1	453	2	T44661	nosD protein [impo
895	25	58.1	374	2	A31382	DNA-binding protei	968	25	58.1	456	2	E70829	probable membrane
896	25	58.1	375	2	T25089	hypothetical prote	969	25	58.1	456	2	T49159	hypothetical prote
897	25	58.1	376	1	G69336	conserved hypochet	970	25	58.1	456	2	T23123	hypothetical prote
898	25	58.1	376	2	T05420	cyclin delta-3 - A	971	25	58.1	457	2	A27449	T-cell surface gly
899	25	58.1	377	2	T10708	adenosylmethionine	972	25	58.1	457	2	G64530	hypothetical prote
900	25	58.1	379	2	JQ2272	formate dehydrogen	973	25	58.1	457	2	C71976	hypothetical prote
901	25	58.1	379	2	G81712	1-deoxy-D-xylose	974	25	58.1	460	2	T21678	hypothetical prote
902	25	58.1	379	2	A34780	vermillion protein	975	25	58.1	461	2	T11819	glycerol-3-phospha
903	25	58.1	379	2	S44745	C02D5.3 protein -	976	25	58.1	462	2	E82176	sensor histidine k
904	25	58.1	382	2	S01339	exo-alpha-galidas	977	25	58.1	466	2	S22258	copper resistance
905	25	58.1	383	2	G84597	probable XAP-5 pro	978	25	58.1	466	2	T08914	hypothetical prote

979 25 58.1 468 2 S55695 suppressor of fuse  
 980 25 58.1 472 2 A83331 probable two-compo  
 981 25 58.1 473 2 G75033 hypothetical prote  
 982 25 58.1 474 2 T27006 hypothetical prote  
 983 25 58.1 474 2 A64691 type III restricti  
 984 25 58.1 478 2 JQ1301 hemorhagic protei  
 985 25 58.1 479 1 TVCHE2 transcription fact  
 986 25 58.1 484 2 B33501 myosin heavy chain  
 987 25 58.1 484 2 S62185 calcium channel b  
 988 25 58.1 487 2 A46146 steroid receptor h  
 989 25 58.1 489 2 T23124 hypothetical prote  
 990 25 58.1 490 2 AC2458 hypothetical prote  
 991 25 58.1 491 2 S74613 hypothetical prote  
 992 25 58.1 491 2 T46915 hypothetical prote  
 993 25 58.1 492 2 T38211 hypothetical prote  
 994 25 58.1 499 2 S48907 probable purine nu  
 995 25 58.1 500 2 B31047 testosterone 16alp  
 996 25 58.1 501 2 AH1852 hypothetical prote  
 997 25 58.1 506 2 T19787 hypothetical prote  
 998 25 58.1 513 2 S75997 asparagine-tRNA li  
 999 25 58.1 515 2 E86811 glucan 1,6-alpha-g  
 1000 25 58.1 515 2 T37982 hypothetical prote

## ALIGNMENTS

RESULT 1  
 G86324  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C:Accession: G86324  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 ansen, N.P.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maifi, R.; Marziali,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: G86324  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-311 <STO>  
 A:Cross-references: UNIPROT:Q9LMB2; UNIPARC:UPI00000A6002; GB:AE005172; NID:g8954052; PI  
 C:Genetics:  
 A:Map position: 1

Query Match 83.7%; Score 36; DB 2; Length 311;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LQLMDRV 9  
 Db 146 LQLMDRI 153  
 |||||:  
 |||||:

RESULT 2  
 S57329  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S57329; S52834  
 R:Kobayashi, T.; Nishizawa, M.; Hirayama, Y.; Kobayashi, E.; Hino, O.  
 Nucleic Acids Res. 23, 2608-2613, 1995  
 A:Title: cDNA structure, alternative splicing and exon-intron organization of the predi  
 A:Reference number: S57329; MUID:95380273; PMID:7651821  
 A:Accession: S57329

A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1809 <KOB>  
 A:Cross-references: UNIPROT:P49816; UNIPARC:UPI0000168290; EMBL:D50413; NID:g1181080; PI  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995  
 R:Xiao, G.  
 Cell Growth Differ. 6, 1185-1191, 1995

A:Title: Identification of tuberos scleriosis 2 messenger RNA splice variants that are  
 A:Reference number: I52834; MUID:96063895; PMID:8519695  
 A:Accession: I52834  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA

A:Residues: 1-931 'K', 933-1513 'C', 1515-1729 'R', 1731-1809 <RES>  
 A:Cross-references: UNIPARC:UPI0000137741; EMBL:U24150; NID:g1061324; PIDN:AAC52289.1; P  
 Query Match 81.4%; Score 35; DB 2; Length 1809;  
 Best Local Similarity 87.5%; Pred. No. 56;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
 Db 444 NLQLLMDR 451  
 |||||:  
 |||||:

RESULT 3  
 T13854  
 C:Species: Drosophila melanogaster  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: T13854  
 R:Valdeolmillos, A.M.; Vallares, R.; Buesa, J.M.; Gonzalez-Crespo, S.; Martinez, A.; Bar  
 DNA Cell Biol. 8, 699-706, 1998  
 A:Title: Molecular cloning and expression of stromalin protein from Drosophila melanogaster  
 A:Reference number: Z17798  
 A:Accession: T13854  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1116 <VAL>  
 A:Cross-references: UNIPROT:O18415; UNIPARC:UPI0000082E2E; EMBL:Y14277; NID:e1202704; PI  
 C:Genetics:  
 A:Cross-references: FlyBase:FBgn0020616

Query Match 79.1%; Score 34; DB 2; Length 1116;  
 Best Local Similarity 66.7%; Pred. No. 54;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
 Db 630 NLQALLDRI 638  
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 |||||:

RESULT 4  
 E98065  
 C:Species: Streptococcus pneumoniae  
 C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
 C:Accession: E98065  
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Bargett, S.; DeHoff, B.S.; E  
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
 y, P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 183, 5709-5717, 2001  
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
 A:Reference number: A97872; MUID:21429245; PMID:11544234  
 A:Accession: E98065  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-283 <KUT>  
 A:Cross-references: UNIPROT:Q8DNT6; UNIPARC:UPI00000E368C; GB:AE007317; PIDN:AAL00354.1;  
 C:Genetics:  
 A:Gene: spr1550

Query Match 74.4%; Score 32; DB 2; Length 283;  
 Best Local Similarity 66.7%; Pred. No. 32;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
 |||||:  
 Db 172 NLPLLDRI 180

RESULT 5  
 F69306  
 hypothetical protein AF0454 - Archaeoglobus fulgidus  
 C:Species: Archaeoglobus fulgidus  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C:Accession: F69306  
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 ; Fleisheimann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 384-370, 1997  
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
 A:Reference number: A69250; MUID:98049343; PMID:9389475  
 A:Accession: F69306  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-305 <KLE>  
 A:Cross-references: UNIPROT:O29795; UNIPARC:UPI00000570D9; GB:AE001073; GB:AE000782; NID

Query Match 74.4%; Score 32; DB 2; Length 305;  
 Best Local Similarity 66.7%; Pred. No. 35;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
 |||||:  
 Db 222 NLALLVDRI 230

RESULT 6  
 S73730  
 MG307 homolog H08\_orf5720 - Mycoplasma pneumoniae (strain ATCC 29342)  
 C:Species: Mycoplasma pneumoniae  
 A:Variety: ATCC 29342  
 C:Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C:Accession: S73730  
 R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.  
 Nucleic Acids Res. 24, 4420-4449, 1996  
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
 A:Reference number: S73327; MUID:97105885; PMID:8948633  
 A:Accession: S73730  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-572 <HIM>  
 A:Cross-references: UNIPROT:P75341; UNIPARC:UPI000013AACE; EMBL:AE000039; GB:U00089; NID  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
 C:Genetics:  
 A:Genetic code: SGC3

Query Match 74.4%; Score 32; DB 2; Length 572;  
 Best Local Similarity 66.7%; Pred. No. 70;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
 |||||:  
 Db 428 NNQLLDRI 436

RESULT 7  
 S73731  
 probable lipoprotein A05\_orf1244 - Mycoplasma pneumoniae (strain ATCC 29342)  
 N:Alternate names: MG307 homolog A05\_orf1244  
 C:Species: Mycoplasma pneumoniae  
 A:Variety: ATCC 29342

C:Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C:Accession: S73731  
 R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.  
 Nucleic Acids Res. 24, 4420-4449, 1996  
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
 A:Reference number: S73327; MUID:97105885; PMID:8948633  
 A:Accession: S73731  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1244 <HIM>  
 A:Cross-references: UNIPROT:P75342; UNIPARC:UPI00001395E1; EMBL:AE000039; GB:U00089; NID  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
 C:Genetics:  
 A:Genetic code: SGC3  
 C:Superfamily: Mycoplasma hypothetical protein MG309

Query Match 74.4%; Score 32; DB 2; Length 1244;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
 |||||:  
 Db 1082 NNQLLDRI 1090

RESULT 8  
 B72697  
 hypothetical protein APE0994 - Aeropyrum pernix (strain K1)  
 C:Species: Aeropyrum pernix  
 C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
 C:Accession: B72697  
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka  
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;  
 DNA Res. 6, 83-101, 1999  
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy  
 A:Reference number: A72450; MUID:99310339; PMID:10382966  
 A:Accession: B72697  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-258 <KAW>  
 A:Cross-references: UNIPROT:Q9YDB9; UNIPARC:UPI000005DD87; DDBJ:AP0000060; NID:G5104188;  
 A:Experimental source: strain K1  
 C:Genetics:  
 A:Gene: APE0994

Query Match 72.1%; Score 31; DB 2; Length 258;  
 Best Local Similarity 75.0%; Pred. No. 48;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9  
 |||||:  
 Db 224 LRLLMDRV 231

RESULT 9  
 D69791  
 conserved hypothetical protein yead - Bacillus subtilis  
 C:Species: Bacillus subtilis  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C:Accession: D69791  
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F  
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
 Y.; M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero  
 keuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: D63791  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-270 <KUN>  
A;Cross-references: UNIPROT:P94475; UNIPARC:UPI0000060013; GB:Z99107; GB:AL009126; NID:9  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: Yeal

Query Match 72.1%; Score 31; DB 2; Length 270;  
Best Local Similarity 87.5%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDR 8  
Db 115 NLFLLMDR 122  
||| ||| |||

RESULT 10  
AE2416  
hypothetical protein all4885 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AE2416  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AE2416  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-291 <KUR>  
A;Cross-references: UNIPROT:Q8YMP8; UNIPARC:UPI00000CECA6; GB:BA000019; PIDN:BA076584.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all4885

Query Match 72.1%; Score 31; DB 2; Length 291;  
Best Local Similarity 75.0%; Pred. No. 55;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDR 8  
Db 170 NLQKIMDR 177  
||| ||| |||

RESULT 11  
S74826  
NADH2 dehydrogenase (EC 1.6.99.3) - *Synechocystis* sp. (strain PCC 6803)  
N;Alternate names: protein slr0851  
C;Species: *Synechocystis* sp.  
A;Variety: PCC 6803  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S74826  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
s.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S74826  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-445 <KAN>  
A;Cross-references: UNIPROT:P73739; UNIPARC:UPI00000D340F; EMBL:D90909; GB:AB001339; NID  
A;Note: the nucleotide sequence was submitted to the EMBL data Library, June 1996  
C;Genetics:  
A;Gene: ndh

C;Superfamily: NADH dehydrogenase  
C;Keywords: electron transfer; FAD; flavoprotein; NAD; oxidoreductase

Query Match 72.1%; Score 31; DB 1; Length 445;  
Best Local Similarity 55.6%; Pred. No. 88;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDR 9  
Db 76 NRVLMMDR 84  
||:|||||

RESULT 12  
C84420  
hypothetical protein At2g01070 [imported] - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: C84420  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: AB4420; MUID:20083487; PMID:10617197  
A;Accession: C84420  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-467 <STO>  
A;Cross-references: UNIPROT:Q9SVJ9; UNIPARC:UPI00000A92A8; GB:AE002093; NID:G6598622; P  
C;Genetics:  
A;Gene: At2g01070  
A;Map position: 2

Query Match 72.1%; Score 31; DB 2; Length 467;  
Best Local Similarity 62.5%; Pred. No. 93;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDR 8  
Db 411 NMKLMMDR 418  
||:|||||

RESULT 13  
E84811  
hypothetical protein At2g38960 [imported] - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 05-Oct-2004  
C;Accession: E84811  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: AB4420; MUID:20083487; PMID:10617197  
A;Accession: E84811  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-519 <STO>  
A;Cross-references: UNIPROT:Q9ZV11; UNIPARC:UPI00000A4229; GB:AE002093; NID:G3928083; P  
C;Genetics:  
A;Gene: At2g38960  
A;Map position: 2  
C;Superfamily: Endoplasmic oxidoreductin 1 precursor

Query Match 72.1%; Score 31; DB 2; Length 519;  
Best Local Similarity 77.8%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDR 9  
Db 267 NUTLLMDR 275  
||| ||| |||



RESULT 14  
A00192  
conserved hypothetical protein [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: A90192  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: A90192  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-582 <KUR>  
A;Cross-references: UNIPROT:Q97ZV6; UNIPARC:UPI0000064271; GB:AE006641; NID:gl3813624; F  
C;Genetics:  
A;Gene: SS00469

Query Match 72.1%; Score 31; DB 2; Length 582;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|||:|:|:  
Db 571 NLDLLKDR I 579

RESULT 15  
JN0657  
methyltransferase (EC 2.1.1.-) - Salmonella typhimurium  
C;Species: Salmonella typhimurium  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 05-Oct-2004  
C;Accession: JN0657  
R;Bartois, V.; De Backer, O.; Colson, C.  
Gene 127, 105-110, 1993  
A;Title: Sequence of the Salmonella typhimurium StyLT1 restriction-modification genes: H  
A;Reference number: JN0657; MUID:93252265; PMID:8387444  
A;Accession: JN0657  
A;Molecule type: DNA  
A;Residues: 1-651 <DNR>  
A;Cross-references: UNIPROT:P40814; UNIPARC:UPI0000179684; GB:M90544  
C;Comment: This enzyme belongs to the type-III restriction-modification system and is ne  
C;Genetics:  
A;Gene: mod  
C;Superfamily: type III restriction-modification system methyltransferase  
C;Keywords: DNA binding; methyltransferase; restriction modification system  
F;134-137/Region: S-adenosylmethionine binding #status predicted

Query Match 72.1%; Score 31; DB 2; Length 651;  
Best Local Similarity 55.6%; Pred. No. 1.3e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|||:|:|:  
Db 215 NLKLMWDE I 223

RESULT 16  
AD0546  
site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) - Salmonella enteri  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 05-Oct-2004  
C;Accession: AD0546  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AD0546  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-652 <PAR>  
A;Cross-references: UNIPARC:UPI000005A271; GB:AL513382; PIDN:CAD08812.1; PID:gl6501627;  
C;Genetics:  
A;Gene: mod  
C;Superfamily: type III restriction-modification system methyltransferase  
C;Keywords: methyltransferase; S-adenosylmethionine

Query Match 72.1%; Score 31; DB 2; Length 652;  
Best Local Similarity 55.6%; Pred. No. 1.3e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|||:|:|:  
Db 216 NLKLMWDE I 224

RESULT 17  
A72076  
hypothetical protein CP0290 [imported] - Chlamydophila pneumoniae (strains CWL029 and A  
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: A72076; AB1594  
R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.  
Nature Genet. 21, 385-389, 1999  
A;Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.  
A;Reference number: A72000; MUID:99206606; PMID:10192388  
A;Accession: A72076  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-672 <ARN>  
A;Cross-references: UNIPROT:Q9Z887; UNIPARC:UPI00000C2212; GB:AE001630; GB:AE001363; NI  
A;Experimental source: strain CWL029  
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg  
Nucleic Acids Res. 28, 1397-1406, 2000  
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A;Reference number: AB1500; MUID:20150255; PMID:10684935  
A;Accession: AB1594  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-672 <REA>  
A;Cross-references: UNIPARC:UPI00000C2212; GB:AE002190; GB:AE002161; NID:g7189209; PIDN  
A;Experimental source: strain AR39, HL cells  
C;Genetics:  
A;Gene: CP0290  
C;Superfamily: Chlamydia hypothetical protein CPn0462

Query Match 72.1%; Score 31; DB 2; Length 672;  
Best Local Similarity 56.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|||:|:|:  
Db 507 NLQLASDR I 515

RESULT 18  
B86548  
hypothetical protein CPJ0462 [imported] - Chlamydophila pneumoniae (strain J138)  
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: B86548  
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I  
Nucleic Acids Res. 28, 2311-2314, 2000  
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A;Reference number: AB6491; MUID:20330349; PMID:10871362  
A;Accession: B86548  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-672 <STO>

A;Cross-references: UNIPROT:Q9Z887; UNIPARC:UPI00000C2212; GB:BA000008; NID:g9878832; PID:1708 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
A;Experimental source: strain J138  
C:Genetics:  
A;Gene: CFJ0462  
C:Superfamily: Chlamydia hypothetical protein CPn0462

Query Match 72.1%; Score 31; DB 2; Length 672;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NQLQMDRV 9  
Db 507 NQLASDRI 515  
|||:|:|:  
|:|:|:|:

RESULT 19  
JQ0647  
preprotein translocase secA - Bacillus subtilis  
N:Alternate names: Div protein; secA protein homolog  
C:Species: Bacillus subtilis  
C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 05-Oct-2004  
C:Accession: JQ0647; S17771; F69704  
R:Sadaie, Y.; Takamatsu, H.; Nakamura, K.; Yamane, K.  
Gene 98, 101-105, 1991  
A:Title: Sequencing reveals similarity of the wild-type divA gene of Bacillus subtilis to  
A:Reference number: JN0145; MUID:91192600; PMID:1901557  
A:Accession: JQ0647  
A:Molecule type: DNA  
A:Residues: 1-841 <SAD>  
A:Cross-references: UNIPROT:P28366; UNIPARC:UPI0000060B13; GB:D10279; DDBJ:D90218; NID:g9878832  
R:Overhoff, B.; Klein, M.; Spies, M.; Freudl, R.  
Mol. Gen. Genet. 228, 417-423, 1991  
A:Title: Identification of a gene fragment which codes for the 364 amino-terminal amino  
export apparatus in gram-positive and gram-negative bacteria.  
A:Reference number: S17771; MUID:91375427; PMID:1832735  
A:Accession: S17771  
A:Molecule type: DNA  
A:Residues: 1-125, '1', 127-364 <OVE>  
A:Cross-references: UNIPARC:UPI000016E95A; EMBL:X62035; NID:g48979; PIDN:CAA43977.1; PID:1708  
R:Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni  
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningshtein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tostato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: F69704  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-841 <KUN>  
A:Cross-references: UNIPARC:UPI0000060B13; GB:Z99122; GB:AL009126; NID:g2636029; PIDN:CA  
A:Experimental source: strain 168  
C:Comment: This pleiotropic protein is required for cell division, sporulation, septatio  
C:Comment: The "nucleotide-binding motif B" and "DEAD motif" features as annotated are c  
is adjacent to the identified motif and a third conserved motif is approximately 120-140  
C:Genetics:  
A:Gene: secA; div  
C:Superfamily: preprotein translocase, subunit SecA  
C:Keywords: ATP; membrane-associated complex; P-loop; protein transport; sporulation  
F:100-107/Region: nucleotide-binding motif A (P-loop) #status atypical  
F:203-208/Region: nucleotide-binding motif B  
F:207-210/Region: DEXH motif

Query Match 72.1%; Score 31; DB 2; Length 841;  
Best Local Similarity 62.5%; Pred. No. 1.8e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IQLLMDRV 9  
Db 685 LELIMDRI 692  
|:|:|:|:  
|:|:|:|:

RESULT 20  
E97473  
1708 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: E97473  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: E97473  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-861 <KUR>  
A:Cross-references: UNIPROT:Q8UGU8; UNIPARC:UPI00000D19A9; GB:AE007869; PIDN:AAK86742.1,  
C:Genetics:  
A:Gene: AGR\_C1708  
A:Map position: circular chromosome  
C:Superfamily: probable cation-transporting ATPase APE1454; ATPase nucleotide-binding do

Query Match 72.1%; Score 31; DB 2; Length 861;  
Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IQLLMDRV 9  
Db 443 IQLLVDRV 450  
|:|:|:|:  
|:|:|:|:

RESULT 21  
AI2691  
copper transporting ATPase Atu0937 [imported] - Agrobacterium tumefaciens (strain C58, I  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AI2691  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Y.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AI2691  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-861 <KUR>  
A:Cross-references: UNIPROT:Q8UGU8; UNIPARC:UPI00000D19A9; GB:AE008688; PIDN:AAL41951.1,  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu0937  
A:Map position: circular chromosome  
C:Superfamily: probable cation-transporting ATPase APE1454; ATPase nucleotide-binding do

Query Match 72.1%; Score 31; DB 2; Length 861;  
Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IQLLMDRV 9  
Db 443 IQLLVDRV 450  
|:|:|:|:  
|:|:|:|:

```
RESULT 22
A33602
DNA-directed DNA polymerase (EC 2.7.7.7) REV3 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein P2535; protein YPL167c
C;Species: Saccharomyces cerevisiae
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A33602; S65178; S69432
R;Morrison, A.; Christensen, R.B.; Alley, J.; Beck, A.K.; Bernstein, E.G.; Lemontt, J.F.
J. Bacteriol. 171, 5659-5667, 1989
A;Title: REV3, a Saccharomyces cerevisiae gene whose function is required for induced mu
A;Reference number: A33602; MUID:90008808; PMID:2676986
A;Accession: A33602
A;Molecule type: DNA
A;Residues: 1-1504 <MOR>
A;Cross-references: UNIPROT:P14284; UNIPARC:UPI0000129839; GB:M29683; NID:g172386; PIDN:
A;Experimental source: strain S288C
R;Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65154
A;Accession: S65178
A;Molecule type: DNA
A;Residues: 1-1504 <PUP>
A;Cross-references: UNIPARC:UPI0000129839; EMBL:Z73523; NID:g1370352; PIDN:CAA97873.1; P
R;Purnelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies
ogue to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant
A;Reference number: S69428
A;Accession: S69432
A;Molecule type: DNA
A;Residues: 1-1504 <PUW>
A;Cross-references: UNIPARC:UPI0000129839; EMBL:X96770; NID:g1403537; PIDN:CAA65554.1; P
C;Genetics:
A;Gene: SGD:REV3; PS01
A;Cross-references: SGD:S0006088; MIPS:YPL167c
A;Map position: 16L
C;Superfamily: yeast DNA-directed DNA polymerase REV3
C;Keywords: DNA binding; nucleotidyltransferase
Query Match 72.1%; Score 31; DB 2; Length 1504;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLQLLMDR 8
:||||:|
Db 237 DLQLLDR 244
:||||:|
RESULT 23
T09329
XILP1 protein - human herpesvirus 6 (strain U1102)
C;Species: human herpesvirus 6
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09329
R;Nicholas, J.; Martin, M.
J. Virol. 68, 597-610, 1994
A;Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hu
A;Reference number: Z16644; MUID:94118404; PMID:8289364
A;Accession: T09329
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-129 <NIC>
A;Cross-references: UNIPROT:Q65058; UNIPARC:UPI000000EFACC; EMBL:L25528; NID:g451932; PID
C;Genetics:
A;Gene: XILP1
Query Match 69.8%; Score 30; DB 2; Length 129;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NLQLLMDR 9
:||||:|
```

```
Db 33 NLELLYERV 41
RESULT 24
F91130
hypothetical protein ECs4014 [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91130
R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91130
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <HAY>
A;Cross-references: UNIPROT:Q8XAC4; UNIPROT:Q8FDA9; UNIPARC:UPI000000D070D; GB:BA0000007;
A;Experimental source: strain O157:H7, substrain RMD 050952
C;Genetics:
A;Gene: ECs4014
Query Match 69.8%; Score 30; DB 2; Length 144;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NLQLLMDRV 9
:||||:|
Db 93 NLQLLEMV 101
:||||:|
RESULT 25
F85975
hypothetical protein Z4488 [imported] - Escherichia coli (strain O157:H7, substrain BD
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F85975
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F85975
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <STO>
A;Cross-references: UNIPROT:Q8XAC4; UNIPROT:Q8FDA9; UNIPARC:UPI000000D070D; GB:AE005174;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4488
Query Match 69.8%; Score 30; DB 2; Length 144;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NLQLLMDRV 9
:||||:|
Db 93 NLQLLEMV 101
:||||:|
RESULT 26
T44404
adenylate kinase (EC 2.7.4.3) [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44404; C83669
R;Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.
Biosci. Biotechnol. Biochem. 63, 452-455, 1999
A;Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene
A;Reference number: Z23756; MUID:99209008; PMID:10192928
A;Accession: T44404
A;Status: preliminary; translated from GB/EMBL/DBJ
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A:Molecule type: DNA  
A:Residues: 1-217 <TAK>  
A:Cross-references: UNIPROT:P38372; UNIPARC:UPI000012DBB0; EMBL:AB017508; NID:94512395;  
A:Experimental source: strain C-125  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: AB83650; MUID:20512582; PMID:11058132  
A:Accession: C83669  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-217 <STO>  
A:Cross-references: UNIPARC:UPI000012DBB0; GB:AP001507; GB:BA000004; NID:g10172612; PIDN  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: adk  
C:Superfamily: adenylate kinase  
C:Keywords: phosphotransferase

Query Match 69.8%; Score 30; DB 2; Length 217;  
Best Local Similarity 85.7%; Pred. No. 66;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLLMDRV 9  
|:|||||  
Db 118 QLLMDRL 124  
|:|||||

RESULT 27  
AB1147  
carboxylesterase homolog lmo0580 [imported] - Listeria monocytogenes (strain EGD-e)  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
A:Accession: AE1147  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1147  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-218 <GLA>  
A:Cross-references: UNIPROT:Q8Y9E9; UNIPARC:UPI0000551E5; GB:NC\_003210; PIDN:CAC98659.1  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0580

Query Match 69.8%; Score 30; DB 2; Length 218;  
Best Local Similarity 85.7%; Pred. No. 66;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LOLLMDR 8  
|:|||||  
Db 38 LELLMDR 44  
|:|||||

RESULT 28  
AE1506  
weakly carboxylesterase homolog lin0589 [imported] - Listeria innocua (strain Clp11262)  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
A:Accession: AE1506  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1506  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-219 <GLA>  
A:Cross-references: UNIPROT:Q92E71; UNIPARC:UPI00000CC2A6; GB:AL592022; PIDN:CAC95821.1  
A:Experimental source: strain Clp11262  
C:Genetics:  
A:Gene: lin0589

Query Match 69.8%; Score 30; DB 2; Length 219;  
Best Local Similarity 85.7%; Pred. No. 66;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LOLLMDR 8  
|:|||||  
Db 38 LELLMDR 44  
|:|||||

RESULT 29  
A75304  
ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain RL)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
A:Accession: A75304  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RL.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: A75304  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-227 <WHI>  
A:Cross-references: UNIPROT:Q9RS3; UNIPARC:UPI00000D3F58; GB:AE002052; GB:AE000513; NII  
A:Experimental source: strain RL  
C:Genetics:  
A:Gene: DR2192  
A:Map position: 1  
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 69.8%; Score 30; DB 2; Length 227;  
Best Local Similarity 85.7%; Pred. No. 69;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLLMDRV 9  
|:|||||  
Db 125 QLLMDRV 131  
|:|||||

RESULT 30  
TI9750  
hypothetical protein C35C5.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
A:Accession: TI9750  
R:White, S.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z19173  
A:Accession: TI9750  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-244 <WIL>  
A:Cross-references: UNIPARC:UPI000017B80F; EMBL:Z78417; PIDN:CAB01687.1; GSPDB:GN00028;  
A:Experimental source: clone C35C5  
C:Genetics:  
A:Gene: CESP:C35C5.7  
A:Map position: X  
A:introns: 51/1; 67/2; 103/3; 150/2; 201/3

Query Match 69.8%; Score 30; DB 2; Length 244;  
Best Local Similarity 62.5%; Pred. No. 74;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLLMDR 8  
||:|:|

Db 166 NLRILLDR 173

RESULT 31  
E86339  
protein F2D10.16 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E86339  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: E86339  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-252 <STO>  
A:Cross-references: UNIPROT:Q9LM87; UNIPARC:UPI00000A443C; GB:AE005172; NID:g8886927; P1  
C:Genetics:  
A:Gene: F2D10.16  
A:Map position: 1

Query Match 69.8%; Score 30; DB 2; Length 252;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NQLLMDRV 9  
|:|:|

Db 56 NTSLLLDV 64

RESULT 32  
E87726  
DNA-directed DNA polymerase (EC 2.7.7.7) - Rickettsia conorii (strain Malish 7)  
C:Species: Rickettsia conorii  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: E87726  
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R Science 293, 2093-2098, 2001  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:11557893  
A:Accession: E87726  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-269 <KUR>  
A:Cross-references: UNIPROT:Q92J56; UNIPARC:UPI00000CBCEB; GB:AE006914; PIDN:AAL02751.1;  
C:Genetics:  
A:Gene: hdb  
C:Keywords: nucleotidyltransferase

Query Match 69.8%; Score 30; DB 2; Length 269;  
Best Local Similarity 66.7%; Pred. No. 83;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NQLLMDRV 9  
||:|:|

Db 196 NLLLMNRI 204

RESULT 33  
T15820  
hypothetical protein C52B11.2 - Caenorhabditis elegans

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLLMDR 8  
||:|:|

Db 166 NLRILLDR 173

RESULT 31  
E86339  
protein F2D10.16 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E86339  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: E86339  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-252 <STO>  
A:Cross-references: UNIPROT:Q9LM87; UNIPARC:UPI00000A443C; GB:AE005172; NID:g8886927; P1  
C:Genetics:  
A:Gene: F2D10.16  
A:Map position: 1

Query Match 69.8%; Score 30; DB 2; Length 252;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NQLLMDRV 9  
|:|:|

Db 56 NTSLLLDV 64

RESULT 32  
E87726  
DNA-directed DNA polymerase (EC 2.7.7.7) - Rickettsia conorii (strain Malish 7)  
C:Species: Rickettsia conorii  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: E87726  
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R Science 293, 2093-2098, 2001  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:11557893  
A:Accession: E87726  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-269 <KUR>  
A:Cross-references: UNIPROT:Q92J56; UNIPARC:UPI00000CBCEB; GB:AE006914; PIDN:AAL02751.1;  
C:Genetics:  
A:Gene: hdb  
C:Keywords: nucleotidyltransferase

Query Match 69.8%; Score 30; DB 2; Length 269;  
Best Local Similarity 66.7%; Pred. No. 83;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NQLLMDRV 9  
||:|:|

Db 196 NLLLMNRI 204

RESULT 33  
T15820  
hypothetical protein C52B11.2 - Caenorhabditis elegans

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLLMDR 8  
||:|:|

Db 166 NLRILLDR 173

RESULT 31  
E86339  
protein F2D10.16 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E86339  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: E86339  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-252 <STO>  
A:Cross-references: UNIPROT:Q9LM87; UNIPARC:UPI00000A443C; GB:AE005172; NID:g8886927; P1  
C:Genetics:  
A:Gene: F2D10.16  
A:Map position: 1

Query Match 69.8%; Score 30; DB 2; Length 252;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NQLLMDRV 9  
|:|:|

Db 56 NTSLLLDV 64

RESULT 32  
E87726  
DNA-directed DNA polymerase (EC 2.7.7.7) - Rickettsia conorii (strain Malish 7)  
C:Species: Rickettsia conorii  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: E87726  
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R Science 293, 2093-2098, 2001  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:11557893  
A:Accession: E87726  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-269 <KUR>  
A:Cross-references: UNIPROT:Q92J56; UNIPARC:UPI00000CBCEB; GB:AE006914; PIDN:AAL02751.1;  
C:Genetics:  
A:Gene: hdb  
C:Keywords: nucleotidyltransferase

Query Match 69.8%; Score 30; DB 2; Length 269;  
Best Local Similarity 66.7%; Pred. No. 83;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NQLLMDRV 9  
||:|:|

Db 196 NLLLMNRI 204

RESULT 33  
T15820  
hypothetical protein C52B11.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T15820  
R:Martin, J.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid C52B11.  
A:Reference number: Z18411  
A:Accession: T15820  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-272 <MAR>  
A:Cross-references: UNIPROT:Q18776; UNIPARC:UPI000007A41E; EMBL:U41276; NID:gl086884; P2  
A:Experimental source: strain Bristol N2  
C:Genetics:  
A:Gene: CESP:C52B11.2  
A:Introns: 12/1; 91/3; 190/3; 221/3

Query Match 69.8%; Score 30; DB 2; Length 272;  
Best Local Similarity 71.4%; Pred. No. 84;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLLMDRV 9  
||:|:|

Db 174 QLIMDRI 180

RESULT 34  
B64077  
bis(5'-nucleosyl)-tetraphosphatase (symmetrical) (EC 3.6.1.41) - Haemophilus influenzae  
N:Alternate names: diadenosine tetraphosphatase (symmetrical)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: B64077  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: B64077  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-275 <TIGR>  
A:Cross-references: UNIPROT:P44751; UNIPARC:UPI0000125BPA; GB:U32737; GB:L42023; NID:gl  
A:Experimental source: strain Rd KW20  
C:Genetics:  
A:Note: TIGR:HI0551  
C:Function:  
A:Pathway: purine metabolism  
C:Superfamily: bis(5'-nucleosyl)-tetraphosphatase (symmetrical); phosphoesterase core h  
C:Keywords: hydrolase  
P:2-67/Domain: phosphoesterase core homology <PEC>

Query Match 69.8%; Score 30; DB 1; Length 275;  
Best Local Similarity 75.0%; Pred. No. 85;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMDRV 9  
||:|:|

Db 16 LQLLDV 23

RESULT 35  
E89113  
hypothetical protein MTH1843 - Methanobacterium thermoautotrophicum (strain Delta H)  
C:Species: Methanobacterium thermoautotrophicum  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: E89113  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwnani, N. K.; Church, G.M.; Daniele, C.J.; Mao, J.; Rice, P.; Nossling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: funcn  
A;Reference number: A69000; MUID:98037514; PMID:9371463  
A;Accession: E69113  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-284 <MTH>  
A;Cross-references: UNIPROT:O27871; UNIPARC:UPI0000062C0E; GB:AE0000937; GB:AE000666; NID  
C;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH1843

Query Match 69.8%; Score 30; DB 2; Length 284;  
Best Local Similarity 85.7%; Pred. No. 88;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLQLLMD 7  
|||:||||  
Db 57 NLRLIMD 63

RESULT 36  
T01637  
gene R protein - *Acinetobacter calcoaceticus* (fragment)  
C;Species: *Acinetobacter calcoaceticus*  
C;Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 22-Jun-1999  
C;Accession: T01637; G32252  
R;Goosen, N.; Horeman, H.P.A.; Huinen, R.G.M.; van de Putte, P.  
J. Bacteriol. 171, 447-455, 1989  
A;Title: *Acinetobacter calcoaceticus* genes involved in biosynthesis of the coenzyme pyrro  
A;Reference number: A32252; MUID:89123056; PMID:2536663  
A;Accession: T01637  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-316 <GOO>  
A;Cross-references: UNIPARC:UPI000016E135; EMBL:X06452; NID:G38740; PIDN:CAA29758.1; PID  
A;Experimental source: strain LMD 79.41  
C;Superfamily: membrane dipeptidase

Query Match 69.8%; Score 30; DB 2; Length 316;  
Best Local Similarity 66.7%; Pred. No. 99;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9  
:|:|||||  
Db 281 HLEYLMDRV 289

RESULT 37  
T23840  
hypothetical protein M88.4 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T23840  
R;Sulston, J.  
submitted to the EMBL Data Library, June 1994  
A;Reference number: Z19806  
A;Accession: T23840  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-333 <WIL>  
A;Cross-references: UNIPROT:O21602; UNIPARC:UPI0000179CCD; EMBL:Z34802; PIDN:CAA84335.2;  
A;Experimental source: clone M88  
C;Genetics:  
A;Gene: CESP:M88.4  
A;Map position: 3  
A;Introns: 31/3; 55/3; 93/2; 140/3; 168/2; 224/3; 279/2

Query Match 69.8%; Score 30; DB 2; Length 333;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLQLLMDR 8  
|||||:  
Db 154 NLQLLSR 161

RESULT 40  
H90168  
GTP-binding protein (hflX) [imported] - *Sulfolobus solfataricus*  
C;Species: *Sulfolobus solfataricus*  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: H90168  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

Db 138 NLQLLSR 145

## RESULT 38

E71801  
probable o-sialoglycoprotein endopeptidase - *Helicobacter pylori* (strain J99)  
C;Species: *Helicobacter pylori*  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: E71801  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: E71801

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-340 &lt;ARN&gt;

A;Cross-references: UNIPROT:Q9ZJ27; UNIPARC:UPI000012B2F3; GB:AE001570; GB:AE001439; NID

A;Experimental source: strain J99

C;Genetics:

A;Gene: ydix

C;Superfamily: O-sialoglycoprotein endopeptidase

Query Match 69.8%; Score 30; DB 2; Length 340;

Best Local Similarity 66.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9

|||:||||

Db 54 NLPLLSRV 62

## RESULT 39

D88431

protein M88.4 [imported] - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C;Accession: D88431

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects/C\_ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: D88431

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 &lt;STO&gt;

A;Cross-references: UNIPROT:Q21602; UNIPARC:UPI0000179CCE; GB:chr\_III; PIDN:CAA84335.1;

C;Genetics:

A;Gene: M88.4

A;Map position: 3

Query Match 69.8%; Score 30; DB 2; Length 349;

Best Local Similarity 75.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLQLLMDR 8

|||||:  
Db 154 NLQLLSR 161

## RESULT 40

H90168

GTP-binding protein (hflX) [imported] - *Sulfolobus solfataricus*C;Species: *Sulfolobus solfataricus*

C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C;Accession: H90168

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: H90168  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-356 <KUR>  
A;Cross-references: UNIPROT:Q980M3; UNIPARC:UPI00000641E9; GB:AE006641; NID:g13813407; R  
C;Genetics:  
A;Gene: hflX

Query Match 69.8%; Score 30; DB 2; Length 356;  
Best Local Similarity 55.6%; Pred. No. 1.1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|||:|:|  
Db 340 NLELLRDKI 348

RESULT 41  
PC4295  
aspartate-tRNA ligase (EC 6.1.1.12) - Pseudomonas aeruginosa (fragment)  
C;Species: Pseudomonas aeruginosa  
C;Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: PC4295  
R;Hisida, T.; Iwasaki, H.; Ishioka, K.; Shinagawa, H.  
Gene 182, 63-70, 1996  
A;Title: Molecular analysis of the Pseudomonas aeruginosa genes, ruvA, ruvB and ruvC, in  
A;Reference number: JC5476; MUID:97136691; PMID:8982068  
A;Accession: PC4295  
A;Molecule type: DNA  
A;Residues: 1-361 <HIS>  
A;Cross-references: UNIPROT:Q51422; UNIPARC:UPI000016FC87; DBJ:D83138; NID:g1183837; P  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: asps

C;Function:  
A;Description: activates amino acid and transfers it to specific tRNA molecule  
A;Pathway: protein biosynthesis  
C;Superfamily: lysine-tRNA ligase  
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 69.8%; Score 30; DB 2; Length 361;  
Best Local Similarity 55.6%; Pred. No. 1.2e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|||:|:|  
Db 149 NLNVILDRV 157

RESULT 42  
T48449  
fatty acid elongase-like protein - Arabidopsis thaliana  
N;Alternate names: protein T32M21.130  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48449  
R;Bevan, M.; Terry, N.; Ardiles, W.; Buysschaert, C.; Dasseville, R.; De Clerck, R.; De  
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.P.X.  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24487  
A;Accession: T48449  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-464 <BEV>  
A;Cross-references: UNIPROT:Q9LZ72; UNIPARC:UPI000000C62A; EMBL:AL162875  
A;Experimental source: cultivar Columbia; BAC clone T32M21  
C;Genetics:

A;Map position: 5  
A;Note: T32M21.130  
C;Superfamily: very-long-chain 3-ketoacyl-CoA synthase

Query Match 69.8%; Score 30; DB 2; Length 464;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|||:|:|  
Db 291 NLQVLLPRV 299

RESULT 43  
T48328  
importin alpha-like protein - Arabidopsis thaliana  
N;Alternate names: protein F15A17.100  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48328  
R;Bevan, M.; Terry, N.; Ardiles, W.; Buysschaert, C.; Dasseville, R.; De Clerck, R.; De  
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.P.X.  
submitted to the Protein Sequence Database, April 2000  
A;Reference number: Z24491  
A;Accession: T48328  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-483 <BEV>  
A;Cross-references: UNIPROT:Q9LYX8; UNIPARC:UPI000009C59F; EMBL:AL163002  
A;Experimental source: cultivar Columbia; BAC clone F15A17  
C;Genetics:

A;Map position: 5  
A;Introns: 18/1; 92/2; 143/3; 178/1; 239/3; 266/2; 316/3; 327/3; 429/3  
A;Note: F15A17.100  
C;Superfamily: pendulin

Query Match 69.8%; Score 30; DB 2; Length 483;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9  
|||:|:|  
Db 298 LQLLIDRL 305

RESULT 44  
C82138  
conserved hypothetical protein VC1931 [imported] - Vibrio cholerae (strain N16961 serog  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: C82138  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: C82138  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-508 <HEI>  
A;Cross-references: UNIPROT:Q9KQB7; UNIPARC:UPI00000C3155; GB:AE004269; GB:AE003852; NI  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC1931  
A;Map position: 1  
C;Superfamily: hypothetical protein b1706

Query Match 69.8%; Score 30; DB 2; Length 508;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|||:|:|  
Db 215 NLKLLADKV 223

```
RESULT 45
T41092
hypothetical protein SPCC16C4.02c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41092
R:Purnelle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21964
A:Accession: T41092
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-548 <PUR>
A:Cross-references: UNIPROT:O74447; UNIPARC:UPI000006AE1E; EMBL:AL031535; PIDN:CAA20741.
A:Experimental source: strain 972h-; cosmid c16C4
C:Genetics:
A:Gene: SPDB:SPCC16C4.02C
A:Map position: 3
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPCC16C4.02c

Query Match      69.8%; Score 30; DB 2; Length 548;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQQLMDRV 9
||| ||| |
Db 256 NLQPLMDAV 264

RESULT 46
E83524
aspartyl-tRNA synthetase PA0963 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: E83524
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: E83524
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <STO>
A:Cross-references: UNIPROT:Q51422; UNIPARC:UPI00001363AB; GB:AE004530; GB:AE004091; NID:21470413
A:Experimental source: strain PA01
C:Genetics:
A:Gene: asps; PA0963
C:Superfamily: lysine-tRNA ligase

Query Match      69.8%; Score 30; DB 2; Length 591;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQQLMDRV 9
||| ||| |
Db 379 NLNVILDRV 387

RESULT 47
AF0079
RNA polymerase sigma factor RpoD [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF0079
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
```

```
A:Accession: AF0079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-612 <KUR>
A:Cross-references: UNIPROT:Q8Z171; UNIPARC:UPI00000CD701; GB:AL590842; PIDN:CAC89497.1.
C:Genetics:
A:Gene: rpoD
C:Superfamily: transcription initiation factor sigma 70; transcription initiation factor sigma 70

Query Match      69.8%; Score 30; DB 2; Length 612;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9
||| ||| |
Db 271 NMRAMMDRV 279

RESULT 48
TI2531
hypothetical protein DKFp434B194.1 - human
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 05-Oct-2004
C:Accession: TI2531
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: TI2531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-837 <WAM>
A:Cross-references: UNIPROT:Q9UBB9; UNIPARC:UPI0000137191; EMBL:AL080147
A:Experimental source: adult testis; clone DKFp434B194
C:Genetics:
A:Note: DKFp434B194.1
C:Superfamily: tuftelin-interacting protein 11

Query Match      69.8%; Score 30; DB 2; Length 837;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMD 7
||| ||| |
Db 323 NLQLLID 329

RESULT 49
A70634
probable mmpL1 protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: A70634
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70634
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-958 <COL>
A:Cross-references: UNIPROT:P95211; UNIPARC:UPI000012F26E; GB:Z84725; GB:AL123456; NID:21470413
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: mmpL1

Query Match      69.8%; Score 30; DB 2; Length 958;
Best Local Similarity 77.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
```



Db 499 NLQNLKDRV 507

## RESULT 50

AI2046

ABC transporter ATP-binding protein alr1927 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: AI2046

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AI2046

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1011 &lt;KUR&gt;

A;Cross-references: UNIPROT:Q8YVP7; UNIPARC:UPI00000CE265; GB:BA000019; PIDN:BAE73626.1;

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alr1927

Query Match

Best Local Similarity 69.8%; Score 30; DB 2; Length 1011;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLLMDRV 9

Db 475 QLLMDRV 481

Search completed: May 9, 2006, 02:25:17  
Job time : 28.4 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:25:44 ; Search time 80.8 Seconds  
(without alignments)  
46.540 Million cell updates/sec

Title: US-09-870-216C-11  
Perfect score: 43  
Sequence: 1 NLQLLMDRV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pgp:  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pgp:  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pgp:  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pgp:  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pgp:  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pgp:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	9	3	US-09-870-216C-11
2	43	100.0	9	4	Sequence 11, Appl
3	43	100.0	256	3	Sequence 1353, Ap
4	43	100.0	352	3	Sequence 2, Appli
5	43	100.0	352	4	Sequence 2, Appli
6	43	100.0	352	4	Sequence 347, App
7	36	83.7	311	5	US-10-408-765A-347
8	35	81.4	180	4	US-10-739-930-6423
9	35	81.4	180	5	US-10-264-237-1883
10	35	81.4	180	5	US-10-734-049A-220
11	35	81.4	180	5	US-10-965-898-43
12	35	81.4	239	3	US-09-925-300-1229
13	34	79.1	371	4	US-10-425-115-35256
14	34	79.1	372	4	Sequence 59828, A
15	34	79.1	1116	6	US-11-097-143-6447
16	33	76.7	874	4	US-10-163-214-13
17	33	76.7	987	4	US-10-437-963-113606
18	32	74.4	125	3	US-09-867-550-422
19	32	74.4	155	4	US-10-425-115-357844
20	32	74.4	178	4	US-10-424-599-233102
21	32	74.4	203	4	US-10-369-493-11994
22	32	74.4	250	5	US-10-617-320-2880
23	32	74.4	423	4	US-10-437-963-166526
24	32	74.4	2637	3	US-09-961-527A-5
25	32	74.4	4080	4	US-10-307-817-138
26	32	74.4	4624	4	US-10-408-765A-2991
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29	31	72.1	162	4	US-10-437-963-142657	Sequence 142657,
30	31	72.1	175	4	US-10-437-963-125323	Sequence 125323,
31	31	72.1	229	4	US-10-425-115-218767	Sequence 218767,
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33	31	72.1	270	4	US-10-627-476-676	Sequence 676, App
34	31	72.1	320	4	US-10-425-114-63198	Sequence 63198, A
35	31	72.1	336	4	US-10-425-115-345058	Sequence 345058,
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37	31	72.1	430	6	US-11-097-143-13443	Sequence 13443, A
38	31	72.1	455	5	US-10-739-930-10942	Sequence 10942, A
39	31	72.1	529	5	US-10-848-111-4	Sequence 4, Appli
40	31	72.1	542	4	US-10-289-762-496	Sequence 496, App
41	31	72.1	823	4	US-10-425-115-340748	Sequence 340748,
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43	31	72.1	838	4	US-10-369-493-11738	Sequence 11738, A
44	31	72.1	838	4	US-10-369-493-14794	Sequence 14794, A
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46	31	72.1	1504	4	US-10-369-493-22466	Sequence 22466, A
47	31	72.1	2424	6	US-11-097-143-31560	Sequence 31560, A
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63	30	69.8	340	4	US-10-335-977-5181	Sequence 5181, Ap
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83	30	69.8	753	3	US-09-925-302-760	Sequence 760, App
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91	30	69.8	1120	5	US-10-617-320-3602	Sequence 104637,
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93	30	69.8	1385	4	US-11-097-143-7206	Sequence 12087, A
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117	29	67.4	204	4	US-10-767-701-38770	Sequence 38770, A	190	29	67.4	1381	3	US-10-806-899-45	Sequence 45, Appl
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119	29	67.4	209	5	US-10-472-928-2026	Sequence 2026, Ap	192	29	67.4	1381	5	US-10-925-369-8	Sequence 8, Appl
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121	29	67.4	209	5	US-10-958-216-34	Sequence 34, Appl	194	29	67.4	1387	5	US-10-925-369-10	Sequence 10, Appl
122	29	67.4	228	4	US-10-724-972A-6176	Sequence 6176, Ap	195	29	67.4	1392	3	US-10-930-871-18	Sequence 18, Appl
123	29	67.4	228	4	US-10-724-972A-7188	Sequence 7188, Ap	196	29	67.4	1392	5	US-10-925-369-18	Sequence 18, Appl
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127	29	67.4	269	5	US-10-476-597-133	Sequence 153, App	200	29	67.4	1430	6	US-10-806-899-48	Sequence 48, Appl
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133	29	67.4	340	3	US-09-882-227-412	Sequence 412, App	206	29	67.4	1510	5	US-10-806-899-46	Sequence 46, Appl
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136	29	67.4	340	4	US-10-649-273-6	Sequence 6, Appl	209	29	67.4	1681	4	US-10-429-681-3	Sequence 3, Appl
137	29	67.4	340	4	US-10-651-722-6	Sequence 6, Appl	210	29	67.4	1757	4	US-10-758-672A-15	Sequence 15, Appl
138	29	67.4	342	5	US-10-779-597-161	Sequence 161, App	211	29	67.4	1757	5	US-10-758-636A-15	Sequence 15, Appl
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141	29	67.4	425	4	US-10-282-122A-61270	Sequence 61270, A	214	29	67.4	1942	5	US-10-806-899-58	Sequence 58, Appl
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154	29	67.4	550	5	US-10-491-183-7	Sequence 7, Appl	227	29	67.4	2009	4	US-10-451-126A-2	Sequence 2, Appl
155	29	67.4	559	4	US-10-425-114-49495	Sequence 49495, A	228	29	67.4	2009	4	US-10-451-126A-4	Sequence 4, Appl
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157	29	67.4	563	5	US-10-732-923-522	Sequence 522, App	230	29	67.4	2009	4	US-10-451-126A-10	Sequence 10, Appl
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162	29	67.4	587	5	US-10-972-963-132	Sequence 132, App	235	29	67.4	2009	5	US-10-806-899-27	Sequence 27, Appl
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166	29	67.4	655	4	US-10-283-122A-53165	Sequence 53165, A	239	29	67.4	2009	5	US-10-806-899-31	Sequence 31, Appl
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171	29	67.4	814	5	US-10-781-581-185	Sequence 185, App	244	29	67.4	2009	5	US-10-806-899-36	Sequence 36, Appl
172	29	67.4	814	5	US-10-756-149-5188	Sequence 5188, Ap	245	29	67.4	2009	5	US-10-806-899-37	Sequence 37, Appl
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275	28	65.1	137	4	US-10-425-114-71699	Sequence 71699, A	348	28	65.1	341	4	US-10-241-743-142	Sequence 142, App
276	28	65.1	158	4	US-10-767-701-41639	Sequence 41639, A	349	28	65.1	341	4	US-10-440-523-142	Sequence 142, App
277	28	65.1	161	4	US-10-437-963-155878	Sequence 155878, A	350	28	65.1	341	4	US-10-440-503-142	Sequence 142, App
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286	28	65.1	185	5	US-10-494-364-19	Sequence 19, Appl	359	28	65.1	369	4	US-10-425-114-65706	Sequence 65706, A
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415	28	65.1	523	4	US-10-006-130A-282	Sequence 282, App	488	28	65.1	928	4	US-10-473-576-16	Sequence 16, Appli
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436	28	65.1	523	4	US-10-013-906A-282	Sequence 282, App	509	28	65.1	1763	5	US-10-783-989-7	Sequence 7, Appli
437	28	65.1	523	4	US-10-015-388A-282	Sequence 282, App	510	28	65.1	1849	4	US-10-437-963-128461	Sequence 128461,
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446	28	65.1	523	4	US-10-006-746A-282	Sequence 282, App	519	27	62.8	38	4	US-10-425-115-330217	Sequence 330217,
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543	27	62.8	99	4	US-10-424-599-197792	Sequence 197792, A	616	27	62.8	245	4	US-10-143-114-214	Sequence 214, App
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551	27	62.8	123	4	US-10-424-599-180430	Sequence 180430, A	624	27	62.8	245	4	US-10-123-236-214	Sequence 214, App
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556	27	62.8	134	4	US-10-767-701-35764	Sequence 35764, A	629	27	62.8	245	4	US-10-123-292-214	Sequence 214, App
557	27	62.8	136	4	US-10-425-114-42199	Sequence 42199, A	630	27	62.8	245	4	US-10-123-903-214	Sequence 214, App
558	27	62.8	136	4	US-10-767-701-56389	Sequence 56389, A	631	27	62.8	245	4	US-10-124-819-214	Sequence 214, App
559	27	62.8	138	4	US-10-029-386-28615	Sequence 28615, A	632	27	62.8	245	4	US-10-124-822-214	Sequence 214, App
560	27	62.8	138	4	US-10-108-260A-3976	Sequence 3976, Ap	633	27	62.8	245	4	US-10-140-925-214	Sequence 214, App
561	27	62.8	148	4	US-10-767-701-55659	Sequence 55659, A	634	27	62.8	245	4	US-10-160-498-214	Sequence 214, App
562	27	62.8	148	5	US-10-450-763-31548	Sequence 31548, A	635	27	62.8	245	4	US-10-124-824-214	Sequence 214, App
563	27	62.8	153	5	US-10-732-923-22773	Sequence 22773, A	636	27	62.8	245	4	US-10-127-825A-214	Sequence 214, App
564	27	62.8	155	4	US-10-343-552-497	Sequence 497, App	637	27	62.8	245	4	US-10-127-829A-214	Sequence 214, App
565	27	62.8	156	4	US-10-174-693-272	Sequence 272, App	638	27	62.8	245	4	US-10-127-835A-214	Sequence 214, App
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570	27	62.8	167	4	US-10-767-701-40255	Sequence 40255, A	643	27	62.8	245	4	US-10-131-818A-214	Sequence 214, App
571	27	62.8	168	4	US-10-767-701-40148	Sequence 40148, A	644	27	62.8	245	4	US-10-131-823A-214	Sequence 214, App
572	27	62.8	179	4	US-10-437-963-195625	Sequence 195625, A	645	27	62.8	245	4	US-10-131-824A-214	Sequence 214, App
573	27	62.8	180	3	US-09-858-580-24	Sequence 24, Appl	646	27	62.8	245	4	US-10-131-830A-214	Sequence 214, App
574	27	62.8	180	3	US-09-847-172-24	Sequence 24, Appl	647	27	62.8	245	4	US-10-131-837A-214	Sequence 214, App
575	27	62.8	180	5	US-10-941-152-24	Sequence 24, Appl	648	27	62.8	245	4	US-10-137-872A-214	Sequence 214, App
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577	27	62.8	184	5	US-10-490-147A-12	Sequence 12, Appl	650	27	62.8	245	4	US-10-147-502-214	Sequence 214, App
578	27	62.8	185	3	US-09-858-580-2	Sequence 2, Appl	651	27	62.8	245	4	US-10-147-515-214	Sequence 214, App
579	27	62.8	185	3	US-09-847-172-2	Sequence 2, Appl	652	27	62.8	245	4	US-10-147-517-214	Sequence 214, App
580	27	62.8	185	5	US-10-941-152-2	Sequence 2, Appl	653	27	62.8	245	4	US-10-147-526-214	Sequence 214, App
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592	27	62.8	212	4	US-10-767-701-56277	Sequence 56277, A	665	27	62.8	245	4	US-10-125-922-214	Sequence 214, App
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596	27	62.8	225	4	US-10-437-963-197213	Sequence 197213, A	669	27	62.8	245	4	US-10-147-519-214	Sequence 214, App
597	27	62.8	227	6	US-11-097-143-39942	Sequence 39942, A	670	27	62.8	245	4	US-10-157-782-214	Sequence 214, App
598	27	62.8	228	3	US-08-976-063C-14	Sequence 14, Appl	671	27	62.8	245	4	US-10-152-395-214	Sequence 214, App
599	27	62.8	228	3	US-09-750-986D-14	Sequence 14, Appl	672	27	62.8	245	4	US-10-125-926A-214	Sequence 214, App
600	27	62.8	230	5	US-10-873-467-90	Sequence 90, Appl	673	27	62.8	245	4	US-10-125-930A-214	Sequence 214, App
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604	27	62.8	244	4	US-10-125-540-438	Sequence 438, App	677	27	62.8	245	4	US-10-127-842A-214	Sequence 214, App
605	27	62.8	245	4	US-10-028-072-214	Sequence 214, App	678	27	62.8	245	4	US-10-127-843A-214	Sequence 214, App
606	27	62.8	245	4	US-10-140-808-214	Sequence 214, App	679	27	62.8	245	4	US-10-127-845A-214	Sequence 214, App
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608	27	62.8	245	4	US-10-123-904-214	Sequence 214, App	681	27	62.8	245	4	US-10-127-848A-214	Sequence 214, App
609	27	62.8	245	4	US-10-140-470-214	Sequence 214, App	682	27	62.8	245	4	US-10-127-849A-214	Sequence 214, App
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993 27 62.8 245 4 US-10-146-794-214 Sequence 214, App
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998 27 62.8 245 4 US-10-152-376-214 Sequence 214, App
999 27 62.8 245 4 US-10-152-381-214 Sequence 214, App
1000 27 62.8 245 4 US-10-152-400-214 Sequence 214, App
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## ALIGNMENTS

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RESULT 1
US-09-870-216C-11
; Sequence 11, Application US/09870216C
; Publication No. US20040138135A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881210100
; CURRENT APPLICATION NUMBER: US/09/870,216C
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/209,391
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/226,256
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/257,008
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-216C-11
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Query Match 100.0%; Score 43; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 NLQLLMDRV 9
Db 1 NLQLLMDRV 9

RESULT 2
US-10-017-327-11
; Sequence 11, Application US/10017327
; Publication No. US20020155471A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND
; TITLE OF INVENTION: METHODS FOR USING SAME
; FILE REFERENCE: G2 2101.20
; CURRENT APPLICATION NUMBER: US/10/017,327
; CURRENT FILING DATE: 2001-12-06
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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-327-11

Query Match 100.0%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 NLQLLMDRV 9
Db 1 NLQLLMDRV 9

RESULT 3
US-09-925-300-1353
; Sequence 1353, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1353
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1353

Query Match 100.0%; Score 43; DB 3; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 NLQLLMDRV 9
Db 146 NLQLLMDRV 154

RESULT 4
US-09-870-216C-2
; Sequence 2, Application US/09870216C
; Publication No. US20040138135A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881210100
; CURRENT APPLICATION NUMBER: US/09/870,216C
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/209,391
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/226,256
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/257,008
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-870-216C-2

Query Match      100.0%; Score 43; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 242 NLQLLMDRV 250

RESULT 5
US-10-017-327-2
; Sequence 2, Application US/10017327
; Publication No. US20020155471A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND
; FILE REFERENCE: GZ 2101.20
; CURRENT APPLICATION NUMBER: US/10/017,327
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-017-327-2

Query Match      100.0%; Score 43; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 242 NLQLLMDRV 250

RESULT 6
US-10-408-765A-347
; Sequence 347, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-347

Query Match      100.0%; Score 43; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 242 NLQLLMDRV 250

RESULT 7
US-10-739-930-6423
; Sequence 6423, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6423
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ARATH-23APR03-C3789_1.p
; US-10-739-930-6423

Query Match      83.7%; Score 36; DB 5; Length 311;
Best Local Similarity 87.5%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9
Db 146 LQLLMDRV 153

RESULT 8
US-10-264-237-1883
; Sequence 1883, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1883
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-237-1883

Query Match      81.4%; Score 35; DB 4; Length 180;
Best Local Similarity 87.5%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 8
Db 23 NLQLLMDRV 30

RESULT 9
US-10-734-049A-220
; Sequence 220, Application US/10734049A
; Publication No. US20050042624A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; APPLICANT: SHICHIGO, Shigeki
; TITLE OF INVENTION: TUMOR ANTIGEN
; FILE REFERENCE: Q-78382
; CURRENT APPLICATION NUMBER: US/10/734,049A
; CURRENT FILING DATE: 2003-12-12
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; PRIOR APPLICATION NUMBER: PCT/JP02/05799  
; PRIOR FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: JP 2001/177058  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: JP 2001/250728  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 408  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 220  
; LENGTH: 180  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-734-049A-220

Query Match 81.4%; Score 35; DB 5; Length 180;  
Best Local Similarity 87.5%; Pred. No. 63;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLQLMDR 8  
Db 23 NLQLVDR 30

RESULT 10  
US-10-734-049A-277  
; Sequence 277, Application US/10734049A  
; Publication No. US20050042624A1  
; GENERAL INFORMATION:  
; APPLICANT: ITOH, Kyogo  
; TITLE OF INVENTION: TUMOR ANTIGEN  
; FILE REFERENCE: Q-78382  
; CURRENT APPLICATION NUMBER: US/10/734,049A  
; PRIOR FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: PCT/JP02/05799  
; PRIOR FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: JP 2001/177058  
; PRIOR FILING DATE: 2001-08-12  
; PRIOR APPLICATION NUMBER: JP 2001/250728  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 408  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 277  
; LENGTH: 180  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-734-049A-277

Query Match 81.4%; Score 35; DB 5; Length 180;  
Best Local Similarity 87.5%; Pred. No. 63;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLQLMDR 8  
Db 23 NLQLVDR 30

RESULT 11  
US-10-965-898-43  
; Sequence 43, Application US/10965898  
; Publication No. US20050084936A1  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Presti  
; Bandman, Olga  
; Hillman, Jennifer L.  
; Au-Young, Janice  
; Tang, Y. Tom  
; Yue, Henry  
; Shah, Purvi  
; Guegler, Karl J.  
; Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY PROTEINS  
; NUMBER OF SEQUENCES: 150

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/965,898  
; FILING DATE: 18-Oct-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/001,403  
; FILING DATE: 31-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BILLINGS, LUCY J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0455 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 180 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BONTNOT01  
; CLONE: 2637177  
; SEQUENCE DESCRIPTION: SEQ ID NO: 43 :  
US-10-965-898-43

Query Match 81.4%; Score 35; DB 5; Length 180;  
Best Local Similarity 87.5%; Pred. No. 63;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLQLMDR 8  
Db 23 NLQLVDR 30

RESULT 12  
US-09-925-300-1229  
; Sequence 1229, Application US/09925300  
; Patent No. US2002015181A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1229  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-300-1229

Query Match 81.4%; Score 35; DB 3; Length 239;  
Best Local Similarity 87.5%; Pred. No. 85;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



Db 195 NLQLLLDK 202  
|||||:|:

RESULT 17  
US-10-437-963-113606  
; Sequence 113606, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 113606  
; LENGTH: 987  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_17378C.1.pap  
US-10-437-963-113606

Query Match 76.7%; Score 33; DB 4; Length 987;  
Best Local Similarity 66.7%; Pred. No. 9.5e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 NLQLLMDRV 9  
:|||||:  
Db 564 DLQLLVDR 572

RESULT 18  
US-09-867-550-422  
; Sequence 422, Application US/09867550  
; Patent No. US20020082206A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Mehraban, Fuad,  
; APPLICANT: Conley, Pamela  
; APPLICANT: Law, Debbie  
; APPLICANT: Topper, James  
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and  
; FILE REFERENCE: 21402-013 (Cura-313)  
; CURRENT APPLICATION NUMBER: US/09/867,550  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: USSN 60/208,427  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 2125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 422  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-867-550-422

Query Match 74.4%; Score 32; DB 3; Length 125;  
Best Local Similarity 75.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 NLQLLMDR 8  
|||||:|:  
Db 22 NLQLLLDQ 29

RESULT 19  
US-10-425-115-357844  
; Sequence 357844, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 357844  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(155)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_89523C.1.pap  
US-10-425-115-357844

Query Match 74.4%; Score 32; DB 4; Length 155;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 NLQLLMDRV 9  
:|||||:  
Db 144 NLTLFMDRI 152

RESULT 20  
US-10-424-599-233102  
; Sequence 233102, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 233102  
; LENGTH: 178  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_52515C.1.pap  
US-10-424-599-233102

Query Match 74.4%; Score 32; DB 4; Length 178;  
Best Local Similarity 75.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 NLQLLMDR 8  
|||||:|:  
Db 76 NLQLVMDQ 83

RESULT 21  
US-10-369-493-11994  
; Sequence 11994, Application US/10369493  
; Publication No. US20030233675A1

```
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11994
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
; US-10-369-493-11994

Query Match      74.4%; Score 32; DB 4; Length 203;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LQLMDRV 9
Db      125 LQLMDRV 132

RESULT 22
US-10-617-320-2880
; Sequence 2880, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/617,320
; FILING DATE: 10-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2880:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...250
; SEQUENCE DESCRIPTION: SEQ ID NO: 2880:
US-10-617-320-2880

Query Match      74.4%; Score 32; DB 5; Length 250;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLMDRV 9
Db      196 NLPLLDRI 204

RESULT 23
US-10-437-963-166526
; Sequence 166526, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166526
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65226C.1.pap
; US-10-437-963-166526

Query Match      74.4%; Score 32; DB 4; Length 423;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLMDRV 9
Db      354 NLQLAMDKL 362

RESULT 24
US-09-961-527A-5
; Sequence 5, Application US/09961527A
; Patent No. US20020142324A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Turgeon, B. Gillian
; APPLICANT: Yoder, Olen
; APPLICANT: Wu, Jianguo
; TITLE OF INVENTION: Fungal target genes and methods to identify those genes
; FILE REFERENCE: TM0129-UT
; CURRENT APPLICATION NUMBER: US/09/961,527A
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/234,673
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/234,650
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 19
```

; SEQ ID NO 5  
; LENGTH: 2697  
; TYPE: PRT  
; ORGANISM: Cochliobolus  
US-09-961-527A-5

Query Match 74.4%; Score 32; DB 3; Length 2697;  
Best Local Similarity 75.0%; Pred. No. 4.4e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLLMDRV 9  
|||  
Db 605 LQLLMDRI 612

## RESULT 25

US-10-307-817-138  
; Sequence 138, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 138  
; LENGTH: 4080  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-307-817-138

Query Match 74.4%; Score 32; DB 4; Length 4080;  
Best Local Similarity 66.7%; Pred. No. 6.8e+03;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9  
:|:|:|  
Db 796 DLELLMDRV 804

## RESULT 26

US-10-408-765A-2991  
; Sequence 2991, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Faby, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2991  
; LENGTH: 4624  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-2991

Query Match 74.4%; Score 32; DB 4; Length 4624;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9  
:|:|:|

Db 812 DLELLMDRV 820

## RESULT 27

US-10-437-963-113390  
; Sequence 113390, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 113390  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_17182C.1.pep  
US-10-437-963-113390

Query Match 72.1%; Score 31; DB 4; Length 156;  
Best Local Similarity 66.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9  
:|:|:|  
Db 94 NVLSMDRV 102

## RESULT 28

US-10-425-115-325709  
; Sequence 325709, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 325709  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_60115C.1.pep  
US-10-425-115-325709

Query Match 72.1%; Score 31; DB 4; Length 160;  
Best Local Similarity 87.5%; Pred. No. 3.4e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLLMDRV 9  
|||  
Db 151 LQLLMDRV 158

## RESULT 29

US-10-437-963-142657



; Sequence 142657, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 142657  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(162)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_43642C.1.pap  
US-10-437-963-142657

Query Match 72.1%; Score 31; DB 4; Length 162;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
|::| ||||  
DB 20 NVLSMDRV 28

RESULT 30  
US-10-437-963-125323  
; Sequence 125323, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 125323  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_27979C.1.pap  
US-10-437-963-125323

Query Match 72.1%; Score 31; DB 4; Length 175;  
Best Local Similarity 77.8%; Pred. No. 3.8e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
||| ||||  
DB 80 NLPLLYDRV 88

RESULT 31  
US-10-425-115-218767  
; Sequence 218767, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 218767  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(229)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_131106C.1.pap  
US-10-425-115-218767

Query Match 72.1%; Score 31; DB 4; Length 229;  
Best Local Similarity 77.8%; Pred. No. 5e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
||| ||||  
DB 138 NLULLDRV 146

RESULT 32  
US-09-738-626-5133  
; Sequence 5133, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 5133  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-5133

Query Match 72.1%; Score 31; DB 3; Length 270;  
Best Local Similarity 66.7%; Pred. No. 6e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 NLQLLMDRV 9
Db      22 NLPLIVDRV 30

RESULT 33
US-10-627-476-676
; Sequence 676, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Zelderhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125PCPN
; CURRENT APPLICATION NUMBER: US/10/627,476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 676
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-627-476-676

Query Match      72.1%; Score 31; DB 4; Length 270;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
Db      22 NLPLIVDRV 30

RESULT 34
US-10-425-114-63198
; Sequence 63198, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
```

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; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63198
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017286D01_FLI.pep
US-10-425-114-63198

Query Match      72.1%; Score 31; DB 4; Length 320;
Best Local Similarity 77.8%; Pred. No. 7.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
Db      122 NLPLIVDRV 130

RESULT 35
US-10-425-115-345058
; Sequence 345058, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345058
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_7785C.1.pep
US-10-425-115-345058

Query Match      72.1%; Score 31; DB 4; Length 336;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
Db      138 NLPLIVDRV 146

RESULT 36
US-10-680-860A-24
; Sequence 24, Application US/10680860A
; Publication No. US20050202528A1
; GENERAL INFORMATION:
; APPLICANT: BLONDELET-ROUAULT, Marie-Helene
; APPLICANT: DOMINGUEZ, Helene
; APPLICANT: DARBON-RONGERE, Emmanuelle
; APPLICANT: GERBAUD, Claude
; APPLICANT: GONDRAN, Anne
; APPLICANT: KAREAY, Fatma
; APPLICANT: LACROIX, Patricia
; APPLICANT: OESTREICHER-MERMET-BOUVIER, Nathalie
; APPLICANT: PERNODET, Jean-Luc
; APPLICANT: TUPHILE, Karine
; TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE BIOSYNTHESIS OF SPIRAMYCINS, NUCLEOS
; TITLE OF INVENTION: SEQUENCE ENCODING THESE POLYPEPTIDES AND APPLICATIONS THEREOF
; FILE REFERENCE: FRV2002/0028 US NP
; CURRENT APPLICATION NUMBER: US/10/680,860A
; CURRENT FILING DATE: 2003-10-07
```

; PRIOR APPLICATION NUMBER: FR 0212489  
; PRIOR FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: FR 0302439  
; PRIOR FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: US 60/493,490  
; PRIOR FILING DATE: 2003-08-07  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Streptomyces ambofaciens  
US-10-860-860A-24

Query Match 72.1%; Score 31; DB 5; Length 403;  
Best Local Similarity 75.0%; Pred. No. 9.1e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMDRV 9  
|:|:|:|  
Db 366 LELLDV 373

## RESULT 37

US-11-097-143-13443  
; Sequence 13443, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.

; FILE REFERENCE: CL000728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23

; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13443

; LENGTH: 430

; TYPE: PRT

; ORGANISM: DROSOPHILA

US-11-097-143-13443

Query Match 72.1%; Score 31; DB 6; Length 430;  
Best Local Similarity 75.0%; Pred. No. 9.8e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
|:|:|:|  
Db 172 NLQMLDR 179

## RESULT 38

US-10-739-930-10942  
; Sequence 10942, Application US/10739930  
; Publication No. US20040216190A1

; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 10942  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: TRIAB-23APR03-C8746\_1.p  
US-10-739-930-10942

Query Match 72.1%; Score 31; DB 5; Length 455;  
Best Local Similarity 77.8%; Pred. No. 1e+03;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
|:|:|:|  
Db 266 NLSLLHDRV 274

## RESULT 39

US-10-848-111-4  
; Sequence 4, Application US/10848111  
; Publication No. US20040235107A1

; GENERAL INFORMATION:

; APPLICANT: Rosenberg, Eugene

; APPLICANT: Ron, Elisha

; APPLICANT: Orr, Elisha

; APPLICANT: Paitan, Yossi

; TITLE OF INVENTION: GENE CLUSTER

; FILE REFERENCE: 27757

; CURRENT APPLICATION NUMBER: US/10/848,111

; CURRENT FILING DATE: 2004-05-19

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-10-848-111-4

Query Match 72.1%; Score 31; DB 5; Length 529;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMDRV 9  
|:|:|:|  
Db 48 LQTLMDRI 55

## RESULT 40

US-10-289-762-496

; Sequence 496, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Grifais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 496

; LENGTH: 542

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-496

```
Query Match          72.1%; Score 31; DB 4; Length 542;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 531 NLQLASDRI 539

RESULT 41
US-10-425-115-340748
; Sequence 340748, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 340748
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_73932C.1.pep
US-10-425-115-340748

Query Match          72.1%; Score 31; DB 4; Length 823;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 573 NLQALVDRM 581

RESULT 42
US-10-369-493-14960
; Sequence 14960, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14960
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14960

Query Match          72.1%; Score 31; DB 4; Length 833;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9
Db 426 IQLLVDRV 433

RESULT 43
US-10-369-493-11738
; Sequence 11738, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11738
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11738

Query Match          72.1%; Score 31; DB 4; Length 838;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9
Db 430 IQLLVDRV 437

RESULT 44
US-10-369-493-14794
; Sequence 14794, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14794
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14794

Query Match          72.1%; Score 31; DB 4; Length 838;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9
Db 430 IQLLVDRV 437

RESULT 45
US-10-287-226-330
; Sequence 330, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
```

; APPLICANT: Agee, Michele L.,  
; APPLICANT: Alsobrook, John P.,  
; APPLICANT: Berghs, Constance,  
; APPLICANT: Boldog, Ference,  
; APPLICANT: Burgeas, Catherine E.,  
; APPLICANT: Chant, John S.,  
; APPLICANT: Chaudhuri, Amitabha,  
; APPLICANT: DiPippo, Vincent A.,  
; APPLICANT: Edinger, Shlomit R.,  
; APPLICANT: Eisen, Andrew,  
; APPLICANT: Ellerman, Karen,  
; APPLICANT: Gangolli, Esha A.,  
; APPLICANT: Gorman, Linda,  
; APPLICANT: Gerlach, Valerie,  
; APPLICANT: Ji, Weizhen,  
; APPLICANT: Kekuda, Ramesh,  
; APPLICANT: Khramtsov, Nikolai,  
; APPLICANT: Li, Li,  
; APPLICANT: Malvankar, Uriel M.,  
; APPLICANT: MacDougall, John R.,  
; APPLICANT: Mezes, Peter S.,  
; APPLICANT: Miller, Charles E.,  
; APPLICANT: Millet, Isabelle,  
; APPLICANT: Ooi, Chean Eng,  
; APPLICANT: Ort, Tatiana,  
; APPLICANT: Padigar, Muralidhara,  
; APPLICANT: Patturajan, Meera,  
; APPLICANT: Rastelli, Luca,  
; APPLICANT: Rieger, Daniel K.,  
; APPLICANT: Rothenberg, Mark E.,  
; APPLICANT: Shenoy, Suresh G.,  
; APPLICANT: Spaderna, Steven K.,  
; APPLICANT: Spytek, Kimberley A.,  
; APPLICANT: Taupier, Jr., Raymond J.,  
; APPLICANT: Vernet, Corine A.M.,  
; APPLICANT: Zerhusen, Bryan D.,  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-480C  
; CURRENT APPLICATION NUMBER: US/10/287,226  
; CURRENT FILING DATE: 2002-11-04  
; PRIOR APPLICATION NUMBER: 60/334,421  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/354,392  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/360,148  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: 60/364,000  
; PRIOR FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: 60/404,821  
; PRIOR FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: 60/334,526  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/354,409  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/364,227  
; PRIOR FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: 60/334,027  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/331,641  
; PRIOR FILING DATE: 2001-11-20  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 673  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 330  
; LENGTH: 916  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-226-330

Query Match 72.1%; Score 31; DB 4; Length 916;  
Best Local Similarity 75.0%; Pred. No. 2.2e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
:|||||:  
Db 740 HLQLMDK 747

## RESULT 46

US-10-369-493-22466  
; Sequence 22466, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22466  
; LENGTH: 1504  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-22466

Query Match 72.1%; Score 31; DB 4; Length 1504;  
Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
:|||||:  
Db 237 DLQLMDR 244

## RESULT 47

US-11-097-143-31560  
; Sequence 31560, Application US/11097143  
; Publication No. US2005020858A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31560  
; LENGTH: 2424  
; TYPE: PRT

```
; ORGANISM: DROSOPHILA
US-11-097-143-31560

Query Match      72.1%; Score 31; DB 6; Length 2424;
Best Local Similarity 55.6%; Pred. No. 6.1e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLMDRV 9
Db      848 NLQIMDDI 856

RESULT 48
US-10-335-977-6139
; Sequence 6139, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandagouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...55
; SEQUENCE DESCRIPTION: SEQ ID NO: 6139:
US-10-335-977-6139

Query Match      69.8%; Score 30; DB 4; Length 55;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLQLLMD 7
Db      45 NLQLLVD 51

RESULT 49
US-10-425-115-362529

; Sequence 362529, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 362529
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(130)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_93801C.1.pap
US-10-425-115-362529

Query Match      69.8%; Score 30; DB 4; Length 130;
Best Local Similarity 77.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 NLQLMDRV 9
Db      25 NLQLLKDLV 33

RESULT 50
US-10-104-047-2471
; Sequence 2471, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2471
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2471

Query Match      69.8%; Score 30; DB 4; Length 132;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLMDR 8
Db      74 NLQNMMDR 81

Search completed: May 9, 2006, 02:35:46
Job time : 94.8 secs
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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:28:58 ; Search time 12.8 Seconds  
(without alignments)  
32.544 Million cell updates/sec

Title: US-09-870-216C-11

Perfect score: 43

Sequence: 1 NLOQLMDRV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New.\*

- 1: /SIDSS/ptodata/2/pubpaa/US08\_NEW\_PUB.pep1.\*
- 2: /SIDSS/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /SIDSS/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /SIDSS/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /SIDSS/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 6: /SIDSS/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 7: /SIDSS/ptodata/2/pubpaa/US10\_NEW\_PUB.pep1.\*
- 8: /SIDSS/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 9: /SIDSS/ptodata/2/pubpaa/US10\_NEW\_PUB.pep1.\*
- 10: /SIDSS/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 11: /SIDSS/ptodata/2/pubpaa/US11\_NEW\_PUB.pep1.\*
- 12: /SIDSS/ptodata/2/pubpaa/US60\_NEW\_PUB.pep1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	302	9	US-10-853-807A-45
2	43	100.0	347	9	US-10-853-807A-45
3	43	100.0	352	9	US-10-878-556A-40
4	36	83.7	260	11	US-11-096-568A-33949
5	36	83.7	311	11	US-11-096-568A-33948
6	36	83.7	345	11	US-11-096-568A-33947
7	34	79.1	310	11	US-11-096-568A-19252
8	34	79.1	348	11	US-11-096-568A-19251
9	33	76.7	509	9	US-10-506-454-1111
10	32	74.4	457	11	US-11-096-568A-30182
11	32	74.4	480	11	US-11-096-568A-30181
12	32	74.4	518	11	US-11-096-568A-30180
13	32	74.4	572	11	US-11-052-554A-129
14	32	74.4	1444	11	US-11-052-554A-130
15	31	72.1	270	11	US-11-082-389-38
16	31	72.1	841	11	US-11-216-333-2
17	30	69.8	132	11	US-11-072-512-2471
18	30	69.8	165	11	US-11-096-568A-18308
19	30	69.8	194	11	US-11-096-568A-18307
20	30	69.8	198	11	US-11-096-568A-10913
21	30	69.8	201	11	US-11-096-568A-18306

22	69.8	218	11	US-11-045-004-1366	Sequence 1366, Ap
23	69.8	308	11	US-11-096-568A-10912	Sequence 10912, A
24	69.8	335	11	US-11-096-568A-10911	Sequence 10911, A
25	69.8	1763	8	US-10-504-120-21	Sequence 21, Appl
26	69.8	1807	8	US-10-504-120-22	Sequence 22, Appl
27	67.4	379	11	US-11-096-568A-17169	Sequence 17169, A
28	67.4	390	11	US-11-096-568A-21913	Sequence 21913, A
29	67.4	424	11	US-11-045-004-1627	Sequence 1627, Ap
30	67.4	587	8	US-10-511-937-2407	Sequence 2407, Ap
31	67.4	726	11	US-11-052-554A-127	Sequence 127, App
32	67.4	752	11	US-11-188-298-4158	Sequence 4158, Ap
33	67.4	862	11	US-11-188-298-7416	Sequence 7416, Ap
34	67.4	1060	11	US-11-079-463-10154	Sequence 10154, A
35	67.4	1216	9	US-10-873-528-12	Sequence 12, Appl
36	67.4	1406	10	US-11-263-326-171	Sequence 171, App
37	67.4	1795	10	US-11-263-326-124	Sequence 124, App
38	67.4	1855	10	US-11-263-326-125	Sequence 125, App
39	67.4	1891	10	US-11-263-326-173	Sequence 173, App
40	67.4	1981	9	US-10-374-954-23	Sequence 23, Appl
41	67.4	1998	9	US-10-374-954-21	Sequence 21, Appl
42	67.4	2009	9	US-10-374-954-2	Sequence 2, Appl
43	67.4	2009	10	US-11-263-326-2	Sequence 2, Appl
44	67.4	2009	10	US-11-263-326-4	Sequence 4, Appl
45	67.4	2009	10	US-11-263-326-6	Sequence 6, Appl
46	67.4	2009	10	US-11-263-326-10	Sequence 10, Appl
47	67.4	2009	10	US-11-263-326-12	Sequence 12, Appl
48	67.4	2009	10	US-11-263-326-121	Sequence 121, App
49	67.4	2009	10	US-11-263-326-122	Sequence 122, App
50	67.4	2009	10	US-11-263-326-123	Sequence 123, App
51	67.4	2009	10	US-11-263-326-126	Sequence 126, App
52	67.4	2009	10	US-11-263-326-127	Sequence 127, App
53	67.4	2009	10	US-11-263-326-167	Sequence 167, App
54	67.4	2009	10	US-11-263-326-168	Sequence 168, App
55	67.4	2009	10	US-11-263-326-169	Sequence 169, App
56	67.4	2009	10	US-11-263-326-170	Sequence 170, App
57	67.4	2009	10	US-11-263-326-172	Sequence 172, App
58	65.1	94	11	US-11-004-399-1053	Sequence 1053, Ap
59	65.1	193	11	US-11-079-463-10040	Sequence 10040, A
60	65.1	218	11	US-11-143-980-33	Sequence 33, Appl
61	65.1	365	11	US-11-229-769-322	Sequence 322, App
62	65.1	383	9	US-10-485-517-356	Sequence 356, App
63	65.1	413	11	US-11-188-298-5417	Sequence 5417, Ap
64	65.1	413	11	US-11-188-298-13659	Sequence 13659, A
65	65.1	416	9	US-10-055-877-168	Sequence 168, App
66	65.1	451	11	US-11-079-463-9559	Sequence 9559, Ap
67	65.1	485	11	US-11-165-211-47	Sequence 47, Appl
68	65.1	485	11	US-11-165-226-57	Sequence 57, Appl
69	65.1	542	11	US-11-229-769-323	Sequence 323, App
70	65.1	543	11	US-11-079-463-6315	Sequence 6315, Ap
71	65.1	754	11	US-11-079-463-8046	Sequence 8046, Ap
72	65.1	856	11	US-11-096-568A-28102	Sequence 28102, A
73	65.1	861	11	US-11-096-568A-28101	Sequence 28101, A
74	65.1	890	11	US-11-096-568A-28100	Sequence 28100, A
75	65.1	917	11	US-11-169-041-145	Sequence 145, App
76	65.1	1146	11	US-11-087-099-723	Sequence 723, App
77	65.1	1151	11	US-11-087-099-9496	Sequence 9496, Ap
78	65.1	1313	11	US-11-091-668-4	Sequence 4, Appl
79	62.8	110	9	US-10-793-626-2152	Sequence 2152, Ap
80	62.8	157	11	US-11-045-004-2748	Sequence 2748, Ap
81	62.8	184	11	US-11-096-568A-215	Sequence 215, App
82	62.8	187	11	US-11-096-568A-15058	Sequence 15058, A
83	62.8	194	9	US-10-986-405-345	Sequence 345, App
84	62.8	203	11	US-11-096-568A-3354	Sequence 3354, Ap
85	62.8	205	9	US-10-453-372-762	Sequence 762, App
86	62.8	221	11	US-11-096-568A-15057	Sequence 15057, A
87	62.8	227	11	US-11-096-568A-15056	Sequence 15056, A
88	62.8	230	11	US-11-074-176-224	Sequence 224, App
89	62.8	238	11	US-11-156-084-221	Sequence 221, App
90	62.8	244	9	US-10-986-405-348	Sequence 348, App
91	62.8	245	9	US-10-131-826A-214	Sequence 214, App
92	62.8	245	9	US-10-973-115B-214	Sequence 214, App
93	62.8	245	9	US-10-137-873A-214	Sequence 214, App
94	62.8	245	9	US-10-152-370-214	Sequence 214, App

95	27	62.8	245	11	US-11-290-153-214	Sequence 214, App	168	26	60.5	246	11	US-11-079-463-8152	Sequence 8152, Ap
96	27	62.8	247	11	US-11-087-099-11393	Sequence 11393, A	169	26	60.5	247	11	US-11-096-568A-29306	Sequence 29306, A
97	27	62.8	256	11	US-11-096-568A-30721	Sequence 30721, A	170	26	60.5	250	11	US-11-096-568A-12005	Sequence 12005, A
98	27	62.8	258	11	US-11-072-512-3541	Sequence 3541, Ap	171	26	60.5	256	11	US-11-087-099-5276	Sequence 5276, Ap
99	27	62.8	267	11	US-11-096-568A-28052	Sequence 28052, A	172	26	60.5	256	11	US-11-096-568A-29305	Sequence 29305, A
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103	27	62.8	297	11	US-11-096-568A-18353	Sequence 18353, A	176	26	60.5	278	11	US-11-096-568A-23004	Sequence 23004, A
104	27	62.8	298	11	US-11-098-686-11250	Sequence 11250, A	177	26	60.5	301	11	US-11-096-568A-12824	Sequence 12824, A
105	27	62.8	301	11	US-11-096-568A-3353	Sequence 3353, Ap	178	26	60.5	301	11	US-11-045-004-182	Sequence 182, App
106	27	62.8	316	11	US-11-087-099-8205	Sequence 8205, Ap	179	26	60.5	302	11	US-11-096-568A-12823	Sequence 12823, A
107	27	62.8	319	11	US-11-096-568A-18352	Sequence 18352, A	180	26	60.5	304	11	US-11-079-463-7891	Sequence 7891, Ap
108	27	62.8	325	11	US-11-188-298-21546	Sequence 21546, A	181	26	60.5	309	11	US-11-188-298-10902	Sequence 10902, A
109	27	62.8	328	11	US-11-152-697-4	Sequence 4, Appl	182	26	60.5	309	11	US-11-188-298-18212	Sequence 18212, A
110	27	62.8	330	11	US-11-045-004-2846	Sequence 2846, Ap	183	26	60.5	310	7	US-09-941-095-88	Sequence 88, Appl
111	27	62.8	339	11	US-11-096-568A-15817	Sequence 15817, A	184	26	60.5	310	11	US-11-198-746-88	Sequence 88, Appl
112	27	62.8	355	11	US-11-087-099-9730	Sequence 9730, Ap	185	26	60.5	310	11	US-11-198-794-88	Sequence 88, Appl
113	27	62.8	362	11	US-11-079-463-6078	Sequence 6078, Ap	186	26	60.5	310	11	US-11-198-657-88	Sequence 88, Appl
114	27	62.8	373	11	US-11-096-568A-3352	Sequence 3352, Ap	187	26	60.5	311	11	US-11-096-568A-29304	Sequence 29304, A
115	27	62.8	384	11	US-11-139-041-326	Sequence 326, App	188	26	60.5	315	7	US-09-941-095-91	Sequence 91, Appl
116	27	62.8	384	11	US-11-139-041-333	Sequence 332, App	189	26	60.5	315	11	US-11-198-746-91	Sequence 91, Appl
117	27	62.8	384	11	US-11-139-041-333	Sequence 333, App	190	26	60.5	315	11	US-11-198-794-91	Sequence 91, Appl
118	27	62.8	392	11	US-11-087-099-4211	Sequence 4211, Ap	191	26	60.5	315	11	US-11-198-657-91	Sequence 91, Appl
119	27	62.8	404	11	US-11-069-642-115	Sequence 115, App	192	26	60.5	322	7	US-09-941-095-89	Sequence 89, Appl
120	27	62.8	411	11	US-11-169-041-206	Sequence 206, App	193	26	60.5	322	11	US-11-198-746-89	Sequence 89, Appl
121	27	62.8	411	11	US-11-100-640-22	Sequence 22, Appl	194	26	60.5	322	11	US-11-198-657-89	Sequence 89, Appl
122	27	62.8	464	11	US-11-251-304-2	Sequence 2, Appl	195	26	60.5	332	11	US-11-198-794-89	Sequence 89, Appl
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126	27	62.8	528	9	US-10-195-883-490	Sequence 490, App	199	26	60.5	345	11	US-11-096-568A-31638	Sequence 31638, A
127	27	62.8	528	9	US-10-195-888-490	Sequence 490, App	200	26	60.5	360	11	US-11-172-740-669	Sequence 669, App
128	27	62.8	528	9	US-10-195-889-490	Sequence 490, App	201	26	60.5	360	11	US-11-172-740-1528	Sequence 1528, Ap
129	27	62.8	531	11	US-11-096-568A-15816	Sequence 15816, A	202	26	60.5	369	11	US-11-096-568A-12822	Sequence 12822, A
130	27	62.8	532	11	US-11-188-298-7161	Sequence 7161, A	203	26	60.5	379	11	US-11-072-512-3298	Sequence 3298, Ap
131	27	62.8	539	11	US-11-188-298-6486	Sequence 6486, Ap	204	26	60.5	384	11	US-11-096-568A-23002	Sequence 23002, A
132	27	62.8	539	11	US-11-188-298-19684	Sequence 19684, A	205	26	60.5	388	11	US-11-079-463-7038	Sequence 7038, Ap
133	27	62.8	541	11	US-11-096-568A-15815	Sequence 15815, A	206	26	60.5	393	11	US-11-087-099-10885	Sequence 10885, A
134	27	62.8	543	9	US-10-453-372-756	Sequence 756, App	207	26	60.5	396	11	US-11-188-298-6723	Sequence 6723, Ap
135	27	62.8	547	11	US-11-203-526-26	Sequence 26, Appl	208	26	60.5	402	11	US-11-098-686-10827	Sequence 10827, A
136	27	62.8	548	9	US-10-453-372-754	Sequence 754, App	209	26	60.5	407	11	US-11-072-175-165	Sequence 165, App
137	27	62.8	548	9	US-10-453-372-768	Sequence 768, App	210	26	60.5	421	11	US-11-098-686-10215	Sequence 10215, A
138	27	62.8	555	9	US-10-453-372-764	Sequence 764, App	211	26	60.5	444	11	US-11-188-298-4499	Sequence 4499, Ap
139	27	62.8	565	11	US-11-045-004-1227	Sequence 1227, Ap	212	26	60.5	450	9	US-10-506-454-1213	Sequence 1213, Ap
140	27	62.8	766	9	US-10-453-372-752	Sequence 752, App	213	26	60.5	457	11	US-11-087-099-2903	Sequence 2903, Ap
141	27	62.8	1109	11	US-11-096-568A-29006	Sequence 29006, A	214	26	60.5	463	11	US-11-264-096-212	Sequence 212, App
142	27	62.8	1115	11	US-11-087-099-9860	Sequence 9860, Ap	215	26	60.5	468	11	US-11-087-099-11555	Sequence 11555, A
143	27	62.8	1137	11	US-11-087-099-9891	Sequence 9891, Ap	216	26	60.5	470	11	US-11-188-298-7546	Sequence 7546, Ap
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145	27	62.8	1237	11	US-11-096-568A-32521	Sequence 32521, A	218	26	60.5	501	11	US-11-188-298-17041	Sequence 17041, A
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148	27	62.8	1976	11	US-11-069-834-52	Sequence 52, Appl	221	26	60.5	521	11	US-11-188-298-11698	Sequence 11698, A
149	27	62.8	1976	11	US-11-069-834-54	Sequence 54, Appl	222	26	60.5	528	7	US-09-941-095-90	Sequence 90, Appl
150	27	62.8	2004	9	US-10-467-657-84	Sequence 84, Appl	223	26	60.5	528	11	US-11-198-746-90	Sequence 90, Appl
151	27	62.8	3113	9	US-10-467-657-6222	Sequence 6222, Ap	224	26	60.5	528	11	US-11-198-794-90	Sequence 90, Appl
152	27	62.8	3113	9	US-10-505-928-325	Sequence 325, App	225	26	60.5	528	11	US-11-198-657-90	Sequence 90, Appl
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160	26	60.5	188	11	US-11-229-769-314	Sequence 314, App	233	26	60.5	548	11	US-11-198-794-86	Sequence 86, Appl
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165	26	60.5	223	11	US-11-188-298-915	Sequence 915, App	238	26	60.5	557	11	US-11-188-298-8022	Sequence 8022, Ap
166	26	60.5	229	9	US-11-188-298-12710	Sequence 12710, A	239	26	60.5	557	11	US-11-188-298-9316	Sequence 9316, Ap
167	26	60.5	229	9	US-10-793-626-88	Sequence 88, Appl	240	26	60.5	565	11	US-11-127-877-68	Sequence 68, Appl
168	26	60.5	244	11	US-11-098-686-10165	Sequence 10165, A	240	26	60.5	565	11		



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243	26	60.5	576	11	US-11-137-465-64	Sequence 64, Appl	316	25	58.1	176	9	US-10-219-061-218	Sequence 218, App
244	26	60.5	592	11	US-11-106-672A-14	Sequence 14, Appl	317	25	58.1	176	9	US-10-219-062-218	Sequence 218, App
245	26	60.5	616	11	US-11-045-004-1892	Sequence 1892, Ap	318	25	58.1	176	9	US-10-219-064-218	Sequence 218, App
246	26	60.5	634	11	US-11-137-465-63	Sequence 63, Appl	319	25	58.1	176	9	US-10-233-134-218	Sequence 218, App
247	26	60.5	659	9	US-10-793-626-1596	Sequence 1596, Ap	320	25	58.1	176	9	US-10-137-873A-98	Sequence 98, Appl
248	26	60.5	686	11	US-11-079-463-6039	Sequence 6039, Ap	321	25	58.1	176	9	US-10-152-370-98	Sequence 98, Appl
249	26	60.5	695	7	US-09-941-095-87	Sequence 87, Appl	322	25	58.1	176	11	US-11-290-153-98	Sequence 98, Appl
250	26	60.5	695	11	US-11-198-746-87	Sequence 87, Appl	323	25	58.1	183	11	US-11-096-568A-6049	Sequence 6049, Ap
251	26	60.5	695	11	US-11-198-794-87	Sequence 87, Appl	324	25	58.1	183	11	US-11-045-004-459	Sequence 459, App
252	26	60.5	695	11	US-11-198-657-87	Sequence 87, Appl	325	25	58.1	188	11	US-11-036-797-37	Sequence 37, Appl
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255	26	60.5	745	11	US-11-087-099-1316	Sequence 1316, Ap	328	25	58.1	197	11	US-11-176-830-794	Sequence 794, App
256	26	60.5	758	11	US-11-087-099-7427	Sequence 7427, Ap	329	25	58.1	197	11	US-11-176-830-795	Sequence 795, App
257	26	60.5	808	9	US-10-523-503-24	Sequence 24, Appl	330	25	58.1	197	11	US-11-176-830-796	Sequence 796, App
258	26	60.5	830	11	US-11-242-730-3	Sequence 3, Appli	331	25	58.1	197	11	US-11-176-830-797	Sequence 797, App
259	26	60.5	832	7	US-09-941-095-4	Sequence 4, Appli	332	25	58.1	197	11	US-11-176-830-798	Sequence 798, App
260	26	60.5	832	11	US-11-065-943-100	Sequence 100, App	333	25	58.1	197	11	US-11-176-830-799	Sequence 799, App
261	26	60.5	832	11	US-11-007-797A-11	Sequence 11, Appl	334	25	58.1	197	11	US-11-176-830-800	Sequence 800, App
262	26	60.5	832	11	US-11-007-642B-11	Sequence 11, Appl	335	25	58.1	197	11	US-11-176-830-801	Sequence 801, App
263	26	60.5	832	11	US-11-198-746-4	Sequence 4, Appli	336	25	58.1	197	11	US-11-176-830-802	Sequence 802, App
264	26	60.5	832	11	US-11-198-794-4	Sequence 4, Appli	337	25	58.1	197	11	US-11-176-830-803	Sequence 803, App
265	26	60.5	832	11	US-11-242-730-1	Sequence 1, Appli	338	25	58.1	197	11	US-11-176-830-804	Sequence 804, App
266	26	60.5	832	11	US-11-198-657-4	Sequence 4, Appli	339	25	58.1	197	11	US-11-176-830-805	Sequence 805, App
267	26	60.5	832	11	US-11-198-657-8	Sequence 8, Appli	340	25	58.1	197	11	US-11-176-830-806	Sequence 806, App
268	26	60.5	832	11	US-11-005-559-26	Sequence 26, Appl	341	25	58.1	197	11	US-11-176-830-807	Sequence 807, App
269	26	60.5	832	11	US-11-005-559-28	Sequence 28, Appl	342	25	58.1	197	11	US-11-176-830-808	Sequence 808, App
270	26	60.5	832	11	US-11-005-559-30	Sequence 30, Appl	343	25	58.1	197	11	US-11-176-830-809	Sequence 809, App
271	26	60.5	833	7	US-09-941-095-8	Sequence 8, Appli	344	25	58.1	197	11	US-11-176-830-810	Sequence 810, App
272	26	60.5	833	7	US-09-941-095-85	Sequence 85, Appl	345	25	58.1	197	11	US-11-176-830-811	Sequence 811, App
273	26	60.5	833	11	US-11-198-746-8	Sequence 8, Appli	346	25	58.1	197	11	US-11-176-830-812	Sequence 812, App
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281	26	60.5	982	11	US-11-079-463-8232	Sequence 8232, Ap	354	25	58.1	197	11	US-11-176-830-820	Sequence 820, App
282	26	60.5	1007	9	US-10-467-657-8514	Sequence 8514, Ap	355	25	58.1	197	11	US-11-176-830-821	Sequence 821, App
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284	26	60.5	1099	11	US-11-213-326-10	Sequence 10, Appl	357	25	58.1	197	11	US-11-176-830-823	Sequence 823, App
285	26	60.5	1124	11	US-11-195-197-9	Sequence 9, Appli	358	25	58.1	197	11	US-11-176-830-824	Sequence 824, App
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287	26	60.5	1145	11	US-11-087-099-11401	Sequence 11401, A	360	25	58.1	197	11	US-11-176-830-826	Sequence 826, App
288	26	60.5	1156	11	US-11-087-099-4316	Sequence 4316, Ap	361	25	58.1	197	11	US-11-176-830-827	Sequence 827, App
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290	26	60.5	3475	11	US-11-087-099-10885	Sequence 10885, A	363	25	58.1	197	11	US-11-176-830-829	Sequence 829, App
291	26	60.5	5699	9	US-10-784-004-709	Sequence 709, App	364	25	58.1	197	11	US-11-176-830-830	Sequence 830, App
292	25	58.1	39	9	US-10-895-064-864	Sequence 864, App	365	25	58.1	197	11	US-11-176-830-831	Sequence 831, App
293	25	58.1	39	11	US-11-129-741-864	Sequence 864, App	366	25	58.1	197	11	US-11-176-830-832	Sequence 832, App
294	25	58.1	39	11	US-11-129-741-3861	Sequence 3861, Ap	367	25	58.1	197	11	US-11-176-830-833	Sequence 833, App
295	25	58.1	42	9	US-10-895-064-950	Sequence 950, App	368	25	58.1	197	11	US-11-176-830-834	Sequence 834, App
296	25	58.1	42	11	US-11-129-741-950	Sequence 950, App	369	25	58.1	197	11	US-11-176-830-835	Sequence 835, App
297	25	58.1	44	9	US-10-957-887B-56	Sequence 56, Appl	370	25	58.1	197	11	US-11-176-830-836	Sequence 836, App
298	25	58.1	101	11	US-11-098-686-10869	Sequence 10869, A	371	25	58.1	197	11	US-11-176-830-837	Sequence 837, App
299	25	58.1	113	9	US-10-845-413-284	Sequence 284, App	372	25	58.1	197	11	US-11-176-830-842	Sequence 842, App
300	25	58.1	113	9	US-10-845-413-285	Sequence 285, App	373	25	58.1	197	11	US-11-176-830-843	Sequence 843, App
301	25	58.1	113	9	US-10-845-413-286	Sequence 286, App	374	25	58.1	197	11	US-11-176-830-844	Sequence 844, App
302	25	58.1	113	9	US-10-845-413-312	Sequence 312, App	375	25	58.1	197	11	US-11-176-830-845	Sequence 845, App
303	25	58.1	113	9	US-10-845-413-331	Sequence 331, App	376	25	58.1	197	11	US-11-176-830-846	Sequence 846, App
304	25	58.1	133	9	US-10-467-657-38	Sequence 38, Appl	377	25	58.1	197	11	US-11-176-830-847	Sequence 847, App
305	25	58.1	133	9	US-10-467-657-8452	Sequence 8452, Ap	378	25	58.1	197	11	US-11-176-830-848	Sequence 848, App
306	25	58.1	136	11	US-11-079-463-5273	Sequence 5273, Ap	379	25	58.1	197	11	US-11-176-830-849	Sequence 849, App
307	25	58.1	138	9	US-10-793-626-1254	Sequence 1254, Ap	380	25	58.1	201	11	US-11-087-099-3908	Sequence 3908, Ap
308	25	58.1	138	11	US-11-079-463-6746	Sequence 6746, Ap	381	25	58.1	208	11	US-11-098-686-110	Sequence 110, App
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311	25	58.1	165	11	US-11-087-099-925	Sequence 925, App	384	25	58.1	219	11	US-11-040-595-14	Sequence 14, Appl
312	25	58.1	169	11	US-11-096-568A-17371	Sequence 17371, A	385	25	58.1	227	9	US-10-921-286B-17	Sequence 17, Appl
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388	25	58.1	238	11	US-11-100-183-14	Sequence 14, Appl	461	25	58.1	459	11	US-11-079-463-5558	Sequence 5558, Ap
389	25	58.1	239	11	US-11-156-084-165	Sequence 165, App	462	25	58.1	471	11	US-11-096-568A-10983	Sequence 10983, A
390	25	58.1	239	11	US-11-096-568A-33336	Sequence 33336, A	463	25	58.1	476	11	US-11-188-298-14178	Sequence 14178, A
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392	25	58.1	249	11	US-11-096-568A-6236	Sequence 6236, Ap	465	25	58.1	513	9	US-10-453-372-442	Sequence 442, Appl
393	25	58.1	250	11	US-11-096-568A-6048	Sequence 6048, Ap	466	25	58.1	515	11	US-11-199-233-6	Sequence 6, Appl
394	25	58.1	253	9	US-10-995-561-555	Sequence 555, App	467	25	58.1	520	11	US-11-052-554A-98	Sequence 98, Appl
395	25	58.1	257	11	US-11-096-568A-11406	Sequence 11406, A	468	25	58.1	534	11	US-11-188-298-8000	Sequence 8000, Ap
396	25	58.1	261	9	US-10-131-826A-546	Sequence 546, App	469	25	58.1	535	9	US-10-453-372-436	Sequence 436, App
397	25	58.1	261	9	US-10-063-703-138	Sequence 138, App	470	25	58.1	536	11	US-11-087-099-11686	Sequence 11686, A
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405	25	58.1	261	11	US-11-102-240-138	Sequence 138, App	478	25	58.1	580	8	US-10-505-928-181	Sequence 181, App
406	25	58.1	261	11	US-11-103-195-138	Sequence 138, App	479	25	58.1	580	11	US-11-188-298-20619	Sequence 20619, A
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412	25	58.1	266	11	US-11-096-568A-27128	Sequence 27128, A	485	25	58.1	676	9	US-10-453-372-440	Sequence 440, App
413	25	58.1	269	11	US-11-096-568A-20722	Sequence 20722, A	486	25	58.1	682	11	US-11-185-560-5	Sequence 5, Appl
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419	25	58.1	297	11	US-11-096-568A-33735	Sequence 33735, A	492	25	58.1	703	11	US-11-096-568A-30901	Sequence 30901, A
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422	25	58.1	302	11	US-11-096-568A-29924	Sequence 29924, A	495	25	58.1	734	11	US-11-096-568A-30900	Sequence 30900, A
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425	25	58.1	313	9	US-10-195-883-554	Sequence 554, App	498	25	58.1	737	9	US-10-453-372-448	Sequence 448, App
426	25	58.1	313	9	US-10-195-888-554	Sequence 554, App	499	25	58.1	737	9	US-10-453-372-450	Sequence 450, App
427	25	58.1	313	9	US-10-195-889-554	Sequence 554, App	500	25	58.1	737	9	US-10-453-372-452	Sequence 452, App
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429	25	58.1	315	11	US-11-010-795-28	Sequence 28, Appl	502	25	58.1	737	9	US-10-453-372-456	Sequence 456, App
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432	25	58.1	329	9	US-10-793-626-1460	Sequence 1460, Ap	505	25	58.1	753	11	US-11-188-298-7467	Sequence 7467, Ap
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434	25	58.1	337	11	US-11-087-099-2933	Sequence 2933, Ap	507	25	58.1	788	11	US-11-079-463-5927	Sequence 5927, Ap
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438	25	58.1	357	11	US-11-096-568A-33734	Sequence 33734, A	511	25	58.1	825	11	US-11-188-298-1365	Sequence 1365, Ap
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440	25	58.1	390	11	US-11-087-099-1025	Sequence 1025, Ap	513	25	58.1	837	11	US-11-096-568A-28530	Sequence 28530, A
441	25	58.1	391	11	US-11-087-099-702	Sequence 702, App	514	25	58.1	844	11	US-11-096-568A-28529	Sequence 28529, A
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443	25	58.1	394	11	US-11-087-099-3730	Sequence 3730, Ap	516	25	58.1	861	11	US-11-188-298-12347	Sequence 12347, A
444	25	58.1	394	11	US-11-087-099-5320	Sequence 5320, App	517	25	58.1	891	11	US-11-096-568A-28860	Sequence 28860, A
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446	25	58.1	397	11	US-11-087-099-8667	Sequence 8667, Ap	519	25	58.1	956	11	US-11-079-463-5853	Sequence 5853, Ap
447	25	58.1	397	11	US-11-045-004-762	Sequence 762, App	520	25	58.1	977	11	US-11-072-512-2552	Sequence 2552, Ap
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451	25	58.1	410	11	US-11-079-463-8609	Sequence 8609, Ap	524	25	58.1	1061	11	US-11-000-463-347	Sequence 347, App
452	25	58.1	421	9	US-10-793-626-144	Sequence 144, App	525	25	58.1	1061	11	US-11-124-367A-325	Sequence 325, App
453	25	58.1	424	11	US-11-079-463-9298	Sequence 9298, Ap	526	25	58.1	1091	11	US-11-000-463-348	Sequence 348, App
454	25	58.1	430	11	US-11-045-004-2343	Sequence 2343, Ap	527	25	58.1	1167	9	US-10-455-772-986	Sequence 986, App
455	25	58.1	436	9	US-10-467-657-7578	Sequence 7578, Ap	528	25	58.1	1167	9	US-10-455-772-990	Sequence 990, App
456	25	58.1	437	9	US-10-453-372-438	Sequence 438, App	529	25	58.1	1167	9	US-10-455-772-992	Sequence 992, App
457	25	58.1	446	11	US-11-096-568A-10985	Sequence 10985, A	530	25	58.1	1204	9	US-10-455-772-988	Sequence 988, App
458	25	58.1	453	11	US-11-096-568A-10984	Sequence 10984, A	531	25	58.1	1210	11	US-11-108-172-692	Sequence 692, App
459	25	58.1	453	11	US-11-264-096-2170	Sequence 2170, Ap	532	25	58.1	1238	11	US-11-078-735-21	Sequence 21, Appl

533	25	58.1	1238	11	US-11-050-346-66	Sequence 66, Appl	606	24	55.8	163	11	US-11-087-099-2200	Sequence 2200, Ap
534	25	58.1	1238	11	US-11-103-077-21	Sequence 21, Appl	607	24	55.8	163	11	US-11-079-463-6596	Sequence 6596, Ap
535	25	58.1	1238	11	US-11-058-066-21	Sequence 21, Appl	608	24	55.8	165	11	US-11-188-298-13085	Sequence 13085, A
536	25	58.1	1240	11	US-11-096-568A-30789	Sequence 30789, A	609	24	55.8	167	9	US-10-506-454-440	Sequence 440, App
537	25	58.1	1257	11	US-11-096-568A-30788	Sequence 30788, A	610	24	55.8	169	10	US-11-254-182-21	Sequence 21, Appl
538	25	58.1	1285	11	US-11-079-463-9072	Sequence 3078, Ap	611	24	55.8	169	11	US-11-182-908-21	Sequence 21, Appl
539	25	58.1	1286	11	US-11-096-568A-30787	Sequence 30787, A	612	24	55.8	171	11	US-11-079-463-8876	Sequence 8876, Ap
540	25	58.1	1404	9	US-10-878-556A-169	Sequence 169, App	613	24	55.8	174	11	US-11-079-463-8015	Sequence 8015, Ap
541	25	58.1	1419	11	US-11-124-367A-324	Sequence 324, App	614	24	55.8	175	9	US-10-873-528-90	Sequence 90, Appl
542	25	58.1	1428	11	US-11-124-367A-320	Sequence 320, App	615	24	55.8	176	11	US-11-098-686-10991	Sequence 10991, A
543	25	58.1	1515	9	US-10-915-002-292	Sequence 292, App	616	24	55.8	179	11	US-11-188-298-9668	Sequence 9668, Ap
544	25	58.1	1548	11	US-11-108-172-1095	Sequence 1095, Ap	617	24	55.8	181	11	US-11-188-298-880	Sequence 880, App
545	25	58.1	1613	9	US-10-055-877-145	Sequence 145, App	618	24	55.8	184	11	US-11-087-099-7622	Sequence 7622, App
546	25	58.1	1637	9	US-10-055-877-144	Sequence 144, App	619	24	55.8	194	11	US-11-108-172-1126	Sequence 1126, Ap
547	25	58.1	1652	9	US-10-995-561-663	Sequence 664, App	620	24	55.8	197	11	US-11-087-099-4852	Sequence 4852, Ap
548	25	58.1	1732	9	US-10-055-877-147	Sequence 147, App	621	24	55.8	201	9	US-10-980-388-83	Sequence 83, Appl
549	25	58.1	1897	11	US-11-096-568A-28325	Sequence 28325, A	622	24	55.8	203	11	US-11-096-568A-22000	Sequence 22000, A
550	25	58.1	1938	9	US-10-995-561-661	Sequence 661, App	623	24	55.8	207	11	US-11-096-568A-26695	Sequence 26695, A
551	25	58.1	1938	9	US-10-995-561-662	Sequence 662, App	624	24	55.8	210	11	US-11-212-443-169	Sequence 169, App
552	25	58.1	1954	9	US-10-995-561-660	Sequence 660, App	625	24	55.8	211	11	US-11-087-099-6884	Sequence 6884, Ap
553	25	58.1	1972	9	US-10-995-561-664	Sequence 664, App	626	24	55.8	212	7	US-09-978-360A-426	Sequence 426, App
554	25	58.1	1972	9	US-10-995-561-666	Sequence 666, App	627	24	55.8	212	11	US-11-188-298-15208	Sequence 15208, A
555	25	58.1	2048	11	US-11-285-818-12	Sequence 12, Appl	628	24	55.8	216	11	US-11-183-664-16	Sequence 16, Appl
556	25	58.1	2057	11	US-11-285-818-10	Sequence 10, Appl	629	24	55.8	219	11	US-11-096-568A-17345	Sequence 17345, A
557	25	58.1	2058	11	US-11-072-173-188	Sequence 188, Appl	630	24	55.8	222	11	US-11-212-443-174	Sequence 174, App
558	25	58.1	2058	11	US-11-285-818-17	Sequence 17, Appl	631	24	55.8	222	11	US-11-212-443-175	Sequence 175, App
559	25	58.1	2065	11	US-11-096-568A-28324	Sequence 28324, A	632	24	55.8	222	11	US-11-212-443-176	Sequence 176, App
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561	25	58.1	2312	11	US-11-126-313-34	Sequence 34, Appl	634	24	55.8	226	11	US-11-087-099-3305	Sequence 3305, Ap
562	25	58.1	2617	9	US-10-453-372-740	Sequence 740, App	635	24	55.8	226	11	US-11-087-099-16531	Sequence 16531, A
563	25	58.1	2767	11	US-11-100-640-38	Sequence 38, Appl	636	24	55.8	227	9	US-10-467-657-21279	Sequence 21279, Ap
564	25	58.1	2768	9	US-10-510-101-72	Sequence 72, Appl	637	24	55.8	227	11	US-11-072-512-2179	Sequence 2179, Ap
565	25	58.1	3353	11	US-11-037-243-64	Sequence 64, Appl	638	24	55.8	227	11	US-11-096-568A-7037	Sequence 7037, Ap
566	25	58.1	5024	9	US-10-793-626-2964	Sequence 2964, Ap	639	24	55.8	228	11	US-11-172-740-1665	Sequence 1665, Ap
567	24	55.8	42	11	US-11-226-657-170	Sequence 170, App	640	24	55.8	229	11	US-11-045-004-2041	Sequence 2041, Ap
568	24	55.8	52	9	US-10-467-657-1696	Sequence 1696, Ap	641	24	55.8	234	11	US-11-079-463-8572	Sequence 8572, Ap
569	24	55.8	54	9	US-10-485-517-267	Sequence 267, App	642	24	55.8	238	11	US-11-100-183-22	Sequence 22, Appl
570	24	55.8	93	11	US-11-079-463-7513	Sequence 7513, Ap	643	24	55.8	239	11	US-11-100-183-25	Sequence 25, Appl
571	24	55.8	93	11	US-11-079-463-10343	Sequence 10343, A	644	24	55.8	240	11	US-11-100-183-17	Sequence 17, Appl
572	24	55.8	105	11	US-11-188-298-7033	Sequence 7033, Ap	645	24	55.8	240	11	US-11-212-443-170	Sequence 170, App
573	24	55.8	105	11	US-11-232-408A-34	Sequence 34, Appl	646	24	55.8	241	11	US-11-100-183-19	Sequence 19, Appl
574	24	55.8	107	9	US-10-678-790-61	Sequence 61, Appl	647	24	55.8	241	11	US-11-045-004-1355	Sequence 1355, Ap
575	24	55.8	111	9	US-10-481-935A-259	Sequence 259, App	648	24	55.8	242	11	US-11-045-004-1421	Sequence 1421, Ap
576	24	55.8	113	9	US-10-845-413-280	Sequence 280, App	649	24	55.8	245	11	US-11-079-463-9676	Sequence 9676, Ap
577	24	55.8	113	9	US-10-845-413-281	Sequence 281, App	650	24	55.8	249	9	US-10-506-454-139	Sequence 139, App
578	24	55.8	113	9	US-10-845-413-282	Sequence 282, App	651	24	55.8	249	11	US-11-096-568A-23045	Sequence 23045, A
579	24	55.8	113	9	US-10-845-413-283	Sequence 283, App	652	24	55.8	250	11	US-11-096-568A-1626	Sequence 1626, Ap
580	24	55.8	113	9	US-10-845-413-289	Sequence 289, App	653	24	55.8	251	11	US-11-009-658-36	Sequence 36, Appl
581	24	55.8	113	9	US-10-845-413-291	Sequence 291, App	654	24	55.8	258	11	US-11-172-740-1564	Sequence 1664, Ap
582	24	55.8	113	9	US-10-845-413-294	Sequence 294, App	655	24	55.8	259	11	US-11-079-463-6775	Sequence 6775, Ap
583	24	55.8	113	9	US-10-845-413-296	Sequence 296, App	656	24	55.8	262	11	US-11-072-512-2808	Sequence 2808, Ap
584	24	55.8	113	9	US-10-845-413-308	Sequence 308, App	657	24	55.8	268	11	US-11-218-272-12	Sequence 12, Appl
585	24	55.8	113	9	US-10-845-413-311	Sequence 311, App	658	24	55.8	269	11	US-11-096-568A-26694	Sequence 26694, A
586	24	55.8	113	9	US-10-941-717A-10	Sequence 10, Appl	659	24	55.8	274	8	US-10-511-937-2546	Sequence 2546, Ap
587	24	55.8	119	11	US-11-072-512-2375	Sequence 2375, Ap	660	24	55.8	274	11	US-11-072-512-3079	Sequence 3079, A
588	24	55.8	122	11	US-10-678-790-60	Sequence 60, Appl	661	24	55.8	274	11	US-11-188-298-19599	Sequence 19599, A
589	24	55.8	132	11	US-11-096-568A-6433	Sequence 6433, Ap	662	24	55.8	279	9	US-11-087-099-4795	Sequence 4795, Ap
590	24	55.8	132	11	US-11-087-099-10155	Sequence 10155, A	663	24	55.8	281	9	US-10-481-935A-32	Sequence 32, Appl
591	24	55.8	132	11	US-11-087-099-10155	Sequence 10155, A	664	24	55.8	284	11	US-11-096-568A-4083	Sequence 4083, Ap
592	24	55.8	134	9	US-10-793-626-438	Sequence 438, App	665	24	55.8	286	9	US-10-793-626-2192	Sequence 2192, Ap
593	24	55.8	135	11	US-11-087-099-8998	Sequence 8998, Ap	666	24	55.8	286	9	US-10-481-935A-33	Sequence 33, Appl
594	24	55.8	136	7	US-09-978-360A-744	Sequence 744, App	667	24	55.8	286	11	US-11-096-568A-1625	Sequence 1625, Ap
595	24	55.8	139	11	US-11-079-463-8838	Sequence 8838, Ap	668	24	55.8	286	11	US-11-096-568A-33862	Sequence 33862, A
596	24	55.8	140	11	US-11-087-099-2015	Sequence 2015, Ap	669	24	55.8	287	11	US-11-087-099-3601	Sequence 3601, Ap
597	24	55.8	141	11	US-11-096-568A-13756	Sequence 13756, A	670	24	55.8	288	11	US-11-087-099-10962	Sequence 10962, A
598	24	55.8	143	11	US-11-158-655-8	Sequence 8, Appl	671	24	55.8	290	11	US-11-079-463-7851	Sequence 7851, Ap
599	24	55.8	144	11	US-11-096-568A-6432	Sequence 6432, Ap	672	24	55.8	291	9	US-10-481-935A-36	Sequence 36, Appl
600	24	55.8	144	11	US-11-045-004-1670	Sequence 1670, Ap	673	24	55.8	291	9	US-10-481-935A-39	Sequence 39, Appl
601	24	55.8	147	11	US-11-096-568A-23047	Sequence 23047, A	674	24	55.8	291	11	US-11-065-943-50	Sequence 50, Appl
602	24	55.8	153	11	US-11-087-099-11265	Sequence 11265, A	675	24	55.8	294	11	US-11-188-298-10375	Sequence 10375, A
603	24	55.8	160	11	US-11-087-099-785	Sequence 785, App	676	24	55.8	295	11	US-11-188-298-16043	Sequence 16043, A
604	24	55.8	160	11	US-11-087-099-8405	Sequence 8405, Ap	677	24	55.8	296	9	US-10-481-935A-34	Sequence 34, Appl
605	24	55.8	161	9	US-10-986-405-230	Sequence 230, App	678	24	55.8	296	9	US-10-481-935A-35	Sequence 35, Appl

679	24	55.8	296	9	US-10-481-935A-37	Sequence 37, Appl	752	24	55.8	387	11	US-11-096-568A-25269	Sequence 25269, A
680	24	55.8	296	9	US-10-481-935A-40	Sequence 40, Appl	753	24	55.8	388	9	US-10-527-500-5	Sequence 5, Appl
681	24	55.8	296	9	US-10-525-907-52	Sequence 52, Appl	754	24	55.8	389	11	US-11-188-298-1081	Sequence 1081, Ap
682	24	55.8	298	11	US-11-096-568A-21999	Sequence 21999, A	755	24	55.8	391	11	US-11-087-099-11488	Sequence 11488, A
683	24	55.8	299	11	US-11-096-568A-18196	Sequence 18196, A	756	24	55.8	392	9	US-10-793-626-2794	Sequence 2794, Ap
684	24	55.8	300	11	US-11-087-099-5090	Sequence 5090, Ap	757	24	55.8	392	9	US-10-793-626-2874	Sequence 2874, Ap
685	24	55.8	300	11	US-11-096-568A-9726	Sequence 9726, Ap	758	24	55.8	393	11	US-11-111-239-8	Sequence 8, Appl
686	24	55.8	301	9	US-10-481-935A-38	Sequence 38, Appl	759	24	55.8	394	9	US-10-506-454-156	Sequence 156, App
687	24	55.8	301	9	US-10-481-935A-41	Sequence 41, Appl	760	24	55.8	394	11	US-11-087-099-11230	Sequence 11230, A
688	24	55.8	301	11	US-11-096-568A-4082	Sequence 4082, Ap	761	24	55.8	395	11	US-11-087-099-5231	Sequence 5231, Ap
689	24	55.8	301	11	US-11-096-568A-18195	Sequence 18195, A	762	24	55.8	395	11	US-11-188-298-3141	Sequence 3141, Ap
690	24	55.8	302	11	US-11-096-568A-17344	Sequence 17344, A	763	24	55.8	396	11	US-11-087-099-9889	Sequence 9889, Ap
691	24	55.8	302	11	US-11-045-004-2579	Sequence 2579, Ap	764	24	55.8	397	11	US-11-152-569-8	Sequence 8, Appl
692	24	55.8	303	11	US-11-172-740-74	Sequence 74, Appl	765	24	55.8	397	11	US-11-079-463-6449	Sequence 6449, Ap
693	24	55.8	303	11	US-11-172-740-75	Sequence 75, Appl	766	24	55.8	399	9	US-10-517-939-124	Sequence 124, App
694	24	55.8	303	11	US-11-172-740-77	Sequence 77, Appl	767	24	55.8	399	11	US-11-111-239-10	Sequence 10, Appl
695	24	55.8	307	11	US-11-096-568A-4081	Sequence 4081, Ap	768	24	55.8	402	11	US-11-188-298-7863	Sequence 7863, Ap
696	24	55.8	308	11	US-11-045-004-647	Sequence 647, App	769	24	55.8	402	11	US-11-188-298-14964	Sequence 14964, A
697	24	55.8	310	9	US-10-506-454-396	Sequence 396, Appl	770	24	55.8	405	11	US-11-096-568A-27639	Sequence 27639, A
698	24	55.8	310	11	US-11-178-485-2	Sequence 2, Appl	771	24	55.8	405	11	US-11-096-568A-32155	Sequence 32155, A
699	24	55.8	312	11	US-11-188-298-21947	Sequence 21947, A	772	24	55.8	406	11	US-11-096-568A-7180	Sequence 7180, Ap
700	24	55.8	315	11	US-11-087-099-5820	Sequence 9820, Ap	773	24	55.8	406	11	US-11-096-568A-9725	Sequence 9725, Ap
701	24	55.8	315	11	US-11-096-568A-18194	Sequence 18194, A	774	24	55.8	407	9	US-10-517-939-12	Sequence 12, Appl
702	24	55.8	317	11	US-11-172-740-73	Sequence 73, Appl	775	24	55.8	407	9	US-10-517-939-68	Sequence 68, Appl
703	24	55.8	317	11	US-11-172-740-76	Sequence 76, Appl	776	24	55.8	407	9	US-10-517-939-316	Sequence 316, App
704	24	55.8	319	11	US-11-096-568A-18403	Sequence 18403, A	777	24	55.8	408	9	US-10-467-657-7592	Sequence 7592, Ap
705	24	55.8	320	11	US-11-096-568A-27640	Sequence 27640, A	778	24	55.8	408	9	US-10-467-657-8366	Sequence 8366, Ap
706	24	55.8	323	9	US-10-724-598-10	Sequence 10, Appl	779	24	55.8	410	11	US-11-087-099-1691	Sequence 1691, Ap
707	24	55.8	324	11	US-11-087-099-4100	Sequence 4100, Ap	780	24	55.8	410	11	US-11-096-568A-20785	Sequence 20785, A
708	24	55.8	325	11	US-11-096-568A-25271	Sequence 25271, A	781	24	55.8	414	11	US-11-096-568A-20784	Sequence 20784, A
709	24	55.8	326	9	US-10-467-657-7224	Sequence 7224, Ap	782	24	55.8	416	9	US-10-467-657-5284	Sequence 5284, Ap
710	24	55.8	326	11	US-11-096-568A-1624	Sequence 1624, Ap	783	24	55.8	416	11	US-11-098-686-10509	Sequence 10509, A
711	24	55.8	326	11	US-11-096-568A-26693	Sequence 26693, A	784	24	55.8	416	11	US-11-072-512-2096	Sequence 2096, Ap
712	24	55.8	326	11	US-11-096-568A-33861	Sequence 33861, A	785	24	55.8	418	11	US-11-079-463-8423	Sequence 8423, Ap
713	24	55.8	327	11	US-11-096-568A-33860	Sequence 33860, A	786	24	55.8	420	9	US-10-506-454-559	Sequence 559, App
714	24	55.8	327	11	US-11-045-004-1432	Sequence 1432, Ap	787	24	55.8	420	11	US-11-087-099-6901	Sequence 6901, Ap
715	24	55.8	330	11	US-11-096-568A-17343	Sequence 17343, A	788	24	55.8	423	11	US-11-188-298-15051	Sequence 15051, A
716	24	55.8	331	9	US-10-517-939-50	Sequence 50, Appl	789	24	55.8	423	11	US-11-188-298-19627	Sequence 19627, A
717	24	55.8	331	9	US-10-517-939-266	Sequence 266, Appl	790	24	55.8	423	11	US-11-045-004-554	Sequence 554, App
718	24	55.8	331	11	US-11-087-099-8831	Sequence 8831, Ap	791	24	55.8	425	11	US-11-096-568A-20783	Sequence 20783, A
719	24	55.8	332	11	US-11-096-568A-16504	Sequence 16504, A	792	24	55.8	426	11	US-11-087-099-6894	Sequence 6894, Ap
720	24	55.8	333	9	US-10-517-939-202	Sequence 202, App	793	24	55.8	426	11	US-11-188-298-8052	Sequence 8052, Ap
721	24	55.8	333	9	US-10-517-939-294	Sequence 294, Ap	794	24	55.8	428	11	US-11-216-267-38	Sequence 38, Appl
722	24	55.8	334	11	US-11-079-463-7790	Sequence 7790, Ap	795	24	55.8	428	11	US-11-232-382-38	Sequence 38, Appl
723	24	55.8	335	11	US-11-188-298-12990	Sequence 12990, A	796	24	55.8	428	11	US-11-045-004-410	Sequence 410, App
724	24	55.8	336	11	US-11-087-099-6092	Sequence 6092, Ap	797	24	55.8	430	8	US-10-505-928-127	Sequence 127, App
725	24	55.8	336	11	US-11-087-099-7384	Sequence 7384, Ap	798	24	55.8	430	9	US-10-506-454-1573	Sequence 1573, Ap
726	24	55.8	337	11	US-11-087-099-3273	Sequence 3273, Ap	799	24	55.8	431	11	US-11-031-206-200	Sequence 200, App
727	24	55.8	338	11	US-11-188-298-20263	Sequence 20263, A	800	24	55.8	432	11	US-11-045-004-172	Sequence 172, App
728	24	55.8	342	9	US-10-506-454-1297	Sequence 1297, Ap	801	24	55.8	433	11	US-11-087-099-9015	Sequence 9015, Ap
729	24	55.8	343	11	US-11-207-626A-24	Sequence 24, Appl	802	24	55.8	434	11	US-11-087-099-3939	Sequence 3939, Ap
730	24	55.8	343	11	US-11-188-298-10427	Sequence 10427, A	803	24	55.8	434	11	US-11-096-568A-9724	Sequence 9724, Ap
731	24	55.8	343	11	US-11-045-004-2213	Sequence 2213, Ap	804	24	55.8	442	11	US-11-096-568A-32154	Sequence 32154, A
732	24	55.8	355	11	US-11-206-587-2	Sequence 2, Appl	805	24	55.8	445	11	US-11-087-099-10524	Sequence 10524, A
733	24	55.8	358	11	US-11-096-568A-25270	Sequence 25270, A	806	24	55.8	446	11	US-11-096-568A-32153	Sequence 32153, A
734	24	55.8	363	11	US-11-111-239-6	Sequence 6, Appl	807	24	55.8	447	11	US-11-079-463-10033	Sequence 10033, A
735	24	55.8	364	9	US-10-237-813-10	Sequence 10, Appl	808	24	55.8	451	11	US-11-188-298-13702	Sequence 13702, A
736	24	55.8	367	11	US-11-096-568A-7182	Sequence 7182, Ap	809	24	55.8	452	11	US-11-088-686-10713	Sequence 10713, A
737	24	55.8	368	11	US-11-079-463-6391	Sequence 6391, Ap	810	24	55.8	452	11	US-11-209-388-20	Sequence 20, Appl
738	24	55.8	368	11	US-11-079-463-9461	Sequence 9461, Ap	811	24	55.8	452	11	US-11-079-463-6551	Sequence 6551, Ap
739	24	55.8	371	11	US-11-072-512-2994	Sequence 2994, Ap	812	24	55.8	452	11	US-11-045-004-2456	Sequence 2456, Ap
740	24	55.8	372	11	US-11-188-298-15526	Sequence 15526, A	813	24	55.8	459	9	US-10-467-657-2368	Sequence 2368, Ap
741	24	55.8	375	11	US-11-188-298-8393	Sequence 8393, Ap	814	24	55.8	459	9	US-10-644-807-216	Sequence 216, App
742	24	55.8	376	9	US-10-454-437-412	Sequence 412, App	815	24	55.8	460	9	US-10-481-935A-110	Sequence 110, App
743	24	55.8	376	11	US-11-172-740-780	Sequence 780, App	816	24	55.8	461	11	US-11-054-385-5	Sequence 6, Appl
744	24	55.8	377	11	US-11-087-099-6761	Sequence 6761, Ap	817	24	55.8	461	11	US-11-096-568A-27638	Sequence 27638, A
745	24	55.8	377	11	US-11-188-298-17198	Sequence 17198, A	818	24	55.8	463	11	US-11-079-463-5520	Sequence 5520, Ap
746	24	55.8	378	11	US-11-188-298-17787	Sequence 17787, A	819	24	55.8	463	11	US-11-087-099-7110	Sequence 7110, Ap
747	24	55.8	379	11	US-11-045-004-681	Sequence 681, App	820	24	55.8	471	9	US-10-770-726-68	Sequence 68, Appl
748	24	55.8	381	11	US-11-096-568A-7181	Sequence 7181, Ap	821	24	55.8	471	11	US-11-152-366-31	Sequence 31, Appl
749	24	55.8	384	11	US-11-087-099-11411	Sequence 11411, A	822	24	55.8	471	11	US-11-087-099-11445	Sequence 11445, A
750	24	55.8	385	11	US-11-052-554A-132	Sequence 132, App	823	24	55.8	471	11	US-11-188-298-10558	Sequence 10558, A
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826	24	55.8	472	11	US-11-087-099-10553	Sequence 10553, A	899	24	55.8	630	11	US-11-188-298-8854	Sequence 8854, App
827	24	55.8	473	11	US-11-152-366-32	Sequence 32, Appl	900	24	55.8	632	11	US-11-079-463-8469	Sequence 8469, App
828	24	55.8	473	11	US-11-087-099-528	Sequence 528, App	901	24	55.8	640	11	US-11-188-298-6815	Sequence 6815, App
829	24	55.8	473	11	US-11-087-099-8140	Sequence 8140, App	902	24	55.8	642	8	US-10-505-928-259	Sequence 259, App
830	24	55.8	474	11	US-11-087-099-3692	Sequence 3692, App	903	24	55.8	642	11	US-11-072-175-1172	Sequence 172, App
831	24	55.8	475	11	US-11-087-099-1613	Sequence 1613, App	904	24	55.8	642	11	US-11-188-298-4062	Sequence 4062, App
832	24	55.8	475	11	US-11-087-099-1613	Sequence 1613, App	905	24	55.8	645	11	US-11-154-337-13	Sequence 13, Appl
833	24	55.8	476	11	US-11-152-569-21	Sequence 21, Appl	906	24	55.8	645	11	US-11-223-361-13	Sequence 13, Appl
834	24	55.8	476	11	US-11-096-568A-27606	Sequence 27606, A	907	24	55.8	645	11	US-11-213-557-1	Sequence 1, Appl
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836	24	55.8	477	9	US-10-524-972-106	Sequence 106, App	909	24	55.8	645	11	US-11-234-586-13	Sequence 13, Appl
837	24	55.8	477	11	US-11-098-686-10915	Sequence 10915, A	910	24	55.8	664	11	US-11-080-991-40	Sequence 40, Appl
838	24	55.8	477	11	US-11-087-099-311	Sequence 311, App	911	24	55.8	672	11	US-11-079-463-9531	Sequence 9531, App
839	24	55.8	480	9	US-10-821-234-886	Sequence 886, App	912	24	55.8	672	11	US-11-288-493-26	Sequence 26, Appl
840	24	55.8	480	11	US-11-132-142-6	Sequence 6, Appl	913	24	55.8	673	11	US-11-188-298-1612	Sequence 1612, App
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843	24	55.8	481	11	US-11-087-099-9582	Sequence 9582, App	916	24	55.8	687	11	US-11-212-443-173	Sequence 173, App
844	24	55.8	489	11	US-11-124-607-12	Sequence 12, Appl	917	24	55.8	690	11	US-11-212-443-171	Sequence 171, App
845	24	55.8	490	11	US-11-087-099-5309	Sequence 5309, App	918	24	55.8	690	11	US-11-212-443-172	Sequence 172, App
846	24	55.8	490	11	US-11-188-298-9166	Sequence 9166, App	919	24	55.8	691	11	US-11-098-686-11189	Sequence 11189, A
847	24	55.8	496	11	US-11-188-298-7126	Sequence 7126, App	920	24	55.8	692	11	US-11-024-959-486	Sequence 486, App
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855	24	55.8	502	11	US-11-188-298-19312	Sequence 19312, A	928	24	55.8	710	11	US-11-212-443-28	Sequence 28, Appl
856	24	55.8	506	11	US-11-096-568A-12267	Sequence 12267, A	929	24	55.8	710	11	US-11-212-443-30	Sequence 30, Appl
857	24	55.8	510	11	US-11-194-246-442	Sequence 442, App	930	24	55.8	721	11	US-11-186-284-67	Sequence 67, Appl
858	24	55.8	511	11	US-11-055-822-698	Sequence 698, App	931	24	55.8	729	11	US-11-096-568A-19858	Sequence 19858, A
859	24	55.8	513	9	US-10-915-002-260	Sequence 260, App	932	24	55.8	741	11	US-11-088-306-10	Sequence 10, Appl
860	24	55.8	514	9	US-10-821-234-998	Sequence 998, App	933	24	55.8	741	11	US-11-188-298-8040	Sequence 8040, App
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864	24	55.8	516	11	US-11-087-099-6982	Sequence 6982, App	937	24	55.8	772	11	US-11-087-099-5768	Sequence 5768, App
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870	24	55.8	521	11	US-11-144-947-392	Sequence 392, App	943	24	55.8	834	7	US-09-941-095-6	Sequence 6, Appl
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881	24	55.8	543	11	US-11-188-298-19512	Sequence 19512, A	954	24	55.8	860	11	US-11-172-410-2	Sequence 2, Appl
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886	24	55.8	553	11	US-11-188-298-4058	Sequence 4058, App	959	24	55.8	918	9	US-10-995-561-981	Sequence 981, App
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971 24 55.8 1085 9 US-10-501-035-282 Sequence 282, App  
972 24 55.8 1208 11 US-11-115-639-46 Sequence 46, Appl  
973 24 55.8 1208 11 US-11-115-639-47 Sequence 47, Appl  
974 24 55.8 1208 11 US-11-115-639-48 Sequence 48, Appl  
975 24 55.8 1224 11 US-11-096-568A-27547 Sequence 27547, A  
976 24 55.8 1235 11 US-11-045-004-1385 Sequence 1385, Ap  
977 24 55.8 1236 11 US-11-096-568A-27546 Sequence 27546, A  
978 24 55.8 1240 11 US-11-096-568A-27545 Sequence 27545, A  
979 24 55.8 1248 11 US-11-079-463-7695 Sequence 7695, Ap  
980 24 55.8 1255 9 US-10-770-726-62 Sequence 62, Appl  
981 24 55.8 1255 11 US-11-022-562-213 Sequence 213, App  
982 24 55.8 1255 11 US-11-113-202-10 Sequence 10, Appl  
983 24 55.8 1255 11 US-11-033-039-553 Sequence 553, App  
984 24 55.8 1255 11 US-11-155-288-9 Sequence 9, Appli  
985 24 55.8 1255 11 US-11-202-516-4 Sequence 4, Appli  
986 24 55.8 1255 11 US-11-175-405-2 Sequence 2, Appli  
987 24 55.8 1258 11 US-11-033-039-930 Sequence 930, App  
988 24 55.8 1272 9 US-10-501-035-313 Sequence 313, App  
989 24 55.8 1323 9 US-10-517-939-312 Sequence 312, App  
990 24 55.8 1359 11 US-11-152-569-20 Sequence 20, Appl  
991 24 55.8 1405 9 US-10-995-561-529 Sequence 529, App  
992 24 55.8 1406 9 US-10-995-561-530 Sequence 530, App  
993 24 55.8 1432 10 US-11-301-924-18 Sequence 18, Appl  
994 24 55.8 1436 9 US-10-995-561-531 Sequence 531, App  
995 24 55.8 1451 11 US-11-046-346-1 Sequence 1, Appli  
996 24 55.8 1517 11 US-11-096-568A-27856 Sequence 27856, A  
997 24 55.8 1518 11 US-11-096-568A-27855 Sequence 27855, A  
998 24 55.8 1522 11 US-11-096-568A-27800 Sequence 27800, A  
999 24 55.8 1523 11 US-11-096-568A-27599 Sequence 27599, A  
1000 24 55.8 1678 11 US-11-124-367A-340 Sequence 340, App

ALIGNMENTS

RESULT 1  
US-10-853-807A-46  
; Sequence 46, Application US/10853807A  
; Publication No. US20060034860A1  
; GENERAL INFORMATION:  
; APPLICANT: Hybrigenics  
; TITLE OF INVENTION: Protein-protein interactions in Human Immunodeficiency Virus  
; FILE REFERENCE: B5055AA  
; CURRENT APPLICATION NUMBER: US/10/853,807A  
; CURRENT FILING DATE: 2004-05-26  
; PRIOR APPLICATION NUMBER: US 60/333,346  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: US 60/385,132  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: PCT/EP 02/13868  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: Homosapiens  
; FEATURE:  
; OTHER INFORMATION: Translation of SEQ ID No23  
US-10-853-807A-46

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Best Local Similarity 100.0%; Pred. No. 0.094; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 238 NLQLMDRV 246

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US-10-853-807A-45  
; Sequence 45, Application US/10853807A

; Publication No. US20060034860A1  
; GENERAL INFORMATION:  
; APPLICANT: Hybrigenics  
; TITLE OF INVENTION: Protein-protein interactions in Human Immunodeficiency Virus  
; FILE REFERENCE: B5055AA  
; CURRENT APPLICATION NUMBER: US/10/853,807A  
; CURRENT FILING DATE: 2004-05-26  
; PRIOR APPLICATION NUMBER: US 60/333,346  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: US 60/385,132  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: PCT/EP 02/13868  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 45  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Homosapiens  
; FEATURE:  
; OTHER INFORMATION: Translation of SEQ ID No22  
US-10-853-807A-45

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Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
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Db 237 NLQLMDRV 245

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US-10-878-556A-40  
; Sequence 40, Application US/10878556A  
; Publication No. US20050266399A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffmann La-Roche Inc.  
; TITLE OF INVENTION: HCV regulated protein expression  
; FILE REFERENCE: 21762  
; CURRENT APPLICATION NUMBER: US/10/878,556A  
; CURRENT FILING DATE: 2004-06-28  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: sw\_hum/lf33\_human  
; DATABASE ENTRY DATE: 2000-05-30  
US-10-878-556A-40

Query Match 100.0%; Score 43; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 242 NLQLMDRV 250

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US-11-096-568A-33949  
; Sequence 33949, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01

; NUMBER OF SEQ ID NOS: 34471  
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; LENGTH: 260  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(260)  
; OTHER INFORMATION: Ceres Seq. ID no. 13604603  
US-11-096-568A-33949

Query Match 83.7%; Score 36; DB 11; Length 260;  
Best Local Similarity 87.5%; Pred. No. 2.6; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 95 LQLLMDRI 102

RESULT 5  
US-11-096-568A-33948  
; Sequence 33948, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 33948  
; LENGTH: 311  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
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; OTHER INFORMATION: Ceres Seq. ID no. 13604602  
US-11-096-568A-33948

Query Match 83.7%; Score 36; DB 11; Length 311;  
Best Local Similarity 87.5%; Pred. No. 3.2; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 146 LQLLMDRI 153

RESULT 6  
US-11-096-568A-33947  
; Sequence 33947, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 33947  
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; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
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; NAME/KEY: misc feature  
; LOCATION: (1)..(345)  
; OTHER INFORMATION: Ceres Seq. ID no. 13604601  
US-11-096-568A-33947

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Best Local Similarity 87.5%; Pred. No. 3.6; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9  
| | | | |  
Db 180 LQLLMDRI 187

RESULT 7  
US-11-096-568A-19252  
; Sequence 19252, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 19252  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(310)  
; OTHER INFORMATION: Ceres Seq. ID no. 12372216  
US-11-096-568A-19252

Query Match 79.1%; Score 34; DB 11; Length 310;  
Best Local Similarity 77.8%; Pred. No. 8.7; Indels 1; Gaps 0;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 295 NAKLLMDRV 303

RESULT 8  
US-11-096-568A-19251  
; Sequence 19251, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 19251  
; LENGTH: 348  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(348)  
; OTHER INFORMATION: Ceres Seq. ID no. 12372215  
US-11-096-568A-19251

Query Match 79.1%; Score 34; DB 11; Length 348;  
Best Local Similarity 77.8%; Pred. No. 10; Indels 1; Gaps 0;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
| : | | | | |  
Db 333 NAKLLMDRV 341

RESULT 9  
US-10-506-454-1111

```
; Sequence 1111, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozavavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1111
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
; US-10-506-454-1111

Query Match 76.7%; Score 33; DB 9; Length 509;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9
Db 112 NLQLMDRV 120

RESULT 10
US-11-096-568A-30182
; Sequence 30182, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30182
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(457)
; OTHER INFORMATION: Ceres Seq. ID no. 4948908
; US-11-096-568A-30182

Query Match 74.4%; Score 32; DB 11; Length 457;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMD 7
Db 253 NLQLMD 259

RESULT 11
US-11-096-568A-30181
; Sequence 30181, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30181
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(480)
; OTHER INFORMATION: Ceres Seq. ID no. 4948907
; US-11-096-568A-30181

Query Match 74.4%; Score 32; DB 11; Length 480;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMD 7
Db 276 NLQLMD 282

RESULT 12
US-11-096-568A-30180
; Sequence 30180, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30180
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(518)
; OTHER INFORMATION: Ceres Seq. ID no. 4948906
; US-11-096-568A-30180

Query Match 74.4%; Score 32; DB 11; Length 518;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLMD 7
Db 314 NLQLMD 320

RESULT 13
US-11-052-554A-129
; Sequence 129, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
```



; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 129  
; LENGTH: 572  
; TYPE: PRT  
; ORGANISM: Mycoplasma pneumoniae  
US-11-052-554A-129

Query Match 74.4%; Score 32; DB 11; Length 572;  
Best Local Similarity 66.7%; Pred. No. 48;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLOLLMDRV 9  
| | | | |  
Db 428 NNQLLDRI 436

RESULT 14  
US-11-052-554A-130  
; Sequence 130, Application US/11052554A  
; Publication No. US20050288866A1  
; GENERAL INFORMATION:  
; APPLICANT: Sachdeva, et al.  
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE  
; FILE REFERENCE: 30853/40359A  
; CURRENT APPLICATION NUMBER: US/11/052,554A  
; CURRENT FILING DATE: 2005-02-07  
; PRIOR APPLICATION NUMBER: US 60/589,227  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004  
; PRIOR FILING DATE: 2004-02-06  
; NUMBER OF SEQ ID NOS: 763  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 130  
; LENGTH: 1244  
; TYPE: PRT  
; ORGANISM: Mycoplasma pneumoniae  
US-11-052-554A-130

Query Match 74.4%; Score 32; DB 11; Length 1244;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLOLLMDRV 9  
| | | | |  
Db 1082 NNQLLDRI 1090

RESULT 15  
US-11-082-389-38  
; Sequence 38, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberkauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; FILE REFERENCE: BGI-131CPCN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4

; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 38  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-082-389-38

Query Match 72.1%; Score 31; DB 11; Length 270;  
Best Local Similarity 66.7%; Pred. No. 33;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLOLLMDRV 9  
| | | | |  
Db 22 NLPLIDRV 30

RESULT 16  
US-11-216-333-2  
; Sequence 2, Application US/11216333  
; Publication No. US20060057674A1  
; GENERAL INFORMATION:  
; APPLICANT: Maren Hintz  
; APPLICANT: Roland Freudl  
; APPLICANT: Jorg Feesche  
; APPLICANT: Roland Breves  
; TITLE OF INVENTION: A Translocating Enzyme as a Selection Marker  
; FILE REFERENCE: H 05599 PCT  
; CURRENT APPLICATION NUMBER: US/11/216,333  
; CURRENT FILING DATE: 2005-08-31  
; PRIOR APPLICATION NUMBER: PCT/EP2004/001949  
; PRIOR FILING DATE: 2004-27-2  
; PRIOR APPLICATION NUMBER: DE10309557.8  
; PRIOR FILING DATE: 2003-03-04  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 841  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
US-11-216-333-2

Query Match 72.1%; Score 31; DB 11; Length 841;  
Best Local Similarity 62.5%; Pred. No. 1.3e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9  
| | | | |  
Db 685 LELIMDRI 692

RESULT 17  
US-11-072-512-2471  
; Sequence 2471, Application US/11072512  
; Publication No. US20060029945A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOHIKO  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOYUKI  
; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASUHO, YASUHIKO  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: 084335-0191  
; CURRENT APPLICATION NUMBER: US/11/072,512  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US 60/350,978  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: JP 2001-379298  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2471  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-072-512-2471

Query Match 69.8%; Score 30; DB 11; Length 132;  
Best Local Similarity 75.0%; Pred. No. 24;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDR 8  
|||: |||  
Db 74 NLQMNDR 81

RESULT 18  
US-11-096-568A-18308  
; Sequence 18308, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592FUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 18308  
; LENGTH: 165  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(165)  
; OTHER INFORMATION: Ceres Seq. ID no. 12364312  
US-11-096-568A-18308

Query Match 69.8%; Score 30; DB 11; Length 165;  
Best Local Similarity 75.0%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMDRV 9  
|||: |||  
Db 5 LQLMDRI 12

RESULT 19  
US-11-096-568A-18307  
; Sequence 18307, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592FUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 18307  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(194)  
; OTHER INFORMATION: Ceres Seq. ID no. 12364311  
US-11-096-568A-18307

Query Match 69.8%; Score 30; DB 11; Length 194;  
Best Local Similarity 75.0%; Pred. No. 37;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMDRV 9  
|||: |||  
Db 34 LQLMDRI 41

RESULT 20  
US-11-096-568A-10913  
; Sequence 10913, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592FUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 10913  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(198)  
; OTHER INFORMATION: Ceres Seq. ID no. 13597465  
US-11-096-568A-10913

Query Match 69.8%; Score 30; DB 11; Length 198;  
Best Local Similarity 75.0%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMDRV 9  
|||: |||  
Db 41 LQLMDRI 48

RESULT 21  
US-11-096-568A-18306  
; Sequence 18306, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592FUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 18306  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays

```
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(201)
; OTHER INFORMATION: Ceres Seq. ID no. 12364310
US-11-096-568A-18306

Query Match          69.8%; Score 30; DB 11; Length 201;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLMDRV 9
Db 41 LQLMDRI 48

RESULT 22
US-11-045-004-1366
; Sequence 1366, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESEN, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOOK, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAPED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUP, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1366
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1366

Query Match          69.8%; Score 30; DB 11; Length 218;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLMDR 8
Db 38 LQLMDR 44

RESULT 23
US-11-096-568A-10912
; Sequence 10912, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10912
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(308)
; OTHER INFORMATION: Ceres Seq. ID no. 13597464
US-11-096-568A-10912

Query Match          69.8%; Score 30; DB 11; Length 308;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQLMDRV 9
Db 151 LQLMDRI 158

RESULT 24
US-11-096-568A-10911
; Sequence 10911, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10911
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(335)
; OTHER INFORMATION: Ceres Seq. ID no. 13597463
US-11-096-568A-10911

Query Match          69.8%; Score 30; DB 11; Length 335;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```



; SEQ ID NO 21913  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(390)  
; OTHER INFORMATION: Ceres Seq. ID no. 12406783  
US-11-096-568A-21913

Query Match 67.4%; Score 29; DB 11; Length 390;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NQLQMDRV 9  
|:|:|:|:  
Db 368 NIQLLSKV 376

## RESULT 29

US-11-045-004-1627  
; Sequence 1627, Application US/11045004  
; Publication No. US20060078901A1  
; GENERAL INFORMATION:  
; APPLICANT: BUCHRIESEN, CARMEN  
; APPLICANT: FRANGEUL, LIONEL  
; APPLICANT: COUVE, ELISABETH  
; APPLICANT: RUSNIOK, CHRISTOPHE  
; APPLICANT: FSIHL, HAFIDA  
; APPLICANT: DEHOUX, PIERRE  
; APPLICANT: DUSSURGET, OLIVIER  
; APPLICANT: CHETOUANI, FARID  
; APPLICANT: NEDJARI, HAFID  
; APPLICANT: GLASER, PHILIPPE  
; APPLICANT: KUNST, FRANK  
; APPLICANT: COSSART, PASCAL  
; APPLICANT: DANIELS, JUSTIN  
; APPLICANT: GOEBEL, WERNER  
; APPLICANT: KREFT, JURGEN  
; APPLICANT: KUHN, MICHAEL  
; APPLICANT: NG, EVA  
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO  
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO  
; APPLICANT: GARRIDO-GARCIA, PATRICIA  
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO  
; APPLICANT: AMEND, ALEXANDRA  
; APPLICANT: CHAKRABORTY, TRINAD  
; APPLICANT: DOMANN, EUGEN  
; APPLICANT: HAIN, THORSTEN  
; APPLICANT: BERCHE, PATRICK  
; APPLICANT: CHARBIT, ALAIN  
; APPLICANT: DURANT, LIONEL  
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO  
; APPLICANT: BAQUERO, FERNANDO  
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO  
; APPLICANT: GOMEZ-LOPEZ, NURIA  
; APPLICANT: MADUENIO, ENCARNA  
; APPLICANT: PABLOS, BETRIZ DE  
; APPLICANT: WEHLAND, JURGEN  
; APPLICANT: KARST, UWE  
; APPLICANT: ENTIAN, KARL-DIETER  
; APPLICANT: HAUF, JORG  
; APPLICANT: ROSE, MATTHIAS  
; APPLICANT: VOSS, HAMUT  
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES  
; FILE REFERENCE: 05394.0018-02  
; CURRENT APPLICATION NUMBER: US/11/045,004  
; CURRENT FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: 10/637,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: 10/257,023  
; PRIOR FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: PCT/FR01/01118

; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: FR 00/04,629  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 2854  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1627  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-11-045-004-1627

Query Match 67.4%; Score 29; DB 11; Length 424;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLQLMD 7  
|:|:|:|:  
Db 304 DLQLLMD 310

## RESULT 30

US-10-511-937-2407  
; Sequence 2407, Application US/10511937  
; Publication No. US20060088836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2407  
; LENGTH: 587  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2407

Query Match 67.4%; Score 29; DB 8; Length 587;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLQLMDR 8  
|:|:|:|:  
Db 459 QLQLMDR 464

## RESULT 31

US-11-052-554A-127  
; Sequence 127, Application US/11052554A  
; Publication No. US20050288866A1  
; GENERAL INFORMATION:  
; APPLICANT: Sachdeva, et al.  
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE  
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL  
; FILE REFERENCE: 30853/40359A  
; CURRENT APPLICATION NUMBER: US/11/052,554A  
; CURRENT FILING DATE: 2005-02-07  
; PRIOR APPLICATION NUMBER: US 60/589,227

;  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004  
; PRIOR FILING DATE: 2004-02-06  
; NUMBER OF SEQ ID NOS: 763  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 127  
; LENGTH: 726  
; TYPE: PRT  
; ORGANISM: Mycoplasma pneumoniae  
US-11-052-554A-127

Query Match 67.4%; Score 29; DB 11; Length 726;  
Best Local Similarity 71.4%; Pred. No. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLLMDRV 9  
|||:|:  
Db 565 QLLDRI 571

RESULT 32  
US-11-188-298-4158  
; Sequence 4158, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452) B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 4158  
; LENGTH: 752  
; TYPE: PRT  
; ORGANISM: GIBBERELLA ZEAE PH-1  
US-11-188-298-4158

Query Match 67.4%; Score 29; DB 11; Length 752;  
Best Local Similarity 71.4%; Pred. No. 3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMDR 8  
:|:|:|  
Db 684 IQLMDR 690

RESULT 33  
US-11-188-298-7416  
; Sequence 7416, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452) B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 7416  
; LENGTH: 862  
; TYPE: PRT  
; ORGANISM: Neurospora crassa  
US-11-188-298-7416

Query Match 67.4%; Score 29; DB 11; Length 862;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
||| ||| |:  
;

Db 845 NLQLATDRL 853  
  
RESULT 34  
US-11-079-463-10154  
; Sequence 10154, Application US/11079463  
; Publication No. US20060073161A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRP  
; FILE REFERENCE: PATH00-03DIV2  
; CURRENT APPLICATION NUMBER: US/11/079,463  
; CURRENT FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/128,705  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/540,209  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 10154  
; LENGTH: 1060  
; TYPE: PRT  
; ORGANISM: B. fragilis  
US-11-079-463-10154

Query Match 67.4%; Score 29; DB 11; Length 1060;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
|:|:| |  
Db 134 NWQLLRDAV 142

RESULT 35  
US-10-873-528-12  
; Sequence 12, Application US/10873528  
; Publication No. US20050276814A1  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; CURRENT FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 1216  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-12

Query Match 67.4%; Score 29; DB 9; Length 1216;  
Best Local Similarity 44.4%; Pred. No. 5.2e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
|:|:| |  
Db 272 NVQLILDEI 280

RESULT 36  
US-11-263-326-171  
; Sequence 171, Application US/11263326  
; Publication No. US20060089306A1

```
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US/11/263,326
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 171
; LENGTH: 1406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-171
```

```
Query Match 67.4%; Score 29; DB 10; Length 1406;
Best Local Similarity 55.6%; Pred. No. 6.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 NLQQLMDRV 9
|||: |||:
Db 1011 NLQIAVDRM 1019
```

```
RESULT 37
; Sequence 124, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US/11/263,326
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124
; LENGTH: 1795
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-124
```

```
Query Match 67.4%; Score 29; DB 10; Length 1795;
Best Local Similarity 55.6%; Pred. No. 8.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 NLQQLMDRV 9
|||: |||:
Db 1011 NLQIAVDRM 1019
```

```
RESULT 38
; Sequence 125, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
```

```
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125
; LENGTH: 1855
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-125
```

```
Query Match 67.4%; Score 29; DB 10; Length 1855;
Best Local Similarity 55.6%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 NLQQLMDRV 9
|||: |||:
Db 1011 NLQIAVDRM 1019
```

```
RESULT 39
US-11-263-326-173
; Sequence 173, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US/11/263,326
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173
; LENGTH: 1891
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-173
```

```
Query Match 67.4%; Score 29; DB 10; Length 1891;
Best Local Similarity 55.6%; Pred. No. 8.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 NLQQLMDRV 9
|||: |||:
Db 1011 NLQIAVDRM 1019
```

```
RESULT 40
US-10-374-954-23
; Sequence 23, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
```

```
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-23

Query Match      67.4%; Score 29; DB 9; Length 1981;
Best Local Similarity 55.6%; Pred. No. 9.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLLMDRV 9
Db      983 NLQIAVDRM 991

RESULT 41
US-10-374-954-21
; Sequence 21, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 1998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-21

Query Match      67.4%; Score 29; DB 9; Length 1998;
Best Local Similarity 55.6%; Pred. No. 9.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLLMDRV 9
Db      1000 NLQIAVDRM 1008

RESULT 42
US-10-374-954-2
; Sequence 2, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-4

Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLLMDRV 9
Db      1011 NLQIAVDRM 1019

RESULT 43
US-11-263-326-2
; Sequence 2, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-2

Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLLMDRV 9
Db      1011 NLQIAVDRM 1019

RESULT 44
US-11-263-326-4
; Sequence 4, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-4
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-2

Query Match      67.4%; Score 29; DB 9; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLLMDRV 9
Db      1011 NLQIAVDRM 1019

RESULT 43
US-11-263-326-2
; Sequence 2, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-2

Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLLMDRV 9
Db      1011 NLQIAVDRM 1019

RESULT 44
US-11-263-326-4
; Sequence 4, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-4
```



```
Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQQLMDRV 9
Db      1011 NLQIADVRM 1019

RESULT 45
US-11-263-326-6
; Sequence 6, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 6
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-6

Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQQLMDRV 9
Db      1011 NLQIADVRM 1019

RESULT 46
US-11-263-326-10
; Sequence 10, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 10
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-10

Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQQLMDRV 9
Db      1011 NLQIADVRM 1019

RESULT 47
US-11-263-326-12
; Sequence 12, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 12
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-12

Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQQLMDRV 9
Db      1011 NLQIADVRM 1019

RESULT 48
US-11-263-326-121
; Sequence 121, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 121
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-121

Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQQLMDRV 9
Db      1011 NLQIADVRM 1019
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Search completed: May 9, 2006, 02:36:22  
Job time : 17.8 secs

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Db      1011 NLQIADRM 1019
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RESULT 49
US-11-263-326-122
; Sequence 122, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; PRIOR FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 122
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-122
Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLLMDRV 9
||||: |||:
Db      1011 NLQIADRM 1019

RESULT 50
US-11-263-326-123
; Sequence 123, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; PRIOR FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-123
Query Match      67.4%; Score 29; DB 10; Length 2009;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLLMDRV 9
||||: |||:
Db      1011 NLQIADRM 1019
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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 9, 2006, 02:06:12 ; Search time 99.6 Seconds  
(without alignments)  
63.753 Million cell updates/sec

Title: US-09-870-216C-11

Perfect score: 43  
Sequence: 1 NLQLMDRV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	43	100.0	352	1F33 HUMAN	O15372 homo sapien
3	43	100.0	352	Q53HG0 HUMAN	Q53hg0 homo sapien
4	43	100.0	352	Q53HR0 HUMAN	Q53hr0 homo sapien
5	43	100.0	352	Q61B98 HUMAN	Q61b98 homo sapien
6	43	100.0	352	Q6P9U8 RAT	Q6p9u8 rattus norv
7	38	88.4	315	Q4RFC4 TETNG	Q4rfc4 tetraodon n
8	38	88.4	334	Q5PPY6 XENLA	Q5ppy6 xenopus lae
9	38	88.4	335	Q6AXJ2 BRARE	Q6axj2 brachydanio
10	38	88.4	335	Q6P381 XENTR	Q6p381 xenopus tro
11	38	88.4	348	Q5ZLE6 CHICK	Q5zle6 gallus gall
12	38	88.4	352	1F33 MOUSE	Q91wk2 mus musculu
13	38	88.4	352	Q8BTX5 MOUSE	Q5m910 mus musculu
14	38	88.4	352	Q5M9L0 MOUSE	Q5m9l0 mus musculu
15	37	86.0	352	Q5GJZ5 BOVIN	Q56jz5 bos taurus
16	37	86.0	473	Q8DJU7 SYNEL	Q8dju7 synchococc
17	36	83.7	196	Q94BU3 ARATH	Q94bu3 arabidopsis
18	36	83.7	311	Q8LAP2 ARATH	Q8lap2 arabidopsis
19	36	83.7	311	Q9LMB2 ARATH	Q9lmb2 arabidopsis
20	36	83.7	338	Q5PR67 BRARE	Q5pr67 brachydanio
21	36	83.7	342	Q9LMB3 ARATH	Q9lmb3 arabidopsis
22	36	83.7	1232	Q4Q3R9 LEIMA	Q4q3r9 leishmania
23	35	81.4	180	1NIP7 HUMAN	Q9y221 homo sapien
24	35	81.4	180	1NIP7 MOUSE	Q9cxk8 mus musculu
25	35	81.4	180	1NIP7 RAT	Q9wv50 rattus norv
26	35	81.4	180	Q56P27 FIG	Q56p27 sus scrofa
27	35	81.4	180	Q5R9J1 PONPY	Q5r9j1 pongu pygma
28	35	81.4	180	Q52Q51 FIG	Q52q51 sus scrofa
29	35	81.4	180	Q5RJI7 RAT	Q5rji7 rattus norv
30	35	81.4	1742	Q7TT21 MOUSE	Q7tt21 mus musculu
31	35	81.4	1809	1TSC2 RAT	P49816 rattus norv

32	81.4	1814	1	TSC2 MOUSE	Q61037 mus musculu
33	79.1	149	2	Q6YI26 PAGMA	Q6y126 pagrus majo
34	79.1	285	2	Q31388 CYPCA	Q31388 cyprinus ca
35	79.1	560	2	Q73MF8 TREDE	Q73mf8 treponema d
36	79.1	659	2	Q5EUI0 PLAN	Q5eui0 gemmata sp.
37	79.1	681	1	RPOCL1 ANFO	Q85cl6 anthoceros
38	79.1	808	2	Q6BZ11 DEBHA	Q6bz11 debaryomyce
39	79.1	964	2	Q7UJS8 RHABA	Q7ujs8 rhodospirell
40	79.1	1116	2	O18415 DROME	O18415 drosophila
41	79.1	1127	2	Q9VM62 DROME	Q9vm62 drosophila
42	76.7	219	2	Q52AB0 MAGGR	Q52ab0 magnaporthe
43	76.7	257	2	Q9WBR8 CAUD	Q9wbr8 staphylococ
44	76.7	345	2	Q6F7M9 ACIAD	Q6f7m9 acinetobact
45	76.7	497	2	Q4Q9G4 LEIMA	Q4q9g4 leishmania
46	76.7	509	2	Q8TWC3 METKA	Q8twc3 methanopyru
47	76.7	735	2	Q5CRU7 CRYPV	Q5cru7 cryptospori
48	76.7	735	2	O5CLF9 CRYHO	O5clf9 cryptospori
49	76.7	874	2	Q9XGCL VIGUN	Q9xgcl vigna ungu
50	76.7	944	2	Q5DMW3 CUCWE	Q5dmw3 cucumis mel
51	74.4	35	2	Q8BG77 PSBPK	Q8bg77 pseudomonas
52	74.4	99	2	Q7SFM5 NEUCR	Q7sfm5 neurospora
53	74.4	175	2	Q6ZSS5 HUMAN	Q6zss5 homo sapien
54	74.4	181	2	Q6BGJ7 PARTE	Q6bgj7 paramecium
55	74.4	203	2	Q98PY0 RHILLO	Q98fy0 rhizobium l
56	74.4	204	1	HAMI PROAC	Q6a760 propionibac
57	74.4	222	2	Q6VEA5 PSRSY	Q6vea5 pseudomonas
58	74.4	225	2	Q72E43 DESVH	Q72e43 desulfovibr
59	74.4	243	2	Q5ZOD3 NOCPA	Q5zod3 nocardia fa
60	74.4	262	2	Q99ZF9 STRPV	Q99zf9 streptococc
61	74.4	262	2	Q8P0U8 STRP8	Q8p0u8 streptococc
62	74.4	262	2	Q8K7C1 STRP6	Q8k7c1 streptococc
63	74.4	269	2	Q5XBY1 STRP6	Q5xbv1 streptococc
64	74.4	283	2	Q8DNT6 STRR6	Q8dnt6 streptococc
65	74.4	305	2	Q29795 ARCFU	Q29795 archaeoglob
66	74.4	328	2	Q6HJV4 BACHK	Q6hfv4 bacillus th
67	74.4	328	2	Q81YK5 BACAN	Q81yk5 bacillus ce
68	74.4	328	2	Q637I8 BACCZ	Q637i8 bacillus ce
69	74.4	404	2	Q91AY2 AGKAC	Q91ay2 agkistrodon
70	74.4	419	1	CECR5 MOUSE	Q91wm2 mus musculu
71	74.4	451	2	Q69T21 ORYZA	Q69t21 oryza sativ
72	74.4	452	2	Q7VD67 PROMA	Q7vd67 prochloroco
73	74.4	518	2	Q9FF18 ARATH	Q9ff18 arabidopsis
74	74.4	531	2	Q4FUQ9 AGHAM	Q4fuq9 psychrobact
75	74.4	539	2	Q756G4 ASHGO	Q756g4 ashbya goss
76	74.4	572	1	Y437 MYCPN	P75341 mycoplasma
77	74.4	621	2	Q8DZ67 STRA5	Q8dz67 streptococc
78	74.4	632	2	Q4ICP3 GIBZE	Q4icp3 gibberella
79	74.4	686	2	Q5TX25 ANOGA	Q5tx25 anopheles g
80	74.4	1082	2	Q6BHV5 DEBHA	Q6bhv5 debaryomyce
81	74.4	1161	2	Q7QJQ7 ANOGA	Q7qjq7 anopheles g
82	74.4	1232	2	Q8EL53 OCGIH	Q8el53 oceanobacil
83	74.4	1244	1	Y436 MYCPN	P75342 mycoplasma
84	74.4	4621	1	DYH5 MOUSE	Q8vhe6 mus musculu
85	74.4	4624	1	DYH5 HUMAN	Q8ter3 homo sapien
86	72.1	98	2	Q8ED10 SHEON	Q8ed10 shewanella
87	72.1	113	2	Q8JM90 9NCL	Q8jmn0 mamestra co
88	72.1	163	2	Q41ZH7 GIBZE	Q41zh7 gibberella
89	72.1	186	2	Q8F407 LEPIN	Q8f407 leptospira
90	72.1	186	2	Q72RP9 LEPIE	Q72rp9 leptospira
91	72.1	189	2	Q8FGG9 XANAC	Q8fgg9 xanthomonas
92	72.1	190	2	Q5H4Y2 XANOR	Q5hy2 xanthomonas
93	72.1	206	2	Q74CB5 GEOSL	Q74cb5 geobacter b
94	72.1	208	2	Q8T4J1 DROME	Q8t4j1 drosophila
95	72.1	217	2	Q8IPB0 DROME	Q8ipb0 drosophila
96	72.1	217	2	Q7Q3Z0 ANOGA	Q7q3z0 anopheles g
97	72.1	258	2	Q9YDB9 AERPE	Q9ydb9 aeropyrum p
98	72.1	270	1	YEAD BACS2	P94475 bacillus su
99	72.1	270	2	Q5N002 SYNPN	Q5n002 synchococc
100	72.1	270	2	Q8NQF7 CORGL	Q8ngf7 corynebacte
101	72.1	274	2	Q8DHY9 SYNEL	Q8dhy9 synchococc
102	72.1	280	2	Q8FTG3 COREP	Q8ftg3 corynebacte
103	72.1	286	2	Q9Q8K3 9POXV	Q9q8k3 myxoma viru
104	72.1	286	2	Q9Q8Y1 9POXV	Q9q8y1 rabbit fibr

105	31	72.1	291	2	Q8YMP8	ANASP	Q8Ymp8	anabaena	sp	178	30	69.8	144	2	Q9KIQ1	ECOLI	Q9k1qi	escherichia
106	31	72.1	293	2	QAKMP8	HUMAN	Q4kmp8	homo sapien		179	30	69.8	144	2	Q8FDA9	ECOL6	Q8fda9	escherichia
107	31	72.1	313	2	QANCK5	9M1CC	Q4nck5	arthrobacte		180	30	69.8	144	2	Q83JH7	SHIFL	Q83jh7	shigella fl
108	31	72.1	375	2	Q4T0J7	TETNG	Q4t0j7	tetradodon	n	181	30	69.8	144	2	Q8XAC4	ECOS7	Q8xac4	escherichia
109	31	72.1	380	2	Q65XI3	ORYSA	Q65xi3	oryza sativ		182	30	69.8	146	2	Q8BEM1	9VIRU	Q8bem1	taro bacill
110	31	72.1	410	2	Q63MA0	BURKHA	Q63ma0	burkholderi		183	30	69.8	152	2	Q8VQP3	BURCE	Q8vqp3	burkholderi
111	31	72.1	410	2	Q62D66	BURMA	Q62d66	burkholderi		184	30	69.8	152	2	Q4LLD3	9BURK	Q4lld3	burkholderi
112	31	72.1	422	2	Q8MME6	DROME	Q8mme6	drosophila		185	30	69.8	152	2	Q8MHA8	BRACHD	Q8mha8	brachydanio
113	31	72.1	445	2	Q73739	SYNY3	Q73739	synecocyst		186	30	69.8	153	2	Q8MHA5	BRACHD	Q8mha5	brachydanio
114	31	72.1	467	2	Q9SJV9	ARATH	Q9sjv9	arabidopsis		187	30	69.8	153	2	Q8MHA6	BRACHD	Q8mha6	brachydanio
115	31	72.1	472	1	ER02	ARATH	Q7x914	arabidopsis		188	30	69.8	153	2	Q8MHA7	BRACHD	Q8mha7	brachydanio
116	31	72.1	472	2	Q56Y10	ARATH	Q56y10	arabidopsis		189	30	69.8	153	2	Q8MHB1	BRACHD	Q8mhb1	brachydanio
117	31	72.1	472	2	Q501C9	ARATH	Q501c9	arabidopsis		190	30	69.8	153	2	Q8MHB3	BRACHD	Q8mhb3	brachydanio
118	31	72.1	474	2	Q6AVU2	ORYSA	Q6avu2	oryza sativ		191	30	69.8	153	2	Q8MHB4	BRACHD	Q8mhb4	brachydanio
119	31	72.1	479	2	Q8TQB7	METAC	Q8tqb7	methanosarc		192	30	69.8	153	2	Q8MHA9	BRACHD	Q8mha9	brachydanio
120	31	72.1	487	2	Q518A5	ENTH1	Q518a5	entamoeba h		193	30	69.8	167	2	Q9XF21	CAPCH	Q9xf21	capsicum ch
121	31	72.1	529	2	Q53E02	MYXXXA	Q53e02	myxococcus		194	30	69.8	170	2	Q8GT21	CAPCH	Q8gt21	capsicum ch
122	31	72.1	530	2	Q4NHT7	9M1CC	Q4nht7	arthrobacte		195	30	69.8	171	2	Q86829	PRRSV	Q86829	porcine rep
123	31	72.1	581	2	Q5CHW6	CRYHO	Q5chw6	cryptospori		196	30	69.8	195	2	Q8MHB6	BRACHD	Q8mhb6	brachydanio
124	31	72.1	582	2	Q97ZV6	SULSO	Q97zv6	sulfolobus		197	30	69.8	203	2	Q74J25	LACJO	Q74j25	lactobacill
125	31	72.1	582	2	Q5CQR5	CRYPV	Q5cqr5	cryptospori		198	30	69.8	212	2	Q7P4A4	FUSNV	Q7p4a4	fusobacteri
126	31	72.1	614	2	Q4VPT6	MYXXA	Q4vpt6	myxococcus		199	30	69.8	212	2	Q4FV68	9GAMM	Q4fv68	psychrobact
127	31	72.1	652	1	T3MO	SALTU	P40814	salmonella		200	30	69.8	217	1	KAD	BACHD	P33b72	bacillus ha
128	31	72.1	652	2	Q57SK7	SALCH	Q57sk7	salmonella		201	30	69.8	217	2	Q7P8H8	FUSNV	Q7p8h8	fuobacteri
129	31	72.1	652	2	Q82913	SALTI	Q82913	salmonella		202	30	69.8	218	2	Q8Y9B9	LISMO	Q8y9b9	listeria mo
130	31	72.1	652	2	Q5FPX3	SALPA	Q5fpk3	salmonella		203	30	69.8	219	2	Q92E71	LISIN	Q92e71	listeria in
131	31	72.1	663	2	Q5LE06	ENTHI	Q5le06	entamoeba h		204	30	69.8	220	2	Q722X0	LISMF	Q722x0	listeria mo
132	31	72.1	672	2	Q9Z887	CHLPN	Q9z887	chlamydia p		205	30	69.8	227	2	Q9RSD3	DEIRA	Q9rsd3	deinococcus
133	31	72.1	675	2	Q5A2J7	CANAL	Q5a2j7	candida alb		206	30	69.8	252	2	Q5YXF7	NOCPA	Q5yxf7	nocardia fa
134	31	72.1	677	2	Q8MZE1	DROME	Q8mze1	drosophila		207	30	69.8	252	2	Q9LM87	ARATH	Q9lm87	arabidopsis
135	31	72.1	693	1	EX070	DROME	Q9vqj8	drosophila		208	30	69.8	262	2	Q991V7	9Z2Z2	Q991v7	uncultured
136	31	72.1	698	2	Q6NUE8	XENLA	Q6nue8	xenopus lae		209	30	69.8	263	2	Q6NBA8	RHOPA	Q6nb48	rhodopseudo
137	31	72.1	699	1	CND2	XENLA	Q13067	xenopus lae		210	30	69.8	264	2	Q68XJ5	RLCTY	Q68xj5	rickettsia
138	31	72.1	703	2	Q66KA2	XENTR	Q66ka2	xenopus tro		211	30	69.8	267	2	Q9KTY5	STRCO	Q9kty5	streptomyce
139	31	72.1	731	2	Q4TFU7	TETNG	Q4tfu7	tetradodon	n	212	30	69.8	269	2	Q7PAW2	RICSI	Q7paw2	rickettsia
140	31	72.1	790	2	Q4WT72	AGPFU	Q4wt72	aspergillus		213	30	69.8	269	2	Q92J56	RICCN	Q92j56	rickettsia
141	31	72.1	814	1	CF102	HUMAN	Q62mrv9	homo sapien		214	30	69.8	272	2	Q18776	CABEL	Q18776	caenorhabdi
142	31	72.1	837	2	Q5U2Y6	RAT	Q5u2y6	rattus norv		215	30	69.8	275	1	APAH	HAEN	P44751	haemophilus
143	31	72.1	838	1	TFP11	MOUSE	Q9era6	mus musculus		216	30	69.8	275	2	Q4QMZ7	HA8I8	Q4qmz7	haemophilus
144	31	72.1	841	1	SECA	BACSU	P28366	bacillus su		217	30	69.8	278	2	Q72PA6	LEPIC	Q72pa6	leptospira
145	31	72.1	861	2	Q8UGU8	AGRT5	Q8ugu8	agrobacteri		218	30	69.8	278	2	Q8F741	LEPIN	Q8f741	leptospira
146	31	72.1	865	2	Q4SZU5	TETNG	Q4szu5	tetradodon	n	219	30	69.8	284	2	Q27871	METTH	Q27871	methanobact
147	31	72.1	893	2	Q5B0Q7	EMENI	Q5b0q7	aspergillus		220	30	69.8	312	2	Q60YX6	CAEBR	Q60yx6	caenorhabdi
148	31	72.1	955	2	Q7PQ81	ANOGA	Q7pq81	anopheles g		221	30	69.8	315	1	YPOX	ACICA	P07783	acinetobact
149	31	72.1	965	2	Q5AML7	CANAL	Q5aml7	candida alb		222	30	69.8	324	2	Q610T7	CAEBR	Q610t7	caenorhabdi
150	31	72.1	967	2	Q5AN22	CANAL	Q5an22	candida alb		223	30	69.8	326	2	Q7YPI4	BRACHD	Q7yp14	brachydanio
151	31	72.1	988	1	CIN8	CANGA	Q6fxi5	candida gla		224	30	69.8	330	2	Q7YPI6	BRACHD	Q7yp16	brachydanio
152	31	72.1	1114	2	Q8MME7	DROME	Q8mme7	drosophila		225	30	69.8	332	2	Q7YPI5	BRACHD	Q7yp15	brachydanio
153	31	72.1	1127	2	Q8MME8	DROME	Q8mme8	drosophila		226	30	69.8	336	2	Q95QS2	CABEL	Q95qs2	caenorhabdi
154	31	72.1	1316	2	Q4FWJ3	LEIMA	Q4fwj3	leishmania		227	30	69.8	340	1	GCP	HELPU	Q9xj27	helicobacte
155	31	72.1	1504	1	DPOZ	YEAST	P14284	saccharomyc		228	30	69.8	356	2	Q980M3	SULSO	Q980m3	sulfolobus
156	31	72.1	1522	2	Q5F3R2	CHICK	Q5f3r2	gallus gall		229	30	69.8	365	2	Q21602	CABEL	Q21602	caenorhabdi
157	31	72.1	1596	2	Q5KI58	CRYNE	Q5ki58	cryptococcu		230	30	69.8	390	2	Q6FCR8	ACIAD	Q6fck8	acinetobact
158	31	72.1	1880	2	Q55U87	CRYNE	Q55u87	cryptococcu		231	30	69.8	392	2	Q8MHB7	BRACHD	Q8mhb7	brachydanio
159	31	72.1	2311	2	Q60XZ8	CAEBR	Q60xz8	caenorhabdi		232	30	69.8	399	2	Q5W796	ORYSA	Q5w796	oryza sativ
160	31	72.1	2525	2	Q4Q184	LEIMA	Q4q184	leishmania		233	30	69.8	404	2	Q8TMT9	METAC	Q8tmt9	methanosarc
161	31	72.1	3036	2	Q4PAT2	USTMA	Q4pat2	ustilago ma		234	30	69.8	404	2	Q838Y0	ENTFA	Q838y0	enterococcu
162	31	72.1	3390	2	Q5AUN0	EMENI	Q5aun0	aspergillus		235	30	69.8	421	2	Q7N133	PHOLL	Q7nl33	photorhabdu
163	31	72.1	3896	2	Q4WED0	AGPFU	Q4wed0	aspergillus		236	30	69.8	426	2	Q5AUC7	EMENI	Q5auc7	aspergillus
164	30	69.8	97	1	CH10	BUCTS	Q9f4e4	buchnera ap		237	30	69.8	435	2	Q503S0	BRACHD	Q503s0	brachydanio
165	30	69.8	97	2	Q8GF57	ZYMOO	Q8gf57	zymomonas m		238	30	69.8	446	2	Q5BCM9	EMENI	Q5bcm9	aspergillus
166	30	69.8	105	2	Q9REP7	ZYMOO	Q9rep7	zymomonas m		239	30	69.8	464	2	Q9LZ72	ARATH	Q9lz72	arabidopsis
167	30	69.8	106	2	Q69561	9BETA	Q69561	bacillus ce		240	30	69.8	468	2	Q360N1	DROME	Q360n1	drosophila
168	30	69.8	113	2	Q4MQJ5	BACCE	Q4mqj5	bacillus ce		241	30	69.8	478	2	Q8R4Q7	VITRI	Q8r4q7	vitis ripar
169	30	69.8	113	2	Q6HNV7	BACHK	Q6hnv7	bacillus th		242	30	69.8	480	2	Q5E6G8	VIBF1	Q5e6g8	virbio fisc
170	30	69.8	113	2	Q73E08	BACHK	Q73e08	bacillus ce		243	30	69.8	483	2	Q9LYX8	ARATH	Q9lyx8	arabidopsis
171	30	69.8	113	2	Q811B4	BACCR	Q811b4	bacillus ce		244	30	69.8	487	2	Q9FHD7	ARATH	Q9fhd7	arabidopsis
172	30	69.8	113	2	Q63GE3	BACCC	Q63ge3	bacillus ce		245	30	69.8	489	1	Y1931	VIBCH	Y1931	virbio chol
173	30	69.8	113	2	Q81YY2	BACAN	Q81yy2	bacillus an		246	30	69.8	505	2	Q7PN29	ANOGA	Q7pn29	anopheles g
174	30	69.8	119	2	Q6MXC5	SERMA	Q6mxc5	serratia ma		247	30	69.8	527	2	Q4N006	THEPA	Q4n006	theileria p
175	30	69.8	124	2	Q69058	9BETA	Q69058	human herpe		248	30	69.8	548	1	YCG2	SCHPO	YCG2	schizosacch
176	30	69.8	132	2	Q8NB79	HUMAN	Q8nb79	homo sapien		249	30	69.8	558	2	Q7Q0C3	ANOGA	Q7q0c3	anopheles g
177	30	69.8	142	2	Q4TJJ2	9SPHN	Q4tjj2	erythrobact		250	30	69.8	566	2	Q4IFT4	GIBZE	Q4ift4	gibberella

251	30	69.8	567	2	Q60UJ6_CABBR	Q60uj6	caenorhabdi	324	2104	2	Q5RJ12_BRARE	Q5rj12	brachydanio
252	30	69.8	570	2	Q89HY9_BRAJA	Q89hy9	brachyrhizob	325	2635	2	Q6FS12_CANGA	Q6fs12	candida gla
253	30	69.8	591	1	SYD_PSEAE	Q51422	pseudomonas	326	69.8	2	Q7YWF0_PLAFA	Q7ywf0	plasmodium
254	30	69.8	591	1	SYD_PSESM	Q87y31	pseudomonas	327	3080	2	Q7YWF1_PLAFA	Q7ywf1	plasmodium
255	30	69.8	591	2	Q42WL5_PSESY	Q4zwl5	pseudomonas	328	3096	2	Q7YWF2_PLAFA	Q7ywf2	plasmodium
256	30	69.8	591	2	Q41T48_AZOV1	Q4it48	azotobacter	329	3096	2	Q9BK46_PLAFA	Q9bk46	plasmodium
257	30	69.8	591	2	Q4K7D5_PSEF5	Q4k7d5	pseudomonas	330	3130	2	Q81DX6_PLAP7	Q81dx6	plasmodium
258	30	69.8	591	2	Q7U227_MYCBO	Q7u2d7	mycobacteri	331	3130	2	Q81DX6_PLAP7	Q81dx6	plasmodium
259	30	69.8	603	2	Q7KSD9_DROME	Q7ksd9	drosophila	332	3140	2	Q4SRE1_TETNG	Q4sre1	tetraodon n
260	30	69.8	612	2	Q82I71_YERPE	Q82i71	yersinia pe	333	3152	2	Q7YWE6_PLAFA	Q7ywe6	plasmodium
261	30	69.8	612	2	Q665U2_YERPS	Q665u2	yersinia ps	334	3203	2	Q7YWE7_PLAFA	Q7ywe7	plasmodium
262	30	69.8	613	2	Q4RG46_TETNG	Q4rg46	tetraodon n	335	3254	2	Q7YWE9_PLAP7	Q7ywe9	plasmodium
263	30	69.8	631	2	Q74RR1_YERPE	Q74rr1	yersinia pe	336	3254	2	Q9BK45_PLAP7	Q9bk45	plasmodium
264	30	69.8	632	2	Q8CZR5_YERPE	Q8czr5	yersinia pe	337	3256	2	Q7YWE8_PLAFA	Q7ywe8	plasmodium
265	30	69.8	648	2	Q4Q096_LEIMA	Q4q096	leishmania	338	4543	2	Q9VB44_DROME	Q9vb44	drosophila
266	30	69.8	667	2	Q4R9D5_MACFA	Q4r9d5	macaca fasc	339	67.4	61	Q7WYG6_BACTU	Q7wyg6	bacillus th
267	30	69.8	670	2	Q5HKY4_STAEO	Q5hky4	staphylococ	340	68	2	Q8RA50_TFTTN	Q8ra50	thermoanaer
268	30	69.8	670	2	Q8CQ22_STAEP	Q8cq22	staphylococ	341	68	2	Q17013_ANOGA	Q17013	anopheles g
269	30	69.8	673	2	Q522S5_MAGR	Q522s5	magnaporthe	342	83	2	Q7R558_GIALA	Q7r558	giardia lam
270	30	69.8	673	2	Q7KS65_DROME	Q7ks65	drosophila	343	86	1	RS16_BORPE	Rs16	bordetella
271	30	69.8	681	2	Q9VEA9_DROME	Q9vea9	drosophila	344	86	1	RS16_BORPE	Rs16	bordetella
272	30	69.8	682	2	Q4QFJ7_LEIMA	Q4qfj7	leishmania	345	104	2	Q4LN53_9BURK	Q4ln53	burkholderi
273	30	69.8	684	2	Q9VE51_DROME	Q9ve51	drosophila	346	104	2	Q6MT49_MYCMS	Q6mt49	mycoplasma
274	30	69.8	729	2	Q6CC45_YARLI	Q6cc45	yarrowia li	347	105	1	MDCC_BRAJA	MDcc	brachyrhizob
275	30	69.8	731	2	Q7VK59_HELHP	Q7vk59	helicobacte	348	105	1	MDCC_XANAC	MDcc	xanthomonas
276	30	69.8	733	2	Q9VD46_DROME	Q9vd46	drosophila	349	105	1	MDCC_XANAC	MDcc	xanthomonas
277	30	69.8	771	2	Q5QNE1_ORYSA	Q5qne1	oryza sativ	350	105	2	Q4UZ69_XANCP	Q4uz69	xanthomonas
278	30	69.8	771	2	Q5WY17_LEGFL	Q5wy17	legionella	351	105	2	Q63VB1_BURPS	Q63vb1	burkholderi
279	30	69.8	771	2	Q5X6L3_LEGPA	Q5x6l3	legionella	352	105	2	Q8F4H2_LEPIN	Q8f4h2	leptospira
280	30	69.8	771	2	Q5ZX42_LEGPH	Q5zx42	legionella	353	105	2	Q62FJ3_BURMA	Q62fj3	burkholderi
281	30	69.8	785	2	Q73UJ4_TREDE	Q73uj4	treponema d	354	116	2	Q527V4_CHLPN	Q527v4	chlamydia p
282	30	69.8	801	2	Q51RU1_MAGGR	Q51ru1	magnaporthe	355	126	2	Q5CEFA_CRYHO	Q5cef4	cryptospori
283	30	69.8	804	2	Q5L1L0_GEOKA	Q5l1l0	geobacillus	356	140	2	Q54QX0_DICDI	Q54qx0	dictyosteli
284	30	69.8	824	2	Q66J74_XENLA	Q66j74	xenopus lae	357	140	2	Q54QX0_DICDI	Q54qx0	dictyosteli
285	30	69.8	827	2	Q521I9_CHICK	Q52i19	gallus gall	358	140	2	Q804B7_CAIMO	Q804b7	cairina mos
286	30	69.8	837	1	TFP11_HUMAN	Q9ub99	homo sapien	359	140	2	Q804B7_CAIMO	Q804b7	cairina mos
287	30	69.8	837	2	Q8N523_HUMAN	Q8n523	homo sapien	360	142	2	Q15748_DICDI	Q15748	dictyosteli
288	30	69.8	837	2	Q5H8V8_HUMAN	Q5h8v8	homo sapien	361	144	2	Q61WV3_9CAUD	Q61wv3	methanococ
289	30	69.8	837	2	Q5R5K8_PONPY	Q5r5k8	pongo pygma	362	145	1	Y1180_METJA	Y1180	metanococ
290	30	69.8	855	2	Q4HEK8_CAMCO	Q4hek8	campylobact	363	159	2	Q7B620_PSEPG	Q7b620	pseudomonas
291	30	69.8	862	2	Q4R8S4_TETNG	Q4r8s4	tetraodon n	364	160	2	Q9S480_MYXXA	Q9s480	myxococcus
292	30	69.8	863	2	Q7QRN5_GIALA	Q7qrn5	giardia lam	365	166	2	Q6UYL4_9CAUD	Q6uy14	burkholderi
293	30	69.8	891	2	Q4X128_ASPFU	Q4x128	aspergillus	366	178	2	Q72RA2_LEPIC	Q72ra2	leptospira
294	30	69.8	925	2	Q7ZUM1_BRARE	Q7zum1	brachydanio	367	180	2	Q6DFH9_XENLA	Q6dfh9	xenopus lae
295	30	69.8	958	1	MMPL11_MYCTU	P95211	mycobacteri	368	180	2	Q503P2_BRARE	Q503p2	brachydanio
296	30	69.8	968	2	Q7PTO5_ANOGA	Q7ptq5	anopheles g	369	180	2	Q4T2X8_TETNG	Q4t2x8	tetraodon n
297	30	69.8	986	2	Q87UJ2_PSESM	Q87u22	pseudomonas	370	182	2	Q6JDV2_CHLRE	Q6jd2	chlamydomon
298	30	69.8	986	2	Q4ZL4_PSESY	Q4z214	pseudomonas	371	186	2	Q6LRR0_PHOPR	Q6lrr0	photobacter
299	30	69.8	999	2	Q9U5A3_PLAFA	Q9u5a3	plasmodium	372	187	2	Q90196_9NUCL	Q90196	spodoptera
300	30	69.8	999	2	Q76BD5_ACIBE	Q76bd5	acipenser b	373	193	2	Q5F857_NEIG1	Q5f857	neisseria g
301	30	69.8	1011	2	Q8YVP7_ANASP	Q8yvp7	anabaena sp	374	193	2	Q9JU00_NEIMA	Q9ju00	neisseria m
302	30	69.8	1017	2	Q919E6_BRARE	Q9i9e6	brachydanio	375	193	2	Q9JZQ6_NEIMB	Q9jzq6	neisseria m
303	30	69.8	1018	2	Q9UTR1_SCHPO	Q9utr1	schizosacch	376	196	2	Q84LC2_HELAN	Q84lc2	helianthus
304	30	69.8	1071	2	Q49727_ARATH	Q49727	arabidopsiss	377	199	1	HAML_LEIXX	Haml	leifsonia x
305	30	69.8	1083	2	Q8GE61_HELMO	Q8ge61	heliobacill	378	202	2	Q7UQT2_RHOBA	Q7uqt2	rhodospirell
306	30	69.8	1091	2	Q97RD0_STRPN	Q97rd0	streptococ	379	209	2	Q6H259_BURML	Q6h259	burkholderi
307	30	69.8	1101	2	Q76369_CABEL	Q76369	caenorhabdi	380	209	2	Q83WB1_9BURK	Q83wb1	burkholderi
308	30	69.8	1116	1	DP03A_BACHD	Q9k838	bacillus ha	381	209	2	Q8VP16_9BURK	Q8vp16	burkholderi
309	30	69.8	1116	2	Q8DQ85_STRR6	Q8dq89	streptococ	382	209	2	Q4LHP6_9BURK	Q4lhp6	burkholderi
310	30	69.8	1160	2	Q4HUZ7_GIBZE	Q4hu27	gibberella	383	215	2	Q9KY51_STRCO	Q9ky51	streptomyce
311	30	69.8	1385	2	Q8TOL7_DROME	Q8t017	drosophila	384	216	2	Q912N1_PSEAE	Q912n1	pseudomonas
312	30	69.8	1385	2	Q9VVC7_DROME	Q9vvc7	drosophila	385	217	2	Q6S504_9FABA	Q6s504	glycine fal
313	30	69.8	1579	1	PEP1_YEAST	P32319	saccharomyc	386	217	2	Q8DTL8_STRMU	Q8dtl8	streptococ
314	30	69.8	1612	2	Q6PVX7_OSTTA	Q6pxv7	ostreococcu	387	219	1	F1GLA_HUMAN	F1gla	homo sapien
315	30	69.8	1633	2	Q5NWD5_AZOSE	Q5nwd5	azocarcus sp	388	220	2	P72807_SYNY3	P72807	synecocyst
316	30	69.8	1750	2	Q5QKN8_ORYSA	Q5qkn8	oryza sativ	389	221	2	Q924V6_CAVPO	Q924v6	cavia porce
317	30	69.8	1775	2	Q4LE71_HUMAN	Q4le71	homo sapien	390	223	2	Q6S505_9FABA	Q6s505	glycine lat
318	30	69.8	1807	1	TSC2_HUMAN	P49815	homo sapien	391	223	2	Q6S506_GLYTA	Q6s506	glycine tab
319	30	69.8	1950	2	Q53R17_ORYSA	Q53r17	oryza sativ	392	225	2	Q8UZZ4_9VIRU	Q8uzc4	chelonus in
320	30	69.8	1956	2	Q4T5Z8_TETNG	Q4t5z8	tetraodon n	393	231	1	B10D_BACSU	B10d	bacillus eu
321	30	69.8	1997	2	Q815L6_PLAP7	Q815l6	plasmodium	394	235	2	Q7QLV7_ANOGA	Q7qlv2	anopheles g
322	30	69.8	2016	2	Q7PF90_ANOGA	Q7pf90	anopheles g	395	243	2	Q8NIV2_9MICC	Q8niv2	arthrobacte
323	30	69.8	2041	2	Q81BK6_PLAP7	Q81bk6	plasmodium	396	246	2	Q8PTZ7_METMA	Q8ptz7	methanosarc

397	29	67.4	250	2	Q5C0S8 SCHJA	Q5C0S8 schistosoma	470	29	67.4	492	2	Q87U76 PSESM	Q87u76 pseudomonas
398	29	67.4	252	2	Q5BLD7 BRARE	Q5blD7 brachydanio	471	29	67.4	498	2	Q7NX24 CHRVO	Q7nx24 chryobactce
399	29	67.4	253	2	Q6C4X9 YARLI	Q6c4X9 yarrowia li	472	29	67.4	507	2	Q5N4Z8 SYNRP6	Q5n4Z8 synochococc
400	29	67.4	255	2	Q9H366 HUMAN	Q9h366 homo sapien	473	29	67.4	509	1	C217A FIG	P13100 sus scrofa
401	29	67.4	258	2	Q5D9B4 SCHJA	Q5d9B4 schistosoma	474	29	67.4	512	2	Q6FXF6 CANGA	Q6fxf6 candida gla
402	29	67.4	258	2	Q5DAQ8 SCHJA	Q5daq8 schistosoma	475	29	67.4	515	1	RHO BORBU	P33561 borrelia gla
403	29	67.4	259	2	Q870E4 NEOFRR	Q870e4 neocallinias	476	29	67.4	515	2	Q4U928 THEAN	Q4u928 theileria a
404	29	67.4	259	2	Q4FYC5 LEIMA	Q4fyc5 leishmania	477	29	67.4	515	2	Q662D4 BORGAN	Q662d4 borrelia ga
405	29	67.4	264	2	Q8PZB1 METMA	Q8pzb1 methanosarc	478	29	67.4	518	2	Q8XZV3 RALSO	Q8xZv3 ralstonia s
406	29	67.4	269	2	Q9ZDZ1 RICPR	Q9zdZ1 rickettsia	479	29	67.4	519	2	Q580I1 9TRYP	Q580i1 trypanosoma
407	29	67.4	275	2	Q7PN09 ANOGA	Q7pn09 anopheles g	480	29	67.4	525	2	Q4N1S3 THEPA	Q4n1s3 theileria p
408	29	67.4	276	2	Q8UVC2 PAGBE	Q8uvc2 pagothenia	481	29	67.4	526	2	Q5V0M9 HALMA	Q5v0m9 haloarcula
409	29	67.4	282	2	P93660 BETPR	P93660 beta procum	482	29	67.4	526	2	Q41FC3 GIBZE	Q41fc3 gibberella
410	29	67.4	284	2	Q25696 HELPY	Q25696 helicobacte	483	29	67.4	529	2	Q4N7Y9 THEPA	Q4n7y9 theileria p
411	29	67.4	287	1	Y1641 METJA	Y1641 methanococc	484	29	67.4	533	2	Q6N1W0 RHOPA	Q6n1w0 rhodospseudo
412	29	67.4	288	2	Q618P2 CABBR	Q618p2 caenorhabdi	485	29	67.4	541	2	Q9CF00 LACLA	Q9cf00 lactococcus
413	29	67.4	289	2	Q92M54 HELPU	Q92m54 helicobacte	486	29	67.4	545	2	Q9HZS7 PSEAE	Q9hzs7 pseudomonas
414	29	67.4	292	1	FBX16 HUMAN	Q81x29 homo sapien	487	29	67.4	545	2	Q74BE8 GEOSL	Q74be8 geobactce s
415	29	67.4	311	2	Q6JDV1 CHLRE	Q6jdv1 chlamydomon	488	29	67.4	547	2	Q8Z0A9 ANASP	Q8z0a9 anabaena sp
416	29	67.4	311	2	Q7NTX8 CHRVO	Q7ntx8 chromobacte	489	29	67.4	550	2	Q5JZP5 HUMAN	Q5jzf5 homo sapien
417	29	67.4	312	2	Q5GLJ5 PHAVU	Q5glj5 phaseolus v	490	29	67.4	550	2	Q8N6H3 HUMAP	Q8n6h3 homo sapien
418	29	67.4	322	2	Q97GV4 CLOAB	Q97gv4 clostridium	491	29	67.4	554	2	Q3EZ02 9SP10	Q3ez02 spirochaeta
419	29	67.4	326	2	Q5TTF6 ANOGA	Q5ttf6 anopheles g	492	29	67.4	557	2	Q4NZD9 9DELTA	Q4nzd9 anaeromyxob
420	29	67.4	327	2	Q92US7 RHIME	Q92us7 rhizobium m	493	29	67.4	559	1	YFF1 SCHPO	Q94459 schizosacch
421	29	67.4	329	2	Q9JP86 BACST	Q9jp86 bacillus st	494	29	67.4	561	1	ERO1 KLULA	Q8aip5 kluyveromyc
422	29	67.4	331	1	V012 F0MPV	Q915i9 fowlpox vir	495	29	67.4	561	2	Q54WN3 DICDI	Q54wn3 dictyosteli
423	29	67.4	331	2	Q70HD8 F0MPV	Q70hd8 fowlpox vir	496	29	67.4	566	2	Q81PR3 DROME	Q81pr3 dirosophila
424	29	67.4	335	2	Q8EAV5 SHEON	Q8eav5 shewanella	497	29	67.4	576	2	Q57T24 9TRYP	Q57t24 trypanosoma
425	29	67.4	340	1	GCP HELPY	P55996 helicobacte	498	29	67.4	577	2	Q57E59 BRUSU	Q57e59 brucella ab
426	29	67.4	342	2	Q53CR0 9GAMA	Q53cr0 macaca fusc	499	29	67.4	577	2	Q8G1N1 BRUSU	Q8g1n1 brucella su
427	29	67.4	342	2	Q77NH5 9GAMA	Q77nh5 rhesus monk	500	29	67.4	582	1	Q5N7J0 ORYSA	Q5n7j0 oryza sativ
428	29	67.4	342	2	Q9WRM0 9GAMA	Q9wrM0 macaca mula	501	29	67.4	582	2	Q4FW9 LEIMA	Q4fw9 leishmania
429	29	67.4	348	2	Q628P1 CABBR	Q628f1 caenorhabdi	502	29	67.4	583	2	Q4FW9 LEIMA	Q4fw9 leishmania
430	29	67.4	350	2	Q9UAY5 CABEL	Q9uay5 caenorhabdi	503	29	67.4	587	1	HEMO MOUSE	P22557 homo sapien
431	29	67.4	354	2	Q8F2Z8 LEPIN	Q8f2z8 leptospira	504	29	67.4	587	1	HEMO RAT	P08680 mus musculus
432	29	67.4	354	2	Q72SK9 LEPIE	Q72sk9 leptospira	505	29	67.4	587	1	Q5R557 PONPY	Q5r557 pongo pygma
433	29	67.4	356	2	Q6CSE1 KLULA	Q6cse1 kluyveromyc	506	29	67.4	587	2	Q42C1 RAT	Q42c1 rattus norv
434	29	67.4	367	2	Q8XXK6 RALSO	Q8xxk6 ralstonia s	507	29	67.4	587	2	Q5LB20 BACFN	Q5lb20 bacteroides
435	29	67.4	369	2	Q8ETN1 OCEIH	Q8etn1 oceanobacil	508	29	67.4	588	2	Q6MA16 PARUM	Q6ma16 parachlamyd
436	29	67.4	380	2	Q73X07 MYCPA	Q73x07 mycobacteri	509	29	67.4	591	2	Q56045 9REOV	Q56045 rice ragged
437	29	67.4	380	2	Q6D4S8 ERWINA	Q6d4s8 erwinia car	510	29	67.4	592	2	Q6L404 SOLDE	Q6l404 solanum dem
438	29	67.4	382	2	Q5TPV0 ANOGA	Q5tpv0 anopheles g	511	29	67.4	593	2	Q97GR7 CLOAB	Q97gr7 clostridium
439	29	67.4	385	2	Q6VYW0 ORYSA	Q6vyw0 oryza sativ	512	29	67.4	593	2	Q882M2 PSESM	Q882m2 pseudomonas
440	29	67.4	393	2	Q7VNZ4 HAEDU	Q7vnz4 haemophilus	513	29	67.4	595	2	Q5CUR2 CRYPV	Q5cuf2 cryptospori
441	29	67.4	394	2	Q9CJUB PASMU	Q9cjb8 pasteurella	514	29	67.4	595	2	Q7S5F6 NEUCR	Q7s5f6 neurospora
442	29	67.4	395	2	Q6K6U2 ORYSA	Q6k6u2 oryza sativ	515	29	67.4	606	2	Q7QY14 GALA	Q7qy14 giardia lam
443	29	67.4	395	2	Q4TSV8 9SPHN	Q4tsv8 erythrobaet	516	29	67.4	613	2	Q95ZQ9 CABEL	Q95zq9 caenorhabdi
444	29	67.4	402	2	Q8R1G3 MOUSE	Q8rlg3 mus musculus	517	29	67.4	614	2	Q7N0B4 PHOLI	Q7n0b4 photorhabdu
445	29	67.4	403	1	SHBG MOUSE	P97497 mus musculus	518	29	67.4	618	2	Q52D16 MAGGR	Q52d16 magnaporthe
446	29	67.4	403	2	Q5P214 MOUSE	Q5f214 mus musculus	519	29	67.4	621	2	Q86SD3 CIOIN	Q86sd3 ciona intes
447	29	67.4	407	2	Q51W12 MAGGR	Q51w12 magnaporthe	520	29	67.4	627	2	Q7PS01 ANOGA	Q7ps01 anopheles g
448	29	67.4	421	2	Q7MEI1 VIBVY	Q7mei1 vibrio vuln	521	29	67.4	633	2	Q95Q52 CABEL	Q95q52 caenorhabdi
449	29	67.4	424	2	Q8RNR6 LEGPN	Q8rn6 legionella	522	29	67.4	649	2	Q7KQ93 ANOGA	Q7kq93 anopheles g
450	29	67.4	424	2	Q721J5 LISMF	Q721j5 listeria mo	523	29	67.4	650	2	Q8T426 DROME	Q8t426 drosophila
451	29	67.4	424	2	Q92D50 LIISIN	Q92d50 listeria in	524	29	67.4	653	2	Q8D445 VIBVU	Q8d445 vibrio vuln
452	29	67.4	424	2	Q9S388 LISMO	Q9s388 listeria mo	525	29	67.4	658	2	Q4SRG4 TETNG	Q4srg4 tetraodon n
453	29	67.4	425	2	Q5WT26 LEGPL	Q5wz26 legionella	526	29	67.4	663	2	Q5GVV6 XEIMR	Q5gvv6 xanthomonas
454	29	67.4	426	2	Q5X269 LEGPA	Q5x269 legionella	527	29	67.4	665	2	Q4Q387 LEIMA	Q4q387 leishmania
455	29	67.4	426	2	Q5ZSQ9 LEGPH	Q5zsq9 legionella	528	29	67.4	668	2	Q4WP51 ASPFU	Q4wp51 aspergillus
456	29	67.4	445	2	Q4Q1H4 LEIMA	Q4q1h4 leishmania	529	29	67.4	670	2	Q8YZX5 ANASP	Q8yzx5 anabaena sp
457	29	67.4	452	2	Q4J9K2 SULAC	Q4j9k2 sulfolobus	530	29	67.4	674	2	Q7MFL8 VIBVY	Q7mfl8 vibrio vuln
458	29	67.4	458	2	Q61HM9 CABBR	Q61hm9 caenorhabdi	531	29	67.4	678	2	P87168 SCHRO	P87168 schizosacch
459	29	67.4	460	2	Q6G489 BARHE	Q6g489 bartonella	532	29	67.4	680	2	Q8TNL9 METAC	Q8tnl9 methanosarc
460	29	67.4	463	2	Q7XYH5 CAPAN	Q7xyh5 capsicum an	533	29	67.4	688	2	Q8VNX1 BACTV	Q8vnx1 bacillus ch
461	29	67.4	465	2	Q89RD3 BRAJA	Q89rd3 bradyrhizob	534	29	67.4	688	2	Q7T0P8 XENLA	Q7t0p8 xenopus lae
462	29	67.4	469	1	ER01 ARATH	Q9c7s7 arabidopsis	535	29	67.4	689	2	Q4S171 TETNG	Q4s171 tetraodon n
463	29	67.4	469	2	Q6BGF3 PARTE	Q6bgf3 paramecium m	536	29	67.4	692	2	Q6UEH6 GALME	Q6ueh6 gallieria me
464	29	67.4	470	2	Q92RX5 RHIME	Q92rx5 rhizobium m	537	29	67.4	697	2	Q76208 HYPCU	Q76208 hyphacria
465	29	67.4	472	2	Q8YG93 BRUME	Q8yg93 brucella me	538	29	67.4	700	2	Q5TMB5 9VIRU	Q5tmb5 helicobactid
466	29	67.4	479	2	Q6VAB0 9DEIO	Q6vab0 deinococcus	539	29	67.4	705	2	Q4TLF3 9SPHN	Q4tlf3 erythrobaet
467	29	67.4	481	2	Q4H5Y8 STERE	Q4h5y8 stavia reba	540	29	67.4	708	2	Q7PFY2 ANOGA	Q7pfy2 anopheles g
468	29	67.4	491	2	Q91367 PSEAE	Q91367 pseudomonas	541	29	67.4	726	1	Y440 MYCPN	P75338 mycoplasma
469	29	67.4	491	2	Q882T1 PSESM	Q882t1 pseudomonas	542	29	67.4				

543	29	67.4	739	2	Q4IAU8_GIBZE	Q4IAU8 gibberella	616	29	67.4	1687	1	VIT2_FUNHE	Q98993 fundulus he
544	29	67.4	739	2	Q9HC16_HUMAN	Q9hc16 homo sapien	617	29	67.4	1734	2	Q5WR04_ANGJA	Q5wr04 anguilla ja
545	29	67.4	742	2	Q4S8F4_TETNG	Q4s8f4 tetraodon n	618	29	67.4	1742	2	Q5UBV4_ANGJA	Q5ubv4 anguilla ja
546	29	67.4	743	2	Q9VVK8_DROME	Q9vvnk8 drosophila	619	29	67.4	1757	1	UBR1_MOUSE	O70481 mus musculus
547	29	67.4	746	2	Q21843_CABEL	Q21843 caenorhabdi	620	29	67.4	1814	2	O6WA77_PEA	O6wa77 pisum sativ
548	29	67.4	748	2	Q95Z80_CAEL	Q95z80 caenorhabdi	621	29	67.4	1814	2	O7SZF6_XENIA	O7szf6 xenopus lae
549	29	67.4	751	2	Q7RNF4_PLAYO	Q7rnf4 plasmodium	622	29	67.4	1819	2	Q97K40_CLOAB	Q97k40 clostridium
550	29	67.4	751	2	Q4NHN8_9MICC	Q4nhn8 arthrobacte	623	29	67.4	1875	2	Q5SP25_CRYNE	Q5sp25 cryptococcu
551	29	67.4	752	2	Q4IA08_GIBZE	Q4ia08 gibberella	624	29	67.4	1875	2	Q5KED1_CRYNE	Q5ked1 cryptococcu
552	29	67.4	752	2	Q8LK21_CHLRE	Q8lk21 chlamydomon	625	29	67.4	1876	2	O4P456_USTWA	O4p456 ustilago ma
553	29	67.4	754	2	O6RYX6_BREHE	O6ryx6 brevibacter	626	29	67.4	1892	2	O4G1H1_HUMAN	O4g1h1 homo sapien
554	29	67.4	755	2	O57Y27_9TRYP	O57y27 trypanosoma	627	29	67.4	1892	2	Q8IUJ6_HUMAN	Q8iuj6 homo sapien
555	29	67.4	755	2	Q53NW8_ORYSA	Q53nw8 oryza sativ	628	29	67.4	1998	2	Q585T7_HUMAN	Q585t7 homo sapien
556	29	67.4	787	2	Q8IW25_HUMAN	Q8iw25 homo sapien	629	29	67.4	2009	1	SCN1A_HUMAN	P04774 rattus norv
557	29	67.4	788	2	Q5AU77_EMENI	O5auf7 aspergillus	630	29	67.4	2009	1	SCN1A_RAT	P04774 rattus norv
558	29	67.4	788	2	Q4P8Q3_USTWA	O4p8q3 ustilago ma	631	29	67.4	2028	2	O81129_ARATH	O81129 arabidopsis
559	29	67.4	801	2	O4MX37_BACCE	O4mx37 bacillus ce	632	29	67.4	2051	2	O9SXA1_ARATH	O9sxa1 arabidopsis
560	29	67.4	801	2	Q9REG4_BACCE	Q9reg4 bacillus ce	633	29	67.4	2161	2	O5ZW18_9VIRU	O5zw18 rupestris s
561	29	67.4	801	2	Q7BYC8_BRABR	Q7byc8 bacillus ce	634	29	67.4	2262	2	Q7R5E0_GIALA	O6wa77 pisum sativ
562	29	67.4	810	2	O5RIX7_BRABR	O5rix7 brachydanio	635	29	67.4	2633	2	Q7R5E0_GIALA	O7r5e0 giardia lam
563	29	67.4	814	1	RHG26_HUMAN	O9una1 homo sapien	636	29	67.4	3211	2	O4KJ19_PSBF5	O4k319 pseudomonas
564	29	67.4	819	2	O522T4_MAGGR	O522t4 magnaporthe	637	29	67.4	3469	1	ASPM_SAIBB	P62296 sainri bol
565	29	67.4	823	2	O9LC80_ARTSQ	Q9lc80 arthrobacte	638	29	67.4	3471	1	ASPM_PONPY	P62294 pongo pygma
566	29	67.4	840	2	Q4YU19_PLABE	Q4yu19 plasmodium	639	29	67.4	3473	1	ASPM_AOTVO	P62283 actus vocif
567	29	67.4	847	2	Q6ZQ82_MOUSE	Q6zq82 mus musculus	640	29	67.4	3475	2	O69AX5_CERAE	O69ax5 cercopithec
568	29	67.4	852	2	O5LXB7_SILPO	O5lxb7 silicibacte	641	29	67.4	3476	1	ASPM_GORGO	P62289 gorilla gor
569	29	67.4	858	1	LINES_DROME	O9v4z9 drosophila	642	29	67.4	3476	1	ASPM_MACFA	P62291 macaca fasc
570	29	67.4	862	2	O47424_NEUCR	O47424 neurospora	643	29	67.4	3477	1	ASPM_COLGU	P62287 colobus que
571	29	67.4	874	2	O67R60_SYMTH	Q67r60 symbiobacte	644	29	67.4	3477	1	ASPM_HUMAN	O81xt6 homo sapien
572	29	67.4	875	2	Q5TTS2_ANOGA	Q5tte2 anopheles g	645	29	67.4	3477	1	ASPM_HYLLA	P62290 hylobates l
573	29	67.4	883	2	Q7QC72_ANOGA	Q7qc72 anopheles g	646	29	67.4	3477	1	ASPM_PANTR	P62293 pan troglod
574	29	67.4	904	2	Q54UC2_DICDI	O54uc2 dictyosteli	647	29	67.4	3477	1	Q5VVL3_HUMAN	O5vvl3 homo sapien
575	29	67.4	932	2	Q7VJK1_HELHP	O7vjk1 helicobacte	648	29	67.4	3479	1	ASPM_MACMU	P62292 macaca mula
576	29	67.4	937	2	O6LFP2_PLAF7	O6lfp2 plasmodium	649	29	67.4	4367	1	DYHC_NEUCR	P45443 neurospora
577	29	67.4	938	2	Q4XZ17_PLACH	Q4xz17 plasmodium	650	29	67.4	4830	2	O4PEM9_USTWA	O4pem9 ustilago ma
578	29	67.4	952	1	UVRA_MYCPE	Q8eul1 mycoplasma	651	29	67.4	36	2	O6PR47_SHEEP	O6pr47 ovis aries
579	29	67.4	964	2	Q54PN5_DICDI	Q54pn5 dictyosteli	652	28	65.1	37	2	O6PVS3_SHEEP	O6pvs3 ovis aries
580	29	67.4	976	2	Q53NZ3_ORYSA	Q53nz3 oryza sativ	653	28	65.1	49	2	O5FHR1_LACAC	O5fhr1 lactobacill
581	29	67.4	1017	2	Q64YW0_BACPR	Q64yw0 bacteroides	654	28	65.1	52	2	Q6Z149_ORYSA	O6z149 oryza sativ
582	29	67.4	1023	2	Q8SB11_ORYSA	Q8sb11 oryza sativ	655	28	65.1	69	2	O6GJR4_SHEEP	O6gjr4 ovis aries
583	29	67.4	1023	2	Q7XGB0_ORYSA	Q7xgb0 oryza sativ	656	28	65.1	71	2	O6W188_HILSN	O6w188 rhizobium s
584	29	67.4	1027	2	Q5LHV8_BACFN	Q5lvh8 bacteroides	657	28	65.1	73	2	O89KY1_BRAJA	O89ky1 bradyrhizob
585	29	67.4	1033	2	Q8XQM3_RALSO	Q8xqm3 ralephanti s	658	28	65.1	78	2	Q93JB2_STRCO	Q93jb2 streptomyc
586	29	67.4	1041	2	Q9DKT8_9BETA	Q9dk8 alephanti d	659	28	65.1	100	2	O8KHB3_MYCHO	O8khb3 mycoplasma
587	29	67.4	1050	2	Q4X0U9_ASPFU	O4x0u9 aspergillus	660	28	65.1	100	2	O8KHB4_MYCHO	O8khb4 mycoplasma
588	29	67.4	1057	2	O5B0T1_EMENI	O5b0t1 aspergillus	661	28	65.1	100	2	O8KHB5_MYCHO	O8khb5 mycoplasma
589	29	67.4	1074	2	Q7PTA6_ANOGA	Q7pta6 anopheles g	662	28	65.1	100	2	O8KMI1_MYCHO	O8kmi1 mycoplasma
590	29	67.4	1092	2	P78622_EMENI	P78622 emericella	663	28	65.1	102	2	Q5JXJ9_HUMAN	Q5jxj9 homo sapien
591	29	67.4	1092	2	Q5AZH7_EMENI	Q5azh7 aspergillus	664	28	65.1	103	2	Q5INB6_MAGGR	Q5inb6 magnaporthe
592	29	67.4	1092	2	Q4IQG0_GIBZE	Q4iqg0 gibberella	665	28	65.1	110	2	Q8CD07_MOUSE	Q8cd07 mus musculus
593	29	67.4	1120	2	Q94G17_ORYSA	Q94g17 oryza sativ	666	28	65.1	130	2	O852M7_ORYSA	O852m7 oryza sativ
594	29	67.4	1142	2	Q5VYL4_HUMAN	Q5vyl4 homo sapien	667	28	65.1	131	2	O8T577_PLAFA	O8t577 plasmodium
595	29	67.4	1172	2	Q5YTC3_NOCFA	Q5yc3 nocardia fa	668	28	65.1	134	2	Q6AM04_DESPS	Q6am04 desulfotale
596	29	67.4	1216	2	Q97QP9_STRPN	Q97qp9 streptococc	669	28	65.1	136	2	Q6E220_CAPHI	Q6e220 capra hircu
597	29	67.4	1216	2	Q8DPR6_STRR6	Q8dpr6 streptococc	670	28	65.1	136	2	Q92S92_RHIME	Q92s92 rhizobium m
598	29	67.4	1226	1	KIP4A_XENIA	O4p1784 xenopus lae	671	28	65.1	145	2	Q6S8P5_PLAFA	Q6s8p5 plasmodium
599	29	67.4	1226	2	O6IRM2_XENIA	O6irm2 xenopus lae	672	28	65.1	145	2	O8HZ67_BOSIN	O8hz67 bos indicus
600	29	67.4	1232	2	O4FXD9_LEIMA	O4fxd9 leishmania	673	28	65.1	145	2	O8E677_OCEIH	O8e677 oceanobacil
601	29	67.4	1263	2	Q17373_CABEL	Q17373 caenorhabdi	674	28	65.1	146	2	Q9FFZ6_ARATH	Q9ffz6 arabidopsis
602	29	67.4	1264	2	Q4POM5_USTWA	Q4pom5 ustilago ma	675	28	65.1	155	1	IL2_BOVIN	P05016 bos taurus
603	29	67.4	1297	2	Q5TMP8_ANOGA	Q5tmp8 anopheles g	676	28	65.1	155	1	IL2_BUBBU	O95kp3 bubalus bub
604	29	67.4	1395	2	Q4P950_USTWA	Q4p950 ustilago ma	677	28	65.1	155	1	IL2_CAPHI	P36835 capra hircu
605	29	67.4	1418	2	O81228_PLAF7	O81228 plasmodium	678	28	65.1	155	1	IL2_MOSBE	O5mba8 moschus ber
606	29	67.4	1430	2	Q9VAJ4_DROME	Q9vaj4 drosophila	679	28	65.1	155	1	IL2_SHEEP	P19114 ovis aries
607	29	67.4	1447	2	Q6NNES_DROME	Q6nnes drosophila	680	28	65.1	155	2	O8HYR7_BOVIN	O8hyr7 bos taurus
608	29	67.4	1448	2	Q9V7K2_DROME	Q9v7k2 drosophila	681	28	65.1	155	2	Q5QT38_BOVIN	Q5qt38 bos taurus
609	29	67.4	1476	2	Q6FJ05_CANGA	O6fj05 candida gla	682	28	65.1	155	2	Q5QT37_CAPHI	O5qt37 capra hircu
610	29	67.4	1551	2	Q7QOS0_ANOGA	Q7qos0 anopheles gla	683	28	65.1	155	2	Q4U313_BOSTR	Q4u313 boselaphus
611	29	67.4	1586	2	O52GQ9_MAGGR	O52gq9 magnaporthe	684	28	65.1	156	1	YMG8_BACSU	P71047 bacillus eu
612	29	67.4	1595	2	Q7RVP8_NEUCR	Q7rvp8 neurospora	685	28	65.1	156	2	P71160_BACNO	P71160 bacteroides
613	29	67.4	1596	2	Q9UVY6_SORNA	Q9uyv6 sordaria ma	686	28	65.1	158	2	Q97WJ9_SULSO	Q97wj9 sulfobus
614	29	67.4	1663	2	Q589G6_CONNY	Q589g6 conger myxi	687	28	65.1	162	1	IL2_CEREL	P51747 cervus elap
615	29	67.4	1681	2	Q62467_MOUSE	Q62467 mus musculus	688	28	65.1	165	2	Q5T014_HUMAN	Q5t014 homo sapien

689	28	65.1	168	2	Q6C7R1_YARLI	Q6c7r1	yarrowia li	762	28	65.1	268	1	THIG_NITEU	Q82xi7_nitrosomona
690	28	65.1	173	2	Q51HZ7_MAGGR	Q51hz7	magnaporthe	763	28	65.1	268	2	Q5CF01_CRYHO	Q5cf01_cryptospori
691	28	65.1	174	2	Q9BZR3_HUMAN	Q9bzz3	homo sapien	764	28	65.1	268	2	Q5QN58_ORYSA	Q5qn58_oryza sativ
692	28	65.1	177	1	VG28_BPT4	P13336	bacterioph	765	28	65.1	273	2	Q99QJ1_VIBCH	Q99qj1_vibrio chol
693	28	65.1	177	2	Q6GD32_STAAS	Q6gd32	staphylococ	766	28	65.1	275	2	Q79EX4_PORGI	Q79ex4_porphyromon
694	28	65.1	177	2	Q5HJS9_STAAC	Q5hjs9	staphylococ	767	28	65.1	275	2	Q8VDZ1_MOUSE	Q8vdz1_mus musculus
695	28	65.1	177	2	Q8NYU8_STAAN	Q8nyu8	staphylococ	768	28	65.1	275	2	Q511E1_ENTHI	Q511e1_entamoeba h
696	28	65.1	180	2	Q5T017_HUMAN	Q5t017	homo sapien	769	28	65.1	276	2	Q51A32_ENTHI	Q51a32_entamoeba h
697	28	65.1	180	2	Q7QB77_ANOGA	Q7qbv7	anopheles g	770	28	65.1	277	1	THIG_PROAC	Q6aae4_propionibac
698	28	65.1	182	2	Q5LEG2_SALSA	Q5leg2	salmo salar	771	28	65.1	277	2	Q870X6_NEUCR	Q870x6_neurospora
699	28	65.1	184	1	ARL3_CABEL	Q45379	caenorhabdi	772	28	65.1	277	2	Q8R1F5_MOUSE	Q8r1f5_mus musculus
700	28	65.1	187	2	Q5LHU1_BACFN	Q5lhu1	bacterioides	773	28	65.1	278	1	TCPD_VIBCH	P29491_vibrio chol
701	28	65.1	187	2	Q8VTB1_BACFR	Q8vtb1	bacterioides	774	28	65.1	278	2	Q9HUY3_PSEAE	Q9huy3_pseudomonas
702	28	65.1	190	2	Q9HI84_THEAC	Q9hi84	thermoplaem	775	28	65.1	280	2	Q81EJ8_PLAF7	Q81ej8_plasmodium
703	28	65.1	190	2	Q74HT7_LACJO	Q7hct7	lactobacilli	776	28	65.1	280	2	Q9VL67_DROME	Q9vl67_drosophila
704	28	65.1	190	2	Q9EMI2_AMEPV	Q9em12	amebacta moo	777	28	65.1	281	2	Q3F8U0_9ACTO	Q3f8u0_streptomyce
705	28	65.1	192	2	Q6XYR3_STRSU	Q6xyr3	streptococc	778	28	65.1	281	2	Q44757_BORBU	Q44757_borrelia bu
706	28	65.1	192	2	Q7V7A7_PROMM	Q7v7a7	prochlocco	779	28	65.1	282	2	Q07826_PORGI	Q07826_porphyromon
707	28	65.1	193	2	Q88BZ2_PSEPK	Q8bz22	pseudomonas	780	28	65.1	284	2	Q98PJ9_MYCPU	Q98pj9_mycoplasma
708	28	65.1	194	2	Q4XID1_PLACH	Q4xid1	plasmodium	781	28	65.1	284	2	Q88DJ1_PSEPK	Q88dj1_pseudomonas
709	28	65.1	194	2	Q7VB03_PROMA	Q7vb03	prochlocco	782	28	65.1	292	2	Q8RK99_MYCHO	Q8rk99_mycoplasma
710	28	65.1	195	2	Q6PED9_MOUSE	Q6ped9	mus musculus	783	28	65.1	293	1	MHPC_ECOLI	P77044_escherichia
711	28	65.1	199	1	IL11_HUMAN	P20809	homo sapien	784	28	65.1	294	2	Q8IRV4_DROME	Q8irv4_drosophila
712	28	65.1	199	1	IL11_MACFA	P20808	macaca fasc	785	28	65.1	295	2	Q9NEG2_DROME	Q9neg2_drosophila
713	28	65.1	199	1	IL11_MOUSE	P47873	mus musculus	786	28	65.1	295	2	Q44911_BORBU	Q44911_borrelia bu
714	28	65.1	199	1	IL11_RAT	Q99mf5	rattus norv	787	28	65.1	295	2	Q66126_BORGA	Q66126_borrelia ga
715	28	65.1	199	2	Q95EB4_HUMAN	Q95eb4	homo sapien	788	28	65.1	296	1	EX53_BACSU	P54161_bacillus su
716	28	65.1	203	2	Q8T893_CIOIN	Q8t893	ciona intes	789	28	65.1	296	2	Q4PVJ9_9GAMM	Q4pvj9_psychrobact
717	28	65.1	204	2	Q9BZR4_HUMAN	Q9bzz4	homo sapien	790	28	65.1	296	2	Q726F9_DESVH	Q726f9_desulfovibr
718	28	65.1	204	2	Q72NN4_LEPIC	Q72nn4	leptospira	791	28	65.1	297	1	LIPA_BACCR	Q816a0_bacillus ce
719	28	65.1	204	2	Q8F7W7_LEPIN	Q8f7w7	leptospira	792	28	65.1	297	2	Q7N9J6_PHOLI	Q7n9j6_photorhabdu
720	28	65.1	205	2	Q8DPX7_STRR6	Q8dp7	streptococ	793	28	65.1	298	1	LIPA_BACAN	Q81xm8_bacillus an
721	28	65.1	206	2	Q85F89_SCHJA	Q85f89	schistosoma	794	28	65.1	298	2	Q4MR60_BACCR	Q4mr60_bacillus ce
722	28	65.1	209	1	GIDB_CHRVO	Q7p0a5	chromobacte	795	28	65.1	298	2	Q72YB2_BACCI	Q72yb2_bacillus ce
723	28	65.1	209	2	Q4PHX9_USTMA	Q4phx9	ustilago ma	796	28	65.1	298	2	Q6HBT4_BACCH	Q6hbt4_bacillus th
724	28	65.1	209	2	Q4NQI6_9DELT	Q4nqi6	anaeromyxob	797	28	65.1	298	2	Q63127_BACCC	Q63127_bacillus ce
725	28	65.1	209	2	Q82HR3_STRAW	Q82hr3	streptomyce	798	28	65.1	300	2	Q55EP6_DICDI	Q55ep6_dictyosteli
726	28	65.1	210	2	Q4PAQ4_TETNG	Q4paq4	tetraodon n	799	28	65.1	301	2	Q5E2B0_VIBF1	Q5e2b0_vibrio fiac
727	28	65.1	211	2	Q7X380_9BACT	Q7x380	uncultured	800	28	65.1	302	2	Q986X2_RHILO	Q986x2_rhizobium l
728	28	65.1	211	2	Q8FLJ9_COREF	Q8flj9	corynebacte	801	28	65.1	304	2	Q5ZDI4_ORYSA	Q5zdl4_oryza sativ
729	28	65.1	215	2	Q9W4V2_DROME	Q9w4v2	drosophila	802	28	65.1	308	1	GLSA_PHOLI	Q7n7h7_photorhabdu
730	28	65.1	216	2	Q8MPD7_TABSO	Q8mpd7	taenia soli	803	28	65.1	308	2	Q59KB7_CANAL	Q59kb7_candida alb
731	28	65.1	216	2	Q4K8A4_PSEF5	Q4k8a4	pseudomonas	804	28	65.1	309	2	Q6LTI3_PHOPR	Q6lti3_photobacter
732	28	65.1	216	2	Q72778_HUMAN	Q72778	homo sapien	805	28	65.1	309	2	Q8X5K0_ECO57	Q8x5k0_escherichia
733	28	65.1	221	2	Q4V488_DROME	Q4v488	drosophila	806	28	65.1	310	2	Q9WJ36_HUMAN	Q9w36_homo sapien
734	28	65.1	226	2	Q5TPG5_ANOGA	Q5tpg5	anopheles g	807	28	65.1	311	2	Q4J978_SULAC	Q4j978_sulfolobus
735	28	65.1	227	1	GPMA_NEIMA	Q9tff5	neisseria m	808	28	65.1	311	2	Q580R2_9TRYP	Q580r2_trypanosoma
736	28	65.1	227	2	Q97VQ3_SULSO	Q97vq3	sulfolobus	809	28	65.1	311	2	Q5KVM7_GEOKA	Q5kvm7_geobacillus
737	28	65.1	227	2	Q54DD9_DICDI	Q54dd9	dictyosteli	810	28	65.1	315	2	Q9M1G1_ARATH	Q9m1g1_arabidopsis
738	28	65.1	227	2	Q97MJ8_CLOAB	Q97mj8	clostridium	811	28	65.1	315	2	Q7W172_BORPA	Q7w172_bordetella
739	28	65.1	228	2	Q9F3S2_9BURK	Q9f3s2	cupriavidus	812	28	65.1	315	2	Q7WNW5_BORBR	Q7wnw5_bordetella
740	28	65.1	228	2	Q58AD5_9BURK	Q58ad5	raistonia m	813	28	65.1	317	2	Q7Z5X2_HUMAN	Q7z5x2_homo sapten
741	28	65.1	229	2	Q5Q9A2_HUMAN	Q5q9a2	homo sapien	814	28	65.1	319	2	Q584Q2_9TRYP	Q584q2_trypanosoma
742	28	65.1	229	2	Q5T015_HUMAN	Q5t015	homo sapien	815	28	65.1	322	2	Q63JQ2_BURPS	Q63jq2_burkholderi
743	28	65.1	229	2	Q9HZS3_PSEAE	Q9hzz3	pseudomonas	816	28	65.1	322	2	Q6ZANI_BURMA	Q6zani_burkholderi
744	28	65.1	230	2	Q5LVM1_SILPO	Q5lvn1	silicibacte	817	28	65.1	325	2	Q8YVJ6_ANASP	Q8yv6_anabaena sp
745	28	65.1	235	2	Q4TFJ4_TETNG	Q4tfj4	tetraodon n	818	28	65.1	326	2	Q9HQ03_HALSA	Q9hq03_halobacteri
746	28	65.1	236	2	Q9G5N0_CABEL	Q9g5n0	caenorhabdi	819	28	65.1	326	2	Q4K6S4_PSEF5	Q4k6s4_pseudomonas
747	28	65.1	239	2	Q4STW0_TETNG	Q4stw0	tetraodon n	820	28	65.1	329	2	Q9S6K4_BACTO	Q9s6k4_bacillus th
748	28	65.1	240	1	YAT9_SCHPO	Q10154	schizosacch	821	28	65.1	330	2	Q22929_CABEL	Q22929_caenorhabdi
749	28	65.1	243	2	Q61S79_CABBR	Q61s79	caenorhabdi	822	28	65.1	331	1	ID12_STRMU	Q8dui9_streptococ
750	28	65.1	246	2	Q6GKH0_STAAR	Q6gkh0	staphylococ	823	28	65.1	332	2	Q4FVK3_9GAMM	Q4fvk3_psychrobact
751	28	65.1	247	2	Q9G6S8_HUMAN	Q9g6s8	homo sapien	824	28	65.1	332	2	Q9ZSV3_BACTU	Q9zsv3_bacillus th
752	28	65.1	247	2	Q5T013_HUMAN	Q5t013	homo sapien	825	28	65.1	334	2	Q7U7C2_SINPX	Q7u7c2_synecococc
753	28	65.1	250	2	Q6UQA3_TETNG	Q6uqa3	tetraodon n	826	28	65.1	336	2	Q8M368_TRYCR	Q8m368_trypanosoma
754	28	65.1	258	2	Q7MMW3_PORGI	Q7mmw3	porphyromon	827	28	65.1	337	2	Q5A021_PARDE	Q5a021_paracoccu
755	28	65.1	263	2	Q7RZ20_NEUCR	Q7rzz20	neurospora	828	28	65.1	341	1	DCUP_BRUSE	Q8fyt1_brucella me
756	28	65.1	263	2	Q82Z14_ENTFA	Q82z14	entrococcu	829	28	65.1	341	1	DCUP_BRUSE	Q8fyt1_brucella me
757	28	65.1	263	2	Q6GK46_STAAR	Q6gk46	staphylococ	830	28	65.1	341	2	Q57AJ2_BRUAB	Q57aj2_brucella ab
758	28	65.1	264	2	Q8BQT2_MOUSE	Q8bqt2	mus musculus	831	28	65.1	342	2	Q6RW19_9ZZZZ	Q6rw19_uncultured
759	28	65.1	265	2	Q7P1D9_CHRVO	Q7p1d9	chromobacte	832	28	65.1	342	2	Q61D37_CABBR	Q61d37_caenorhabdi
760	28	65.1	266	2	Q8SV83_ENCCU	Q8sv83	encephalito	833	28	65.1	343	2	P79459_AMBME	P79459_ambystoma m
761	28	65.1	267	2	Q8CC70_MOUSE	Q8cc70	mus musculus	834	28	65.1	344	2	Q8KZ07_9PROT	Q8kz07_uncultured



835	28	65.1	344	2	Q5LMB5_SILPO	Q5lmb5 silicibacte	908	28	65.1	438	2	Q9FLA2_ARATH	Q9fla2 arabidopsis
836	28	65.1	347	2	Q96IH6_HUMAN	Q96ih6 homo sapien	909	28	65.1	438	2	Q814K7_BACCFR	Q814k7 bacillus ce
837	28	65.1	347	2	Q9KAR0_BACHD	Q9kar0 bacillus ha	910	28	65.1	439	2	Q5LEQ8_BACCFR	Q5leq8 bacteroides
838	28	65.1	348	2	Q6BK36_DEBHA	Q6bk36 debaryomyce	911	28	65.1	439	2	Q64SN0_BACFR	Q64sn0 bacteroides
839	28	65.1	348	2	Q8NGP4_HUMAN	Q8ngp4 homo sapien	912	28	65.1	439	2	Q6LJ10_PHOPR	Q6lj10 photobacter
840	28	65.1	348	2	Q9HAP5_HUMAN	Q9hap5 homo sapien	913	28	65.1	443	2	Q5JXK0_HUMAN	Q5jxk0 homo sapien
841	28	65.1	349	2	Q41B69_GIBZE	Q41b69 gibberella	914	28	65.1	443	2	Q7SG00_LEPIC	Q7sg00 leptospira
842	28	65.1	349	2	Q8LQ06_CHLRE	Q8lq06 chlamydomon	915	28	65.1	443	2	Q6QPC5_9ADEN	Q6qpc5 simtan aden
843	28	65.1	350	2	Q8HXL2_GLUOX	Q8hxl2 gluconobact	916	28	65.1	446	2	Q8E016_STRA5	Q8e016 streptococc
844	28	65.1	350	2	Q8HX51_SALSA	Q8hx51 salmo salar	917	28	65.1	446	2	Q8BE61_STRA5	Q8be61 streptococc
845	28	65.1	352	2	Q8ASQ9_ARATH	Q8asq9 arabidopsis	918	28	65.1	447	2	Q8GDN0_PHOJU	Q8gdn0 photorhabdu
846	28	65.1	352	1	FIXB_RHIME	Q98819 rhizobium m	919	28	65.1	449	2	Q9EM03_THERAC	Q9em03 thermoplasm
847	28	65.1	354	2	Q59T99_CANAL	Q59t99 candida alb	920	28	65.1	449	2	Q5FBA7_FUGRU	Q5fba7 fugu rubrip
848	28	65.1	354	2	Q59TJ7_CANAL	Q59tj7 candida alb	921	28	65.1	450	2	Q9XIC6_ARATH	Q9xic6 arabidopsis
849	28	65.1	355	2	Q4R0J8_STRCX	Q4r0j8 streptomyc	922	28	65.1	450	2	Q4RJS8_TETNG	Q4rjs8 tetraodon n
850	28	65.1	355	2	Q8R038_STRCX	Q8r038 streptomyc	923	28	65.1	452	1	SYN MYGWS	Q6mf2 mycoplasma
851	28	65.1	355	2	Q8HX50_SALSA	Q8hx50 salmo salar	924	28	65.1	452	2	Q59EU0_HUMAN	Q59eu0 homo sapien
852	28	65.1	359	2	Q71AE0_9NUCL	Q71ae0 namestra co	925	28	65.1	452	2	P72790_SYNY3	Q72790 synechocyst
853	28	65.1	359	2	Q8UM81_9NUCL	Q8um81 namestra co	926	28	65.1	455	2	Q7MVF5_PORGI	Q7mvf5 porphyromon
854	28	65.1	359	2	Q8QLG2_NPVMC	Q8qlg2 namestra co	927	28	65.1	456	2	Q918S0_COTJA	Q918s0 coturnix co
855	28	65.1	360	1	WNT2_CAEEL	P34989 caenorhabdi	928	28	65.1	461	2	Q6MEQ4_PARUM	Q6meg4 parachlamyd
856	28	65.1	360	2	Q61YS0_CAEBR	Q61ys0 caenorhabdi	929	28	65.1	464	2	Q5L6Y3_CHLAB	Q5l6y3 chlamydophi
857	28	65.1	360	2	Q8EAF9_SHEON	Q8eaf9 shewanella	930	28	65.1	464	2	Q84498_CHLTR	Q84498 chlamydia t
858	28	65.1	362	2	Q7ZAA7_METVO	Q7zaa7 methanococc	931	28	65.1	464	2	Q824L5_CHLCP	Q824l5 chlamydophi
859	28	65.1	363	2	Q4HGG0_CAMCO	Q4hgg0 campylobact	932	28	65.1	464	2	Q927U4_CHLPN	Q927u4 chlamydia p
860	28	65.1	363	2	Q89388_CHVP1	Q89388 paramecium	933	28	65.1	467	2	Q5A126_CANAL	Q5a126 candida alb
861	28	65.1	363	2	Q5UMG5_HALMA	Q5umg5 haloarcula	934	28	65.1	470	2	Q750S7_ASHGO	Q750s7 ashbya goss
862	28	65.1	365	2	Q6AR01_DESPS	Q6ar01 desulfotale	935	28	65.1	471	2	Q568H5_BRARE	Q568h5 brachydanio
863	28	65.1	366	2	Q4IDP9_GIBZE	Q4idp9 gibberella	936	28	65.1	472	2	Q4R704_MACFA	Q4r704 macaca fasc
864	28	65.1	371	2	Q50117_BRARE	Q50117 brachydanio	937	28	65.1	473	2	Q41W70_AZOV1	Q41w70 azotobacter
865	28	65.1	374	2	Q8UYF0_PYRAB	Q8uyf0 pyrococcus	938	28	65.1	474	1	TRME_CANBF	Q7vqv3 candidosac
866	28	65.1	377	2	Q9C1Y2_MOUSE	Q9c1y2 mus musculus	939	28	65.1	475	1	YGMH_SCHPO	Q42965 schizosacch
867	28	65.1	379	2	Q7W810_BORPA	Q7w810 bordetella	940	28	65.1	477	2	Q5U821_BACTT	Q5u821 bacillus th
868	28	65.1	379	2	Q7WM42_BORBR	Q7wm42 bordetella	941	28	65.1	477	2	Q8RLW1_BACTU	Q8rlw1 bacillus th
869	28	65.1	379	2	Q8A3T8_BACTN	Q8a3t8 bacteroides	942	28	65.1	479	2	Q8EY40_LEPIN	Q8ey40 leptospira
870	28	65.1	381	2	Q7U810_SYNPF	Q7u810 synechococc	943	28	65.1	484	1	PEPD_ECOLI	P15288 escherichia
871	28	65.1	384	2	Q30282_ARCFU	Q30282 archaeoglob	944	28	65.1	485	2	Q5DXY6_ECOLI	Q5dxy6 escherichia
872	28	65.1	388	2	Q6PB03_ACTAD	Q6pb03 acinetobact	945	28	65.1	485	2	Q5X137_LEGPA	Q5x137 legionella
873	28	65.1	390	2	Q7QQJ4_GIALA	Q7qqj4 giardia lam	946	28	65.1	485	2	Q8FKM8_ECOL6	Q8fkm8 escherichia
874	28	65.1	392	2	Q5U221_HALMA	Q5uz21 haloarcula	947	28	65.1	485	2	Q83MM9_SHIFL	Q83mm9 shigella fl
875	28	65.1	392	2	Q9RZE4_DEINA	Q9rze4 deinococcus	948	28	65.1	485	2	Q8X7N8_ECO57	Q8x7n8 escherichia
876	28	65.1	394	2	Q17841_CAEEL	Q17841 caenorhabdi	949	28	65.1	487	2	Q580S7_9TRYP	Q580s7 trypanosoma
877	28	65.1	397	2	Q5NM12_FUGRU	Q5nm12 fugu rubrip	950	28	65.1	490	1	Q5WSW3_LEGFL	Q5wsww3 legionella
878	28	65.1	400	2	Q5NM10_LEGPL	Q5nm10 legionella	951	28	65.1	490	1	GCSPB_STAAM	P64219 staphylococ
879	28	65.1	400	2	Q5X4M0_LEGPA	Q5x4m0 legionella	952	28	65.1	490	1	GCSPB_STAAN	P99168 staphylococ
880	28	65.1	400	2	Q5ZUV5_LEGPH	Q5zuv5 legionella	953	28	65.1	490	1	GCSPB_STAAS	Q69394 staphylococ
881	28	65.1	407	2	Q6FT77_CANGA	Q6ft77 candida gla	954	28	65.1	490	1	GCSPB_STAAS	Q69394 staphylococ
882	28	65.1	408	2	Q9MIE9_ARATH	Q9mie9 arabidopsis	955	28	65.1	490	1	GCSPB_STAAM	Q8nmw0 staphylococ
883	28	65.1	408	2	Q6PP46_ACTAD	Q6pp46 acinetobact	956	28	65.1	490	1	Q72X28_BACC1	Q72x28 bacillus ce
884	28	65.1	410	2	Q7SAF9_NEUCR	Q7saf9 neurospora	957	28	65.1	490	2	Q5HFM4_STAAC	Q5hfm4 staphylococ
885	28	65.1	410	2	Q6MB07_PARUM	Q6mb07 parachlamyd	958	28	65.1	492	2	Q4L6N5_STAHT	Q4l6n5 staphylococ
886	28	65.1	413	2	Q7XTM1_ORVSA	Q7xtm1 oryza sativ	959	28	65.1	497	2	Q89GT8_BRAJA	Q89gt8 bradyrhizob
887	28	65.1	413	2	Q9AV74_ORVSA	Q9av74 oryza sativ	960	28	65.1	499	1	CEP57_BOVIN	Q865v0 bos taurus
888	28	65.1	416	2	Q6AJM3_DESPS	Q6ajm3 desulfotale	961	28	65.1	500	1	CEP57_MOUSE	Q86cxr8 homo sapien
889	28	65.1	416	2	Q9PUF2_BOTJA	Q9puf2 bothriops ja	962	28	65.1	500	1	CEP57_MOUSE	Q8cse0 homo musculu
890	28	65.1	417	1	ACLIC_AKGAC	Q9pw36 agkistrodon	963	28	65.1	500	1	K0830_HUMAN	Q94919 homo sapien
891	28	65.1	417	1	MTK1_KLEPN	P25238 klebsiella	964	28	65.1	500	2	Q5JBA6_HUMAN	Q5jba6 homo sapien
892	28	65.1	417	2	Q8PXN4_METWA	Q8pxn4 methanosarc	965	28	65.1	500	2	Q75UY7_9LILI	Q75uy7 zosteria jap
893	28	65.1	417	2	Q9W7S2_AKGAC	Q9w7s2 agkistrodon	966	28	65.1	500	2	Q7YIV6_9LILI	Q7yiv6 zosteria mue
894	28	65.1	419	2	Q9PJQ0_CHLMD	Q9pjq0 chlamydia m	967	28	65.1	500	2	Q7YNT8_9LILI	Q7ynt8 zosteria nov
895	28	65.1	420	2	Q6LX28_METWP	Q6lx28 methanococc	968	28	65.1	500	2	Q7YNU0_9LILI	Q7ynu0 heterozoste
896	28	65.1	421	2	Q4ZN01_PSESY	Q4zn01 pseudomonas	969	28	65.1	500	2	Q7YNU1_9LILI	Q7ynu1 zosteria nol
897	28	65.1	425	2	Q5B4Z7_EMENI	Q5b4z7 aspergillus	970	28	65.1	500	2	Q7YNU2_9LILI	Q7ynu2 zosteria muc
898	28	65.1	425	2	Q9NXL5_HUMAN	Q9nxl5 homo sapien	971	28	65.1	500	2	Q7YNU3_9LILI	Q7ynu3 zosteria cap
899	28	65.1	426	2	Q5RIH9_BRARE	Q5rih9 brachydanio	972	28	65.1	500	2	Q7YNU4_9LILI	Q7ynu4 zosteria jap
900	28	65.1	428	2	Q4UBJ5_THEAN	Q4ubj5 theileria a	973	28	65.1	500	2	Q7YNU5_9LILI	Q7ynu5 zosteria cap
901	28	65.1	429	2	Q4YRX7_PLABE	Q4yrx7 plasmodium	974	28	65.1	501	1	K0830_MOUSE	Q8c522 mus musculu
902	28	65.1	429	2	Q8KFO8_CHLTE	Q8kfg8 chlorobium	975	28	65.1	501	2	Q27479_CAEEL	Q27479 caenorhabdi
903	28	65.1	429	2	Q6P0Z8_BRARE	Q6p0z8 brachydanio	976	28	65.1	501	2	Q4VA96_MOUSE	Q4va96 mus musculu
904	28	65.1	432	2	Q5JN45_ORVSA	Q5jn45 oryza sativ	977	28	65.1	502	2	Q5ZRM9_LEGPH	Q5zrm9 legionella
905	28	65.1	432	2	Q5XGF9_XENTR	Q5xgf9 xenopus tro	978	28	65.1	503	2	Q20040_CAEEL	Q20040 caenorhabdi
906	28	65.1	438	1	MNTH2_PSEAB	Q9rp2 pseudomonas	979	28	65.1	503	2	Q7YNT9_9LILI	Q7ynt9 phyllospadi
907	28	65.1	438	2	Q4IN54_GIBZE	Q4in54 gibberella	980	28	65.1	503	2	Q9M1F1_ARATH	Q9m1f1 arabidopsis

981 28 65.1 506 2 Q8YVB4 ANASP  
 982 28 65.1 507 2 Q5V126 HALMA  
 983 28 65.1 508 2 Q6M9V1 PARUW  
 984 28 65.1 508 2 Q99LHO MOUSE  
 985 28 65.1 511 2 Q6C6M6 YARLI  
 986 28 65.1 511 2 Q4UC15 THEAN  
 987 28 65.1 511 2 Q8MQ61 CAENORHABDI  
 988 28 65.1 511 2 Q983P8 RHILLO  
 989 28 65.1 511 2 Q63IW3 BURPS  
 990 28 65.1 512 2 Q6C7I1 YARLI  
 991 28 65.1 513 2 Q5U655 CRYNE  
 992 28 65.1 513 2 Q8BWV7 MOUSE  
 993 28 65.1 516 2 Q59LT6 CANAL  
 994 28 65.1 517 2 Q59HN5 GRVBI  
 995 28 65.1 519 2 Q8D7S7 VIBVU  
 996 28 65.1 519 2 Q7MEU1 VIBVU  
 997 28 65.1 523 2 Q6UXC4 HUMAN  
 998 28 65.1 523 2 Q8NBP2 HUMAN  
 999 28 65.1 527 2 Q6O9T9 METCA  
 1000 28 65.1 529 2 Q6F823 ACIAD

## ALIGNMENTS

RESULT 1  
 QSEK72\_HUMAN  
 ID Q5BK12 HUMAN PRELIMINARY; PRT; 349 AA.  
 AC Q5BK12;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE EIF353 protein.  
 GN Name=EIF353;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Pituitary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Pituitary;  
 RG NIH MGC Project;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; BC090880; AAH90880.1; -; mRNA.  
 DR InterPro; IPR009081; ACP like.  
 DR InterPro; IPR011989; ARM-like.  
 DR InterPro; IPR003139; D retro matrix.  
 DR InterPro; IPR011992; EF-Hand\_type.

DR InterPro; IPR000555; Mov34\_MPN\_PAD1.  
 DR Pfam; PF01398; Mov34; 1.  
 DR SMART; SM00232; JAB\_MPN; 1.  
 SQ SEQUENCE 349 AA; 39610 MW; 35EB28E07F52C6C7 CRC64;  
 Query Match 100.0%; Score 43; DB 2; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NQLLMDRV 9  
 DB 239 NQLLMDRV 247  
 RESULT 2  
 IF33\_HUMAN  
 ID IF33\_HUMAN STANDARD; PRT; 352 AA.  
 AC O15372;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 10-MAY-2005 (Rel. 39, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Eukaryotic translation initiation factor 3 subunit 3 (eIF-3 gamma)  
 DE (eIF3 p40 subunit) (eIF3h).  
 GN Name=EIF383;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=98001678; PubMed=9341143; DOI=10.1074/jbc.272.43.27042;  
 RA Asano K., Vornlocher H.-P., Richter-Cook N.J., Merrick W.C.,  
 RA Hinnebusch A.G., Hershey J.W.B.;  
 RT "Structure of cDNAs encoding human eukaryotic initiation factor 3  
 subunits. Possible roles in RNA binding and macromolecular assembly.";  
 RL J. Biol. Chem. 272:27042-27052 (1997).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -!- FUNCTION: Binds to the 40S ribosome and promotes the binding of  
 methionyl-tRNAi and mRNA. Associates with the p170 subunit of  
 EIF3.  
 CC -!- SUBUNIT: eIF-3 is composed of at least 12 different subunits.

```
CC -1- SIMILARITY: Contains 1 MPN (JAB/Mov34) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF092576; AAC84044.1; -; mRNA.
CC EMBL; AF092576; AAC84044.1; -; Genomic DNA.
CC EMBL; AF092576; AAC84044.1; JOINED; Genomic DNA.
CC EMBL; AF092570; AAC84044.1; JOINED; Genomic DNA.
CC EMBL; AF092571; AAC84044.1; JOINED; Genomic DNA.
CC EMBL; AF092572; AAC84044.1; JOINED; Genomic DNA.
CC EMBL; AF092573; AAC84044.1; JOINED; Genomic DNA.
CC EMBL; AF092574; AAC84044.1; JOINED; Genomic DNA.
CC EMBL; AF092575; AAC84044.1; JOINED; Genomic DNA.
CC EMBL; BC000386; AAH00386.1; -; mRNA.
CC MEROPS; M67.971; -.
CC Ensembl; ENSG00000147677; Homo sapiens.
CC HGNC; HGNC:3273; EIF33.
CC H-InvDB; HIX0007736; -.
CC Reactome; O15372; -.
CC MIM; 603912; -.
CC GO; GO:0005852; C:eukaryotic translation initiation factor 3...; TAS.
CC GO; GO:0008135; P:translation factor activity, nucleic acid b...; TAS.
CC GO; GO:0006446; P:regulation of translational initiation; TAS.
CC InterPro; IPR000555; Mov34_MPN_PAD1.
CC Pfam; PF01398; Mov34; 1.
CC SMART; SM00232; JAB_MPN; 1.
CC Initiation factor; Protein biosynthesis.
KW CONFLICT 73 73 E -> K (in Ref. 2).
FT CONFLICT 73 73
SQ SEQUENCE 352 AA; 39930 MW; F3A6EFA0CEP587D0 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 242 NLQLLMDRV 250
|||||

RESULT 3
Q53HG0 HUMAN PRELIMINARY; PRT; 352 AA.
AC Q53HG0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa
DE variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK222520; BAD96240.1; -; mRNA.
KW Initiation factor.
FT NON_TER 1
SQ SEQUENCE 352 AA; 39914 MW; F3A6EFB18BE1C7D0 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 242 NLQLLMDRV 250
|||||

RESULT 5
Q6IB98 HUMAN PRELIMINARY; PRT; 352 AA.
ID Q6IB98 HUMAN PRELIMINARY;
AC Q6IB98;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
RN NUCLEOTIDE SEQUENCE.
```

```
RC TISSUE=Cerebellum;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK222520; BAD96340.1; -; mRNA.
KW Initiation factor.
FT NON_TER 1
SQ SEQUENCE 352 AA; 39870 MW; 257134D0D3435547 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 242 NLQLLMDRV 250
|||||

RESULT 4
Q53HR0 HUMAN PRELIMINARY; PRT; 352 AA.
ID Q53HR0 HUMAN PRELIMINARY;
AC Q53HR0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa
DE variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK222520; BAD96240.1; -; mRNA.
KW Initiation factor.
FT NON_TER 1
SQ SEQUENCE 352 AA; 39914 MW; F3A6EFB18BE1C7D0 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 242 NLQLLMDRV 250
|||||

RESULT 5
Q6IB98 HUMAN PRELIMINARY; PRT; 352 AA.
ID Q6IB98 HUMAN PRELIMINARY;
AC Q6IB98;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
RN NUCLEOTIDE SEQUENCE.
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DE EIF3S3 protein (Eukaryotic translation initiation factor 3, subunit 3  
DE gamma, 40kDa).  
GN Name=EIF3S3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RT "Cloning of human full-length cDNAs in BD Creator (TM) System Donor  
RT vector";  
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR456906; CAG33187.1; -; mRNA.  
DR EMBL; BT019594; AAV38401.1; -; mRNA.  
KW Initiation factor.  
SQ SEQUENCE 352 AA; 39930 MW; F3A6EFA0CF587D0 CRC64;  
  
Query Match 100.0%; Score 43; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NQLQLMDRV 9  
Db 242 NQLQLMDRV 250  
|||||  
  
RESULT 6  
ID Q6PSU8\_RAT PRELIMINARY; PRT; 352 AA.  
AC Q6PSU8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Eukaryotic translation initiation factor 3, subunit 3 gamma,  
DE 40kDa.  
GN Name=EIF3S3;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pituitary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapchenko M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pituitary gland;  
RA Strausberg R.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC060586; AAH05086.1; -; mRNA.  
DR RGD; 735178; Eif3e3.  
DR GO; GO:0003743; P:translation initiation factor activity; IEA.  
DR InterPro; IPR000555; Mov34\_MPN\_PADI.  
DR Pfam; PF01398; MOV34; 1.  
DR SMART; SM00232; JAB\_MPN; 1.  
KW Initiation factor.  
SQ SEQUENCE 352 AA; 39905 MW; C06307269ADB343 CRC64;  
  
Query Match 100.0%; Score 43; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NQLQLMDRV 9  
Db 242 NQLQLMDRV 250  
|||||  
  
RESULT 7  
ID Q4RFC4\_TETNG PRELIMINARY; PRT; 315 AA.  
AC Q4RFC4;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome 8 SCAP15119, whole genome shotgun sequence.  
GN ORFNames=GSTENG00035383001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat G., Bottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAG01015119; CAG12908.1; -; Genomic DNA.  
SQ SEQUENCE 315 AA; 36113 MW; 53CC944D7B742C55 CRC64;  
  
Query Match 88.4%; Score 38; DB 2; Length 315;  
Best Local Similarity 88.9%; Pred. No. 17;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NQLQLMDRV 9  
Db 206 SLQLQLMDRV 214  
:|||||

```

RESULT 8
Q5PPY6 XENLA PRELIMINARY; PRT; 334 AA.
ID Q5PPY6 XENLA PRELIMINARY; PRT; 334 AA.
AC Q5PPY6;
DT 01-FEB-2005 (T-EMBLrel. 29, Created)
DT 01-FEB-2005 (T-EMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE LOC496043 protein.
GN Names=LOC496043;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Testis;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Testis;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RG NIH MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087438; AAH87438.1; -; mRNA.
DR ZFIN; ZDB-GENE-040808-19; zgc:101085.
DR GO; GO:0008180; C:signalosome complex; IEA.
DR InterPro; IPR000555; Mov34_MPN_PAD1.
DR Pfam; PF01398; Mov34; 1.
DR SMART; SM00232; JAB_MPN; 1.
KW Initiation factor.
SQ SEQUENCE 334 AA; 38391 MW; 4ED0C8588A009F7 CRC64;
Query Match 88.4%; Score 38; DB 2; Length 334;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLQLLMDRV 9
DB 224 SLQLLMDRV 232
RESULT 9
Q6AXJ2 BRARE PRELIMINARY; PRT; 335 AA.
ID Q6AXJ2 BRARE PRELIMINARY; PRT; 335 AA.
AC Q6AXJ2;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)

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DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Eukaryotic translation initiation factor 3, subunit 3 (Gamma).
GN Name=eif3s3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Singapore local strain; TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Singapore local strain; TISSUE=Embryo;
RG NIH MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079514; AAH79514.1; -; mRNA.
DR ZFIN; ZDB-GENE-040808-19; zgc:101085.
DR GO; GO:0008180; C:signalosome complex; IEA.
DR InterPro; IPR000555; Mov34_MPN_PAD1.
DR Pfam; PF01398; Mov34; 1.
DR SMART; SM00232; JAB_MPN; 1.
KW Initiation factor.
SQ SEQUENCE 335 AA; 38597 MW; 4715E55BEFCC19A CRC64;
Query Match 88.4%; Score 38; DB 2; Length 335;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLQLLMDRV 9
DB 225 SLQLLMDRV 233
RESULT 10
Q6P381 XENTR PRELIMINARY; PRT; 335 AA.
ID Q6P381 XENTR PRELIMINARY; PRT; 335 AA.
AC Q6P381;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75580.
GN Name=MGC75580;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
NCBI_TaxID=8364;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064151; AAH64151.1; -; mRNA.
DR InterPro; IPR000555; Mov34_MPN_PAD1.
DR Pfam; PF01398; Mov34; 1.
DR SMART; SM00232; JAB_MPN; 1.
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 38538 MW; 18D4D446D6561BE9 CRC64;

Query Match 88.4%; Score 38; DB 2; Length 335;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLLMDRV 9
DB 225 SLQLMDRV 233
:|||||

RESULT 11
ID Q5ZLE6 CHICK PRELIMINARY; PRT; 348 AA.
AC Q5ZLE6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04_618;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ719788; CAG31447.1; -; mRNA.
DR GO; GO:0008180; C:signalosome complex; IEA.
DR InterPro; IPR000555; Mov34_MPN_PAD1.
DR Pfam; PF01398; Mov34; 1.
DR SMART; SM00232; JAB_MPN; 1.
KW Hypothetical protein.
SQ SEQUENCE 348 AA; 39537 MW; 034A361FCA60FA61 CRC64;
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Query Match 88.4%; Score 38; DB 2; Length 348;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLLMDRV 9
DB 238 SLQLMDRV 246
:|||||

RESULT 12
ID IF33 MOUSE STANDARD; PRT; 352 AA.
AC Q91WK2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Eukaryotic translation initiation factor 3 subunit 3 (eIF-3 gamma)
DE (eIF3 p40 subunit) (eIF3h).
GN Name=Bif3a3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Eye, and Retina;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds to the 40S ribosome and promotes the binding of
CC methionyl-tRNAi and mRNA. Associates with the p170 subunit of
CC EIF3.
CC -!- SUBUNIT: eIF-3 is composed of at least 12 different subunits.
CC -!- SIMILARITY: Contains 1 MPN (JAB/Mov34) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BC014755; AAH14755.1; -; mRNA.
DR MEROPS; M67.971; -.
DR Ensembl; ENSMUSG00000022312; Mus musculus.
DR MGI; MGI:1915385; Eif3a3.
DR InterPro; IPR000555; Mov34_MPN_PAD1.
DR Pfam; PF01398; Mov34; 1.
DR SMART; SM00232; JAB_MPN; 1.
KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 352 AA; 39832 MW; 96F5AB8E2F41F838 CRC64;

Query Match 88.4%; Score 38; DB 1; Length 352;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 NLQLLMDRV 9  
 ID :|||||  
 Db 242 SLQLLMDRV 250

RESULT 13  
 Q8BTX5 MOUSE  
 ID Q8BTX5\_MOUSE PRELIMINARY; PRT; 352 AA.  
 AC Q8BTX5;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430016K01 product:eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD), full insert sequence.  
 DE Name=Eif383;  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wyszewski B., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RN [3]  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [4]  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 NUCLEOTIDE SEQUENCE.  
 RP

RC STRAIN=NOD; TISSUE=Thymus;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saiton H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami A., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK088436; BAC40351.1; -, mRNA.  
 DR MGI; MGI:1915385; Eif383.  
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.  
 DR InterPro; IPR000555; MOV34\_MPN\_PADI.  
 DR Pfam; PF01398; MOV34; 1.  
 DR SMART; SM00232; JAB\_MPN; 1.  
 KW Initiation factor.  
 SQ SEQUENCE 352 AA; 39846 MW; E6F5A89E2F41F97D CRC64;  
 Query Match 88.4%; Score 38; DB 2; Length 352;  
 Best Local Similarity 88.9%; Pred. No. 19;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 NLQLLMDRV 9  
 Db 242 SLQLLMDRV 250

RESULT 14  
 Q5M9L0 MOUSE  
 ID Q5M9L0\_MOUSE PRELIMINARY; PRT; 352 AA.  
 AC Q5M9L0;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Eukaryotic translation initiation factor 3, subunit 3 (gamma).  
 GN Name=Eif383;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=FVB/N;  
 RC TISSUE=Kidney, and  
 RC Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RA Director MGC Project;  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N;  
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old  
 RC virgin mouse. Taken by biopsy;  
 RG NIH MGC Project;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC086915; AAH86915.1; -; mRNA.  
 DR EMBL; BC091728; AAH91728.1; -; mRNA.  
 KW Initiation factor.  
 SQ SEQUENCE 352 AA; 39832 MW; 96F5A88E2F41F838 CRC64;

Query Match 88.4%; Score 38; DB 2; Length 352;  
 Best Local Similarity 88.9%; Pred. No. 19;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9  
 Db 242 SIQLLMDRV 250  
 :|||||

RESULT 15  
 Q56JZ5 BOVIN  
 ID Q56JZ5\_BOVIN PRELIMINARY; PRT; 352 AA.  
 AC Q56JZ5\_ BOVIN PRELIMINARY;  
 DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
 DE Eukaryotic translation initiation factor 3 subunit 3 gamma.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OC NCBI TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymphoid;  
 RA Xu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;  
 RT "Analysis of sequences obtained from constructed full-length bovine  
 RT cDNA libraries.";  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY911332; AAW82100.1; -; mRNA.  
 KW Initiation factor.  
 SQ SEQUENCE 352 AA; 39906 MW; 29D678DEC880CE8E CRC64;

Query Match 86.0%; Score 37; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQQLMDRV 9  
 Db 243 LQQLMDRV 250  
 :|||||

RESULT 16

Q8DJU7 SYNEL  
 ID Q8DJU7\_SYNEL PRELIMINARY; PRT; 473 AA.  
 AC Q8DJU7\_ SYNEL PRELIMINARY;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE T111125 protein.  
 GN OrderedLocustNames=t111125;  
 OS Synechococcus elongatus (Thermosynechococcus elongatus).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OC NCBI TaxID=32046;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BP-1;  
 EX MEDLINE=2225144; PubMed=12240834;  
 RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,  
 RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,  
 RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the thermophilic cyanobacterium  
 RT Thermosynechococcus elongatus BP-1.";  
 RT DNA Res. 9:123-130(2002).  
 RL EMBL; BA000039; HAC08677.1; -; Genomic\_DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 473 AA; 52173 MW; 1CCD151C50F402C1 CRC64;

Query Match 86.0%; Score 37; DB 2; Length 473;  
 Best Local Similarity 77.8%; Pred. No. 42;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9  
 Db 429 NLQLLMDRV 437  
 :|||||

RESULT 17  
 Q94BU3 ARATH  
 ID Q94BU3\_ARATH PRELIMINARY; PRT; 196 AA.  
 AC Q94BU3\_ ARATH PRELIMINARY;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
 DE T29M8.1/T29M8.1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,  
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,  
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,  
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,  
 RA Davis R.W., Theologis A., Ecker J.R.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,  
 RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY039891; AAK63995.1; -; mRNA.  
 DR EMBL; AY077672; AAL76150.1; -; mRNA.  
 SQ SEQUENCE 196 AA; 21478 MW; 995CA7D4BADF82AA CRC64;



Query Match 83.7%; Score 36; DB 2; Length 196;  
 Best Local Similarity 87.5%; Pred. No. 27;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQMLMDRV 9  
 |||||:  
 Db 146 LQMLMDRI 153

## RESULT 18

Q8LAP2 ARATH  
 ID Q8LAP2 ARATH PRELIMINARY; PRT; 311 AA.  
 AC Q8LAP2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22088475; PubMed=12093376;  
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RT annotation";  
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY087694; AAM65231.1; -; mRNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 311 AA; 34387 MW; 1ACCD30D7260A0A0 CRC64;

Query Match 83.7%; Score 36; DB 2; Length 311;  
 Best Local Similarity 87.5%; Pred. No. 44;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQMLMDRV 9  
 |||||:  
 Db 146 LQMLMDRI 153

## RESULT 19

Q9LMB2 ARATH  
 ID Q9LMB2 ARATH PRELIMINARY; PRT; 311 AA.  
 AC Q9LMB2;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE T29M8.1 protein.  
 GN Name-T29M8.1;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Liu S.-X., Vaysberg M., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H.,  
 RA Toriumi M., Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A.,  
 RA Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,  
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,  
 RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,  
 RA Federspiel N.A., theologis A.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC069143; AAF82225.1; -; Genomic\_DNA.  
 DR PIR; G86324; G86324.

DR GO; GO:0005739; C-mitochondrion; IDA.  
 SQ SEQUENCE 311 AA; 34341 MW; F4CCASBD69623AA0 CRC64;

Query Match 83.7%; Score 36; DB 2; Length 311;  
 Best Local Similarity 87.5%; Pred. No. 44;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQMLMDRV 9  
 |||||:  
 Db 146 LQMLMDRI 153

## RESULT 20

Q5PR67 BRARE  
 ID Q5PR67 BRARE PRELIMINARY; PRT; 338 AA.  
 AC Q5PR67;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Heart;  
 RA Director MGC Project;  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC086809; AAH86809.1; -; mRNA.  
 DR InterPro; IPR000555; Mov34\_MPN\_PAD1.  
 DR Pfam; PF01398; Mov34; 1.  
 DR SMART; SM0232; JAB\_MPN; 1.  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 338 AA; 38806 MW; DE14B7197055EBFA CRC64;

Query Match 83.7%; Score 36; DB 2; Length 338;  
 Best Local Similarity 77.8%; Pred. No. 48;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQMLMDRV 9  
 :|||:  
 Db 228 SLQMLMDRV 236

## RESULT 21

Q9LMB3 ARATH

ID Q9LMB3 ARATH PRELIMINARY; PRT; 342 AA.  
 AC Q9LMB3;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE F14D16.30.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosoids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,  
 RA Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,  
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,  
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,  
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
 RA Ecker J.R.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,  
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 RA Theologis A., Ecker J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC068602; AAF79297.1; -; Genomic DNA.  
 SQ SEQUENCE 342 AA; 38937 MW; 48B2B19ECF26617D CRC64;  
  
 Query Match 83.7%; Score 36; DB 2; Length 342;  
 Best Local Similarity 87.5%; Pred. No. 49;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 LQLMDRV 9  
 Db 146 LQLMDRI 153  
  
 RESULT 22  
 Q4Q3R9 LEIMA  
 ID Q4Q3R9 LEIMA PRELIMINARY; PRT; 1232 AA.  
 AC Q4Q3R9;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=LmjF33.2670;  
 OS Leishmania major.  
 OC Eukaryota; Euzoenzoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Friedlin;  
 RA Peacock C.S., Murphy L., Ivens A.C., Bertiman M., Blackwell J.,  
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,  
 RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR05270; CAJ06739.1; -; Genomic DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1232 AA; 133167 MW; F1F4803BDEB20DFA CRC64;  
  
 Query Match 83.7%; Score 36; DB 2; Length 1232;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 NLQLMDRV 9  
 Db 978 NLQLVLDRI 986

RESULT 23  
 NIP7\_HUMAN  
 ID NIP7\_HUMAN STANDARD; PRT; 180 AA.  
 AC Q9Y221; Q9NZ20;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE 60S ribosome subunit biogenesis protein NIP7 homolog (KD93).  
 DE Name=NIP7;  
 GN ORFNames=CGI-37, HSPC031, HSPC180, OK/SW-cl.76, OK/SW-cl.78;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RX MEDLINE=20272150; PubMed=10810093; DOI=10.1101/gr.10.5.703;  
 RA Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;  
 RT "Identification of novel human genes evolutionarily conserved in  
 RT Caenorhabditis elegans by comparative proteomics.";  
 RL Genome Res. 10:703-713(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).  
 RC TISSUE=Umbilical cord blood;  
 RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;  
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC TISSUE=Colon adenocarcinoma;  
 RA Shichiyo S., Itoh K.;  
 RT "Identification of immuno-peptidmics that are recognized by tumor-  
 RT reactive CTL generated from TIL of colon cancer patients.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
 RC TISSUE=Periodontal ligament;  
 RA Myokai F.;  
 RT "Mechanical stress-induced gene 26-1, 26-2.";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC TISSUE=Skin;  
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]

RP SUBCELLULAR LOCATION, AND IDENTIFICATION BY MASS SPECTROMETRY.  
 RX MEDLINE=22317277; PubMed=12429849; DOI=10.1091/mbc.R02-05-0271;  
 RA Scherl A., Couté Y., Deon C., Calle A., Kindbeiter K., Sanchez J.-C.,  
 RA Greco A., Hochstrasser D.P., Diaz J.-J.,  
 RT "Functional proteomic analysis of human nucleolus";  
 RL Mol. Biol. Cell 13:4100-4109(2002).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS), AND SUBUNIT STRUCTURE.  
 RP PubMed=15522784; DOI=10.1016/j.jeb.2004.06.010;  
 RA Liu J.-F., Wang X.-Q., Wang X.-X., Chen J.-R., Jiang T., An X.-M.,  
 RA Chang W.-R., Liang D.-C.,  
 RT "Crystal structure of KD93, a novel protein expressed in human  
 RT hematopoietic stem/progenitor cells";  
 RL J. Struct. Biol. 148:370-374(2004).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RA Kuzin A.P., Chen Y., Forouhar F., Acton T.B., Shastry R., Ma L.-C.,  
 RA Cooper B., Xiao R., Montelione G., Tong L., Hunt J.F.,  
 RT "Crystal structure of northeast structural genomics consortium target  
 RT HR2118: a human homolog of Saccharomyces cerevisiae NIP7p";  
 RL Submitted (JUN-2004) to the PDB data bank.  
 CC -!- FUNCTION: May play a role in 60S ribosomal subunit synthesis  
 CC (Potential).  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9Y221-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9Y221-2; Sequence=VSP\_012094;  
 CC -!- SIMILARITY: Belongs to the NIP7 family.  
 CC -!- SIMILARITY: Contains 1 PUA domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; AF132971; AAD27746.1; -; mRNA.  
 DR EMBL; AF085360; AAD40195.1; -; mRNA.  
 DR EMBL; AF161528; AAF29143.1; -; mRNA.  
 DR EMBL; AB062398; BAB93485.1; -; mRNA.  
 DR EMBL; AB062479; BAB93504.1; -; mRNA.  
 DR EMBL; AB112439; BAD05056.1; -; mRNA.  
 DR EMBL; BC015941; AAH15941.1; -; mRNA.  
 DR PDB; 1SQW; X-ray; A=1-180.  
 DR PDB; 1TSY; X-ray; A=1-180.  
 DR SWISS-2DPAGE; Q9Y221; HUMAN.  
 DR Ensembl; ENSG0000132603; Homo sapiens.  
 DR InterPro; IPR002478; PUA.  
 DR SMART; SM00359; PUA; 1.  
 DR PROSITE; P50890; PUA; 1.  
 KW 3D-structure; Alternative splicing; Nuclear protein;  
 KW Ribosome biogenesis.  
 FT DOMAIN 94 170 PUA.  
 FT VARSPIC 95 141 Missing (in isoform 2).  
 FT FTID=VSP\_012094.  
 SQ SEQUENCE 180 AA; 20463 MW; FC6CFB2250AA4FC9 CRC64;  
 Query Match 81.4%; Score 35; DB 1; Length 180;  
 Best Local Similarity 87.5%; Pred. No. 41;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NQLQLMDR 8  
 Db 23 NQLQLVDR 30  
 |||||:|  
 RESULT 24  
 NIP7 MOUSE  
 ID\_NIP7\_MOUSE STANDARD; PRT; 180 AA.

AC 09CXK8; Q9D1B4;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE 60S ribosome subunit biogenesis protein NIP7 homolog (Peachy) (KD93).  
 GN Name=Nip7;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic head;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reid D.J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynnshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shizaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: May play a role in 60S ribosomal subunit synthesis  
 CC (Potential).  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).  
 CC -!- SIMILARITY: Belongs to the NIP7 family.

```
CC -!- SIMILARITY: Contains 1 PUA domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AK003739; BAB22972.1; -; mRNA.
CC EMBL; AK014290; BAB23247.1; -; mRNA.
CC EMBL; BC003972; AAH03972.1; -; mRNA.
CC SMR; Q9CXK8; 1-176.
CC MGI; MGI:1913414; 1110017C15Rik.
CC InterPro; IPR002478; PUA.
CC SMART; SM00359; PUA; 1.
CC PROSITE; PS0890; PUA; 1.
KW Nuclear protein; Ribosome biogenesis.
FT DOMAIN 94 170 PUA.
FT CONFLICT 10 10 R -> P (in Ref. 1; BAB22972).
SQ SEQUENCE 180 AA; 20452 MW; 4F1256165370F2AF CRC64;
Query Match 81.4%; Score 35; DB 1; Length 180;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLQLLMDR 8
Db 23 NLQLLVDR 30
|||:|:|
|||:|:|

RESULT 25
NIP7_RAT STANDARD; PRT; 180 AA.
AC Q9WV50;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 60S ribosome subunit biogenesis protein NIP7 homolog (PEachy) (K9D3).
GN Name=Nip7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Wang Z., Tanniswood M.;
RT "Cloning and characterization of pEachy, a rat sequence with homology
RT to Saccharomyces cerevisiae Nip7p.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=pituitary;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: May play a role in 60S ribosomal subunit synthesis
CC (Potential).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -!- SIMILARITY: Belongs to the NIP7 family.
CC -!- SIMILARITY: Contains 1 PUA domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF158186; RAD42887.1; -; mRNA.
CC EMBL; BC059114; RAH59114.1; -; mRNA.
CC SMR; Q9WV50; 1-176.
CC Ensembl; ENSRNOG0000020391; Rattus norvegicus.
```

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DR InterPro; IPR002478; PUA.
DR PROSITE; PS0890; PUA; 1.
KW Nuclear protein; Ribosome biogenesis.
FT DOMAIN 94 170 PUA.
SQ SEQUENCE 180 AA; 20432 MW; B39D7B9EB8E5509A CRC64;
Query Match 81.4%; Score 35; DB 1; Length 180;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLQLLMDR 8
Db 23 NLQLLVDR 30
|||:|:|
|||:|:|

RESULT 26
Q56P27_PIG PRELIMINARY; PRT; 180 AA.
AC Q56P27;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE PUA protein.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC SUB; NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu G.Y., Xiong Z.Y.;
RT "Isolation and prediction of one novel swine gene that is
RT differentially expressed in the longissimus dorsi muscle and backfat
RT tissues from Meishan, Meishan Large White cross and Large White
RT pigs.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY864609; AAX77005.1; -; mRNA.
SQ SEQUENCE 180 AA; 20491 MW; 3F8A4A11E391DDDD CRC64;
Query Match 81.4%; Score 35; DB 2; Length 180;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLQLLMDR 8
Db 23 NLQLLVDR 30
|||:|:|
|||:|:|

RESULT 27
Q5R9J1_PONPY PRELIMINARY; PRT; 180 AA.
AC Q5R9J1;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp468F182.
GN Name=DKFZp468F182;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG The German cDNA Consortium;
RA Bloecker H., Boecker M., Brandt P., Mewes H.W., Weill B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; CR859396; CAH91569.1; -; mRNA.
DR SMR; Q5R9J1; 1-170.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
```



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RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC052449; AAH52449.1; -; mRNA.
DR EMBL; BC060701; AAH60701.1; -; mRNA.
DR Ensembl; ENSMUSG00000002496; Mus musculus.
DR MGI; MGI:102548; Tsc2.
DR GO; GO:0046626; P:regulation of insulin receptor signaling pa. . .; IMP.
DR InterPro; IPR011989; ARM-like.
DR InterPro; IPR000331; Rap-GAP.
DR InterPro; IPR003913; Tuberin.
DR Pfam; PF02145; Rap_GAP; 1.
DR Pfam; PF03542; Tuberin; 1.
DR PRINTS; PR01431; TUBERIN.
DR PROSITE; PS50085; RAPGAP; 1.
KW Anti-oncogene.
SQ SEQUENCE 1742 AA; 194099 MW; 051548778578BF2 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 1742;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLQMDR 8
Db 444 NQLQMDR 451

RESULT 31
TSC2 RAT STANDARD; PRT; 1809 AA.
ID P49816;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tuberin (Tuberous sclerosis 2 homolog protein).
GN Name=Tsc2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4).
RC STRAIN=Wislar; TISSUE=Kidney;
RX MEDLINE=96063895; PubMed=8519695;
RA Xiao G.-H., Jin F., Yeung R.S.;
RT "Identification of tuberous sclerosis 2 messenger RNA splice variants
RT that are conserved and differentially expressed in rat and human
RT tissues.";
RL Cell Growth Differ. 6:1185-1191(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC STRAIN=Long Evans; TISSUE=Brain, and Kidney;
RX MEDLINE=95380273; PubMed=7651821;
RA Kobayashi T., Nishizawa M., Hirayama Y., Kobayashi E., Hino O.;
RT "cDNA structure, alternative splicing and exon-intron organization of
RT the predisposing tuberous sclerosis (Tsc2) gene of the Eker rat
RT model.";
RL Nucleic Acids Res. 23:2608-2613(1995).
RN [3]
RP TUBERIN-RAB5 BINDING.
RX MEDLINE=97197768; PubMed=9045618; DOI=10.1074/jbc.272.10.6097;
RA Xiao G.-H., Shoranejad F., Jin F., Golemis E.A., Yeung R.S.;
RT "The tuberous sclerosis 2 gene product, tuberin, functions as a Rab5
RT GTPase activating protein (GAP) in modulating endocytosis.";
RL J. Biol. Chem. 272:6097-6100(1997).
RN [4]
RP MUTAGENESIS OF ASN-314 AND LEU-713.
RX MEDLINE=99151532; PubMed=10029074;
RA Satake N., Kobayashi T., Kobayashi E., Izumi K., Hino O.;
RT "Isolation and characterization of a rat homologue of the human
RT tuberous sclerosis 1 gene (Tsc1) and analysis of its mutations in rat
RT renal carcinomas";
RL Cancer Res. 59:849-855(1999).

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CC -!- FUNCTION: Implicated as a tumor suppressor. May have a function in
CC vesicular transport, but may also play a role in the regulation of
CC cell growth arrest and in the regulation of transcription mediated
CC by steroid receptors. Interaction between hamartin and tuberin may
CC facilitate vesicular docking. Specifically stimulates the
CC intrinsic GTPase activity of the ras-related protein RAP1A and
CC RAB5. Suggesting a possible mechanism for its role in regulating
CC cellular growth.
CC -!- SUBUNIT: Interacts with hamartin. May also interact with the
CC adapter molecule rabaptin 5. The final complex contains tuberin
CC and rabaptin 5 linked to RAB5 (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P49816-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P49816-2; Sequence=VSP_004481;
CC Name=3;
CC IsoId=P49816-3; Sequence=VSP_004482;
CC Name=4;
CC IsoId=P49816-4; Sequence=VSP_004481, VSP_004482;
CC -!- TISSUE SPECIFICITY: CNS, uterus, heart, skeletal muscle, kidney
CC and spleen.
CC -!- DISEASE: A germline insertion in Tsc2 is the cause of the Eker rat
CC model of inherited cancer susceptibility. Gives rise to a spectrum
CC of epithelial and nonepithelial neoplasms.
CC -!- SIMILARITY: Contains 1 Rap-GAP domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U24150; AAC52289.1; -; mRNA.
CC EMBL; D50413; BAA08914.1; -; mRNA.
CC PIR; S57329; S57329.
CC Ensembl; ENSRNOG00000011375; Rattus norvegicus.
CC RGD; 3908; Tsc2.
CC GO; GO:0005097; P:Rab GTPase activator activity; TAS.
CC GO; GO:0006953; P:acute-phase response; IMP.
CC GO; GO:0008285; P:negative regulation of cell proliferation; IMP.
CC GO; GO:0000074; P:regulation of cell cycle; IMP.
CC GO; GO:0007165; P:signal transduction; IDA.
CC InterPro; IPR011989; ARM-like.
CC InterPro; IPR000331; Rap-GAP.
CC InterPro; IPR003913; Tuberin.
CC Pfam; PF02145; Rap_GAP; 1.
CC Pfam; PF03542; Tuberin; 1.
CC PRINTS; PR01431; TUBERIN.
CC PROSITE; PS50085; RAPGAP; 1.
CC KW Alternative splicing; Anti-oncogene; Cell cycle; GTPase activation.
CC DOMAIN 1533 1760
CC VARSPLIC 947 989
CC VARSPLIC 1272 1294
CC MUTAGEN 314 314
CC MUTAGEN 713 713
CC CONFLICT 932 932
CC CONFLICT 1514 1514
CC CONFLICT 1730 1730
CC SEQUENCE 1809 AA; 201278 MW; 6190BEFB45272664 CRC64;

Query Match 81.4%; Score 35; DB 1; Length 1809;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLQMDR 8
|||||:

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```

Db          444 NLQLLMER 451

RESULT 32
TSC2 MOUSE
ID TSC2_MOUSE STANDARD; PRT: 1814 AA.
AC Q61037; P97723; P97724; P97725; P97727; Q61007; Q61008; Q9WUF6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-MAY-2005 (Rel. 40, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tuberin (Tuberous sclerosis 2 homolog protein).
GN Names=Tsc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS A; B; C; D; E; F AND G).
RC TISSUE=Heart;
RA MEDLINE=96258425; PubMed=8777431;
RX Kim K.K., Pajak L., Wang H., Field L.J.;
RT "Cloning, developmental expression, and evidence for alternative
RT splicing of the murine tuberous sclerosis (TSC2) gene product.";
RL Cell. Mol. Biol. Res. 41:515-526 (1995).
[2]
RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
RA MEDLINE=96430093; PubMed=8833243; DOI=10.1007/s003359900057;
RX Olsson P.G., Schofield J.N., Edwards Y.H., Frischauf A.M.;
RT "Expression and differential splicing of the mouse TSC2 homolog.";
RL Mamm. Genome 7:212-215 (1996).
[3]
RP NUCLEOTIDE SEQUENCE OF 1-199.
RC STRAIN=BALB/c; TISSUE=Leukocyte;
RX MEDLINE=98417643; PubMed=9743625; DOI=10.1006/jmbi.1998.2042;
RA Sarker A.H., Ikeda S., Nakano H., Terato H., Ide H., Inai K.,
RA Akiyama K., Tsutsui K., Bo Z., Kubo K., Yamamoto K., Yasui A.,
RA Yoshida M.C., Seki S.;
RT "Cloning and characterization of a mouse homologue (mNchl1) of
RT Escherichia coli endonuclease III.";
RL J. Mol. Biol. 282:761-774 (1998).
[4]
RP NUCLEOTIDE SEQUENCE OF 119-1805.
RX MEDLINE=20051947; PubMed=10584558;
RA Klymenova E.V., Declue J.E., Walker C.L.;
RT "Genetic variants of the tuberous sclerosis 2 tumour suppressor gene
RT in mouse t haplotypes.";
RL Genet. Res. 74:139-144 (1999).
CC -1- FUNCTION: Implicated as a tumor suppressor. May have a function in
CC vesicular transport, but may also play a role in the regulation of
CC cell growth arrest and in the regulation of transcription mediated
CC by steroid receptors. Interaction between hamartin and tuberin may
CC facilitate vesicular docking. Specifically stimulates the
CC intrinsic GTPase activity of the ras-related protein RAP1A and
CC RAB5. Suggesting a possible mechanism for its role in regulating
CC cellular growth (By similarity).
CC -1- SUBUNIT: Interacts with hamartin. May also interact with the
CC adapter molecule rabaptin 5. The final complex contains tuberin
CC and rabaptin 5 linked to RAB5 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. At steady state found in
CC association with membranes (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=7;
CC Names=G;
CC IsoId=Q61037-1; Sequence=Displayed;
CC Name=A;
CC IsoId=Q61037-2; Sequence=VSP_004473;
CC Name=B;
CC IsoId=Q61037-3; Sequence=VSP_004474;
CC Name=C;
CC IsoId=Q61037-4; Sequence=VSP_004476;
CC Name=D;
CC IsoId=Q61037-5; Sequence=VSP_004478;

Name=E;
IsoId=Q61037-6; Sequence=VSP_004477, VSP_004478, VSP_004479;
Name=F;
IsoId=Q61037-7; Sequence=VSP_004475, VSP_004477, VSP_004478,
VSP_004479, VSP_004480;
-1- TISSUE SPECIFICITY: Widely expressed.
-1- SIMILARITY: Contains 1 Rap-GAP domain.
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removed.
EMBL; U37775; AAA86902.1; -; mRNA.
EMBL; U37775; AAA86901.1; -; mRNA.
EMBL; U37775; AAB18754.1; -; mRNA.
EMBL; AB009371; BAA28845.1; -; Genomic_DNA.
EMBL; AF132986; AAD27867.1; -; mRNA.
DR Ensembl; ENSMUSG00000002496; Mus musculus.
DR MGI; MGI:102548; Tsc2.
DR GO; GO:0046626; P:regulation of insulin receptor signaling pa...; IMP.
DR InterPro; IPR011989; ARM-like.
DR InterPro; IPR012340; OB_NA_ba_sub.
DR InterPro; IPR000331; Rap_GAP.
DR Pfam; PF02145; Rap_GAP; 1.
DR Pfam; PF03542; Tuberin; 1.
DR PRINTS; PR01431; TUBERIN.
DR PROSITE; PS50085; RAPGAP; 1.
KW Alternative splicing; Anti-oncogene; Cell cycle; GTPase activation.
FT DOMAIN 1532 1766 Rap-GAP.
FT VARSPPLIC 79 115 Missing (in isoform A).
FT VARSPPLIC 534 572 Missing (in isoform B).
FT VARSPPLIC 947 990 Missing (in isoform C).
FT VARSPPLIC 947 989 Missing (in isoform F).
FT VARSPPLIC 1245 1258 GHAPVQIVSATGC -> RDTALYKSLVPAAG (in
isoform E and isoform F).
FT VARSPPLIC 1271 1293 Missing (in isoform D, isoform E and
isoform F).
FT VARSPPLIC 1693 1728 GPACKEWRFQGEIVVWALPVVWELTVTILLCHLQ -> M
EGLVDTSVAKIVSDRLNSFVARQWALHAN (in isoform
E and isoform F).
FT VARSPPLIC 1776 1814 Missing (in isoform F).
FT CONFLICT 161 161 Missing (in Ref. 2).
FT CONFLICT 269 269 G -> S (in Ref. 2).
FT CONFLICT 462 462 A -> R (in Ref. 2).
FT CONFLICT 476 476 I -> N (in Ref. 2).
FT CONFLICT 549 549 D -> N (in Ref. 2).
FT CONFLICT 707 707 K -> N (in Ref. 4).
FT CONFLICT 861 862 VP -> AA (in Ref. 2).
FT CONFLICT 1127 1127 R -> P (in Ref. 2).
FT CONFLICT 1665 1665 Missing (in Ref. 2).
SQ SEQUENCE 1814 AA; 202071 MW; 913AB87194AADASB CRC64;

Query Match 81.4%; Score 35; DB 1; Length 1814;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMER 8
DB 444 NLQLLMER 451

RESULT 33

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Q6V1Z6 PAGMA  
ID Q6V1Z6\_PAGMA PRELIMINARY; PRT; 149 AA.  
AC Q6V1Z6;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Translation initiation factor 3 (Fragment).  
OS Pagrus major (Red sea bream) (Chrysophrys major).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;  
OC Sparidae; Pagrus.  
OX NCBI\_TaxID=143350;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spine;  
RA Chen S.L., Xu M.Y., Hu S.L., Li L.;  
RT "Analysis of immune-relevant genes expressed in red sea bream  
RT spleen.";  
RL Aquaculture 240:115-130(2004).  
DR EMBL; AY190743; AAP20218.1; -; mRNA.  
DR GO; GO:0003743; F:translational initiation factor activity; IEA.  
DR InterPro; IPR000555; Mov34\_MPN\_PAD1.  
DR Pfam; PF01398; Mov34; 1.  
KW Initiation factor.  
FT NON\_TER 149  
SQ SEQUENCE 149 AA; 17246 MW; 26DA91A07DF0CB79 CRC64;  
Query Match 79.1%; Score 34; DB 2; Length 149;  
Best Local Similarity 87.5%; Pred. No. 55;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NQLQMLDR 8  
Db 142 SLQQLMLDR 149  
RESULT 34  
Q31388\_CYPCA PRELIMINARY; PRT; 285 AA.  
ID Q31388;  
AC Q31388;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NAR-2004 (TREMBLrel. 26, Last annotation update)  
DE MHC class I protein precursor (Fragment).  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxID=7962;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DOR70;  
RX MEDLINE=96217555; PubMed=8613142; DOI=10.1007/s002510050088;  
RA van Erp S.H., Dixon B., Figueroa F., Egberts E., Stet R.J.;  
RT "Identification and characterization of a novel class I gene in carp  
RT (Cyprinus carpio L.).";  
RL Immunogenetics 44:49-61(1996).  
DR EMBL; X91022; CAA62498.1; -; mRNA.  
DR GO; GO:0042612; C:MHC class I protein complex; IEA.  
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
DR GO; GO:0019882; P:antigen presentation; IEA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR001039; MHC\_I\_alpha\_A1A2.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00129; MHC\_I; 1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR SMART; SM00407; IGcl; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Signal.

FT SIGNAL 1 17 Potential.  
FT NON\_TER 285 285  
SQ SEQUENCE 285 AA; 32801 MW; 74633B20688B9B82 CRC64;  
Query Match 79.1%; Score 34; DB 2; Length 285;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NQLQMLDR 8  
Db 91 NQLQMLDR 98  
RESULT 35  
Q73MF8\_TREDE PRELIMINARY; PRT; 560 AA.  
ID Q73MF8;  
AC Q73MF8;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Phosphofructokinase, pyrophosphate-dependent.  
GN OrderedLocNames=TDE1550;  
OS Treponema denticola.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=158;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 35405 / DSM 14222;  
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;  
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,  
RA Dodson R.J., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,  
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,  
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,  
RA Gebregeorgis E., Geer K., Tshegaye G., Malek J.A., Ayodeji B.,  
RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,  
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,  
RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;  
RT "Comparison of the genome of the oral pathogen Treponema denticola  
RT with other spirochete genomes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).  
DR EMBL; AB017251; AAS12067.1; -; Genomic\_DNA.  
DR TIGR; TDE1550; -.  
DR GO; GO:0005945; C:6-phosphofructokinase complex; IEA.  
DR GO; GO:0003872; E:6-phosphofructokinase activity; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0047334; F:diphosphate-fructose-6-phosphate 1-phosphot. . .; IEA.  
DR GO; GO:0006096; P:glycolysis; IEA.  
DR InterPro; IPR011183; Pfam\_PPI\_PFK.  
DR InterPro; IPR000023; Ppfuckinase.  
DR Pfam; PF00365; PFK; 1.  
DR PIRSF; PIRSF005677; PPI\_PFK\_PfPB; 1.  
DR PRINTS; PR00476; PHFRCTKINASE.  
DR ProDom; PD000707; Ppfuckinase; 1.  
KW Complete proteome.  
SQ SEQUENCE 560 AA; 63141 MW; D5D9695D26343B17 CRC64;  
Query Match 79.1%; Score 34; DB 2; Length 560;  
Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NQLQMLDR 8  
Db 371 SLQQLMLDR 378  
RESULT 36  
Q5EUI0\_9PLAN PRELIMINARY; PRT; 659 AA.  
ID Q5EUI0\_9PLAN PRELIMINARY;  
AC Q5EUI0;  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE Hypothetical protein.



OS Gemmata sp. Wal-1.  
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
OC Planctomycetaceae; Gemmata.  
OX NCBI\_TaxID=235140;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wal-1;  
RX PubMed=15667994; DOI=10.1016/j.femsle.2004.11.034;  
RA Staley J.T., Bouzek H., Jenkins C.;  
RT "Bukaryotic signature proteins of Prostheco bacter dejongei and  
RT Gemmata sp. Wal-1 as revealed by in silico analysis.";  
RL PEMS Microbiol. Lett. 243:9-14(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wal-1;  
RA Campbell J.W.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AY738475; AX07502.1; -; Genomic\_DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
DR ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 659 AA; 72766 MW; 3C4C99C9EA217182 CRC64;  
Query Match 79.1%; Score 34; DB 2; Length 659;  
Best Local Similarity 77.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NLQLMDRV 9  
Db 591 NLTLMDRV 599  
RESULT 37  
RPOC1 ANFTFO STANDARD; PRT; 681 AA.  
AC Q85CL6;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (PEP) (Plastid-  
DE encoded RNA polymerase beta' subunit) (RNA polymerase beta' subunit).  
GN Name-rpoC1; rpoC1 (Hornwort).  
OS Anthoceros formosae (Hornwort).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Anthocerotophyta;  
OC Anthocerotales; Anthocerotaceae; Anthoceros.  
OX NCBI\_TaxID=48387;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA], AND RNA EDITING.  
RC TISSUE=Thallus;  
RX MEDLINE=22415709; PubMed=12527781; DOI=10.1093/nar/gkg155;  
RA Kugita M., Kaneko A., Yamamoto Y., Takeya Y., Matsumoto T.,  
RA Yoshinaga K.;  
RT "The complete nucleotide sequence of the hornwort (Anthoceros  
RT formosae) chloroplast genome: insight into the earliest land plants.";  
RL Nucleic Acids Res. 31:716-721(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE, AND RNA EDITING.  
RC TISSUE=Thallus;  
RX MEDLINE=22598217; PubMed=12711687; DOI=10.1093/nar/gkg327;  
RA Kugita M., Yamamoto Y., Fujikawa T., Matsumoto T., Yoshinaga K.;  
RT "RNA editing in hornwort chloroplasts makes more than half the genes  
RT functional.";  
RL Nucleic Acids Res. 31:2417-2423(2003).  
CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription  
CC of DNA into RNA using the four ribonucleoside triphosphates as  
CC substrates.  
CC -1- CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate  
CC + RNA(n+1).  
CC -1- SUBUNIT: In plastids the minimal PEP RNA polymerase catalytic core  
CC is composed of four subunits: alpha, beta, beta', and beta''. When  
CC a (nuclear-encoded) sigma factor is associated with the core the  
CC holoenzyme is formed, which can initiate transcription (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Chloroplast.  
CC -1- RNA EDITING: Modified\_positions=43, 56, 87, 123, 238, 240, 270,  
CC 273, 290, 296, 335, 341, 344, 355, 368, 375, 384, 390, 398, 406,  
CC 435, 457, 466, 477, 481, 486, 494, 512, 523, 548, 653, 654;  
CC Note=The nonsense codons at positions 240, 344, 375, 494 and 548  
CC are modified to sense codons.  
CC -1- SIMILARITY: Belongs to the RNA polymerase beta' chain family.  
CC RpoC1 subfamily.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; AB086179; BAC55327.1; -; Genomic\_DNA.  
CC EMBL; AB087419; BAC55418.1; -; mRNA.  
CC HSSP; OSKWTU6; LHQM.  
CC HAMAP; MF\_01323; -; 1.  
CC InterPro; IPR000722; RNA\_pol\_A.  
CC InterPro; IPR007080; RNA\_pol\_Rpb1\_1.  
CC InterPro; IPR006592; RNA\_pol\_A\_N.  
CC Pfam; PF04997; RNA\_pol\_Rpb1\_1; 1.  
CC Pfam; PF00623; RPOLA\_N; 1.  
CC SMART; SM00663; RPOLA\_N; 1.  
CC Chloroplast; DNA-directed RNA polymerase; Nucleotidyltransferase;  
KW RNA editing; Transcription; Transferase.  
SQ SEQUENCE 681 AA; 78871 MW; 164735C163338CDB CRC64;  
Query Match 79.1%; Score 34; DB 1; Length 681;  
Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLQLMDR 8  
Db 207 NLQIVMDR 214  
RESULT 38  
Q6BZ11 DEBHA  
ID Q6BZ11\_DEBHA PRELIMINARY; PRT; 808 AA.  
AC Q6BZ11;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Debaryomyces hansenii chromosome A of strain CBS767 of Debaryomyces  
DE hansenii.  
GN OrderedLocusNames=DEHA0A054569;  
OS Debaryomyces hansenii (Yeast) (Torulasporea hansenii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.  
OX NCBI\_TaxID=4959;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 36239 / CBS 767;  
RX PubMed=15229592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E.,  
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barthe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boisrane A., Boyer J., Catolico L., Confanioleri P., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lequr I., Ma L., Muller H.,  
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts.";  
 RL Nature 430:35-44(2004).  
 DR EMBL; CR382133; CAG84513.1; -; Genomic DNA.  
 DR GO; GO:0030127; C:COPII vesicle coat; IEA.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR GO; GO:0005794; C:Golgi apparatus; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0006888; F:ER to Golgi transport; IEA.  
 DR GO; GO:0006886; F:intracellular protein transport; IEA.  
 DR InterPro; IPR007123; Gelsolin.  
 DR InterPro; IPR006900; Sec23 helical.  
 DR InterPro; IPR006896; Sec23\_trunk.  
 DR Pfam; PF00626; Gelsolin; 1.  
 DR Pfam; PF04815; Sec23 helical; 1.  
 DR Pfam; PF04811; Sec23\_trunk; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 808 AA; 91224 MW; C7517D3AD2CABF87 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 808;  
 Best Local Similarity 77.8%; Pred. No. 3.2e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
 |||||  
 Db 792 NLQFWDHV 800  
 |||||

RESULT 39  
 ID Q7UJS8 RHOBX PRELIMINARY; PRT; 964 AA.  
 AC Q7UJS8;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Similar to response regulator aspartate phosphatase rapC.  
 GN OrderedLocusNames=RB11084;  
 OS Rhodopirellula baltica.  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellula.  
 OX NCBI\_TaxID=117;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=1;  
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;  
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
 RA Schlesner H., Amann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 strain 1."; Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
 RL EMBL; BX294152; CAD77153.1; -; Genomic DNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0030090; C:reaction center (sensu Proteobacteria); IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0006118; F:electron transport; IEA.  
 DR GO; GO:0006810; F:transport; IEA.  
 DR InterPro; IPR011031; Multihem cyt.  
 DR InterPro; IPR011990; TPR-like helical.  
 DR PROSITE; PS51008; MULTIHEME\_CYTC; 1.

KW Complete proteome.  
 SQ SEQUENCE 964 AA; 109575 MW; 95158629B29AFFF1 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 964;  
 Best Local Similarity 77.8%; Pred. No. 3.9e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
 |||||  
 Db 879 NLQLLYDKL 887  
 |||||

RESULT 40  
 ID O18415 DROME PRELIMINARY; PRT; 1116 AA.  
 AC O18415;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Nuclear protein SA.  
 GN Name=SA; ORFNames=CG3423;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Canton S.;  
 RA Valdeolmillos A.M., Villares R., Buesa J.M., Gonzalez-Crespo S.,  
 RA Martinez A., Barbero J.L.;  
 RT "Molecular Cloning and Expression of Stromalin Protein from Drosophila  
 RT melanogaster: Homologous to Mammalian Stromalin Family of Nuclear  
 RT Proteins."; DNA Cell Biol. 8:699-706(1998).  
 RL EMBL; Y14277; CAA74654.1; -; mRNA.  
 DR PIR; T13854; T13854.  
 DR Ensembl; CG3423; Drosophila melanogaster.  
 DR FlyBase; FBgn0020616; CG3423.  
 DR FlyBase; FBgn0020616; SA.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0007076; P:mitotic chromosome condensation; IEA.  
 KW Nuclear protein.  
 SQ SEQUENCE 1116 AA; 128793 MW; 1802E8F93C7FB295 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 1116;  
 Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDRV 9  
 |||||  
 Db 630 NLQALLDRI 638  
 |||||

RESULT 41  
 ID Q9VM62 DROME PRELIMINARY; PRT; 1127 AA.  
 AC Q9VM62; Q95RF8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE CG3423-PA (LD34181P).  
 GN Name=SA; ORFNames=CG3423;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 Brannon R.C., Rogers J.H., Blazek R.G., Champagne M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 April J.P., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 Balles R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 Foster C., Gabrielian A., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
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 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
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 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,  
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 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
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 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
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 Science 287:2185-2195 (2000).  
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RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
 Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,  
 Yu C., Rubin G.  
 RT "Drosophila melanogaster release 4 sequence."  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RN NUCLEOTIDE SEQUENCE.  
 RP NUCLEOTIDE SEQUENCE.  
 RG FlyBase;  
 RN Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 [7]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 Munoz J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 Yu C., Lewis S.E., Rubin G.M., Celniker S.,  
 Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF003615; AAF52463.2; -; Genomic\_DNA.  
 DR EMBL; AY061410; AAL28958.1; -; mRNA.  
 DR Ensembl; CG3423; Drosophila melanogaster.  
 DR FlyBase; FBgn0020616; CG3423.  
 DR FlyBase; FBgn0020616; SA.  
 DR GO; GO:0007076; Pmitotic chromosome condensation; IEA.  
 SQ SEQUENCE 1127 AA; 130115 MW; 8DCC0C6934228712 CRC64;  
 Query Match 79.1%; Score 34; DB 2; Length 1127;  
 Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NLOQLMDRV 9  
 DB 641 NLOALLDRI 649  
 RESULT 42  
 Q52AB0 MAGGR PRELIMINARY; PRT; 219 AA.  
 ID Q52AB0 MAGGR PRELIMINARY;  
 AC Q52AB0;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=MG02124.4;  
 OS Magnaporthe grisea 70-15.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
 OX NCBI\_TaxID=242507;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=70-15;  
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
 Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
 Arachchi H., Armbruster J., Bachantang P., Baldwin M., Barry A.,  
 Bayl T., Blitshsteyn B., Bloom T., Blye J., Boguslavsky L.,  
 Borowsky M., Boukhaltier B., Brunache A., Butler J., Calixte N.,  
 Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,  
 Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
 David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
 Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
 Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
 Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,  
 Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
 Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
 Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
 Jaffe D., Jones C., Kamat A., Kamat A., Kamysseis M., Karlsson E.,  
 Kelle C., Kieu A., Klesner P., Kodira C., Kulbokas E., Labutti K.,  
 Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
 Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,  
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 McCarthy M., McDonough S., Mcghee T., Meldrum J., Meneus L.,  
 Mesirov J., Mihalav A., Mihova T., Mikkelsen T., Mienga V., Moru K.,

RA Moses J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'donnell P., Okosawo O., O'leary S., Omotosho B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau K., Ray V., Raymond C.,  
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutnan M., Schubach R., Seaman C., Settipalli S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,  
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,  
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,  
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vaasiliev H.,  
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
RA Zimmer A., Zody M., Lander E.;  
RT "The genome sequence of Magnaporthe grisea";  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Zhu H., Blackmon B.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACU01000405; EAA54139.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 219 AA; 23848 MW; 0F0C147B3849CC48 CRC64;  
  
Query Match 76.7%; Score 33; DB 2; Length 219;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 NQLQLMDRV 9  
Db 202 NQLQLMDRV 210  
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RESULT 43  
Q9M8R8\_9CAUD PRELIMINARY; PRT; 257 AA.  
AC Q9M8R8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Orf 21.  
OS Staphylococcus aureus prophage phIPV83.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=129009;  
RN [1]\_TaxID=129009;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=P83;  
RX PubMed=11210127; DOI=10.1271/bbb.64.2631;  
RA Zou D., Kaneko J., Narita S., Kamio Y.;  
RT "Prophage, phIPV83-pro, carrying panton-valentine leukocidin genes, on  
RT the Staphylococcus aureus P83 chromosome: comparative analysis of the  
RT genome structures of phIPV83-pro, phIPV83, phIPV83, phIPV83, phIPV83,  
RL BioSci. Biotechnol. Biochem. 64:2631-2643 (2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=P83;  
RX MEDLINE=98067870; PubMed=9404084;  
RA Kaneko J., Muramoto K., Kamio Y.;  
RT "Gene of LukF-PV-like component of Pantone-Valentine leukocidin in  
RT Staphylococcus aureus P83 is linked with lukM";  
RL BioSci. Biotechnol. Biochem. 61:1960-1962 (1997).  
DR EMBL; AB044554; BAA97828.1; -; Genomic\_DNA.

SQ SEQUENCE 257 AA; 30023 MW; AC948888FDA94752 CRC64;  
  
Query Match 76.7%; Score 33; DB 2; Length 257;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NQLQLMDRV 9  
Db 151 HIQMLMDRI 159  
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RESULT 44  
Q6F7M9\_ACIAD PRELIMINARY; PRT; 345 AA.  
ID Q6F7M9\_ACIAD PRELIMINARY;  
AC Q6F7M9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=ACIAD3256;  
OS Acinetobacter sp. (strain ADP1).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=62977;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ADP1;  
RX PubMed=15514110; DOI=10.1093/nar/gkh910;  
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,  
RA Labarre L., Crueviller S., Robert C., Duprat S., Wincker P.,  
RA Ornaton L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;  
RT "Unique features revealed by the genome sequence of Acinetobacter sp.  
RT ADP1, a versatile and naturally transformation competent bacterium.";  
RL Nucleic Acids Res. 32:5766-5779 (2004).  
DR EMBL; CR543861; CAG69936.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR InterPro; IPR000157; TIR.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 345 AA; 40855 MW; A4502BABC732F85C CRC64;  
  
Query Match 76.7%; Score 33; DB 2; Length 345;  
Best Local Similarity 55.6%; Pred. No. 2.2e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 NQLQLMDRV 9  
Db 166 NMQLQDRI 174  
||:|||||  
  
RESULT 45  
Q4Q9G4\_LEIMA PRELIMINARY; PRT; 497 AA.  
ID Q4Q9G4\_LEIMA PRELIMINARY;  
AC Q4Q9G4;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE GTP-binding protein-like protein.  
GN ORFNames=LmjF26.0270;  
OS Leishmania major.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RN [1]\_TaxID=5664;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Friedlin;  
RA Peacock C.S., Ivens A.C., Berriman M., Blackwell J.,  
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,  
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CU005265; CAJ04581.1; -; Genomic\_DNA.  
SQ SEQUENCE 497 AA; 56468 MW; FID86485F373BAF8 CRC64;  
  
Query Match 76.7%; Score 33; DB 2; Length 497;

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Best Local Similarity 77.8%; Pred. No. 3.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 390 NLQLMDRV 398

RESULT 46
Q8TWC3 METKA
ID Q8TWC3 METKA PRELIMINARY; PRT; 509 AA.
AC Q8TWC3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Uncharacterized protein specific for M.kandleri, MK-8 family.
GN OrderedLocusNames=MK1112;
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozayavkin S.A.;
RT "The complete genome of hyperthermophilic Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AE010400; AAM02325.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 509 AA; 58194 MW; F7D8A21F7A734AED CRC64;

Query Match 76.7%; Score 33; DB 2; Length 509;
Best Local Similarity 77.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 112 NLQFLMDRV 120

RESULT 47
Q5CRU7 CRYPV
ID Q5CRU7 CRYPV PRELIMINARY; PRT; 735 AA.
AC Q5CRU7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Putative secreted protein, paralog within cryptosporidium-specific HCD
DE multi-gene family.
DE ORFNames=cgd5_1420;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RX PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamsen M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
RA Lanco C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA Banker A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum.";
RL Science 304:441-445(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

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DR EMBL; AABE01000007; EAK88105.1; -; Genomic_DNA.
DR InterPro; IPR002712; CcDB.
DR InterPro; IPR011058; Cyanovirin-N.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001379; Egg lysein.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR000524; HTH GntR.
DR InterPro; IPR001093; IMPDh/GMPrtase.
DR InterPro; IPR012128; Phycocyanin.
DR InterPro; IPR000403; P13/4_kinase_cat.
DR InterPro; IPR009032; Vpu_Cyt.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00478; IMPDH; 1.
SQ SEQUENCE 735 AA; 84495 MW; EB005C8ABEEA9092 CRC64;

Query Match 76.7%; Score 33; DB 2; Length 735;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 722 NLELLLDKI 730

RESULT 48
Q5CLF9 CRYHO
ID Q5CLF9 CRYHO PRELIMINARY; PRT; 735 AA.
AC Q5CLF9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Chro.50241;
OS Cryptosporidium hominis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=237895;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TU502;
RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
RA Fuii D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
RA Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S.,
RA Buck G.A.;
RT "The genome of Cryptosporidium hominis.";
RL Nature 431:1107-1112(2004).
DR EMBL; AAE01000054; EAL37446.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 735 AA; 84584 MW; 3575DE7044E12D85 CRC64;

Query Match 76.7%; Score 33; DB 2; Length 735;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9
Db 722 NLELLLDKI 730

RESULT 49
Q9XGC1 VIGUN
ID Q9XGC1 VIGUN PRELIMINARY; PRT; 874 AA.
AC Q9XGC1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Starch synthase, isoform V (EC 2.4.1.21).
OS Vigna unguiculata (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Vigna.
OX NCBI_TaxID=3917;

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Job time : 136.6 secs

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RN NUCLEOTIDE SEQUENCE.
RP Bhullar S.S., Willmitzer L., Kossmann J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006752; CAB40375.1; -; mRNA.
DR GO; GO:0009501; C:amyloplast; IEA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009011; F:starch synthase activity; IEA.
DR GO; GO:0016757; F:starch synthase activity; IEA.
DR GO; GO:0019252; P:starch biosynthesis; IEA.
DR InterPro; IPR011835; GLGA.
DR TIGRFAMs; TIGR02095; glgA; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 874 AA; 98741 MW; 8561D742868C8399 CRC64;

Query Match 76.7%; Score 33; DB 2; Length 874;
Best Local Similarity 75.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDR 8
DB 195 NLQLLMDK 202

RESULT 50
QSDMW3 CUCME
ID QSDMW3_CUCME PRELIMINARY; PRT; 944 AA.
AC QSDMW3;
DT 10-MAY-2005 (TREMELrel. 30, Created)
DT 10-MAY-2005 (TREMELrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMELrel. 30, Last annotation update)
DE MRGH10.
GN Name=MRGH10;
OS Cucumis melo (Muskmelon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3656;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15902490; DOI=10.1007/s00438-004-1104-7;
RA van Leeuwen H., Garcia-Mas J., Coca M., Puigdomenech P., Monfort A.;
RT "Analysis of the melon genome in regions encompassing TIR-NBS-LRR
RT resistance genes.";
RL Mol. Genet. Genomics 273:240-251(2005).
DR EMBL; AY582736; AAU04758.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042823; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR011713; LRR_3.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR_1; 7.
DR Pfam; PF07725; LRR_3; 1.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERSIST.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
SQ SEQUENCE 944 AA; 107497 MW; FABBCCAA072CAFCE CRC64;

Query Match 76.7%; Score 33; DB 2; Length 944;
Best Local Similarity 75.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLQLLMDR 8
DB 523 NLQLMLVDR 530
```

```
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30109

Query Match      67.4%; Score 29; DB 2; Length 420;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
      |||::||
Db      290 NLQLVVDGV 298

RESULT 49
US-09-248-796A-15391
; Sequence 15391, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15391
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15391

Query Match      67.4%; Score 29; DB 2; Length 508;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LQLLMDRV 9
      |||||
Db      6 LQLLQDRL 13

RESULT 50
US-09-252-991A-22687
; Sequence 22687, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22687
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22687

Query Match      67.4%; Score 29; DB 2; Length 509;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LQLLMDRV 8
      |||||
```

Db 116 LQLLVDR 122

Search completed: May 9, 2006, 02:28:31  
Job time : 32.2 secs

```
QY      1 NLQLMDR 8
      |:|:|:|:|:
Db      40 NIQLLFDK 47

RESULT 44
US-09-818-780-93
; Sequence 93, Application US/09818780
; Patent No. 6677146
; GENERAL INFORMATION:
; APPLICANT: McHenry, Charles
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME
; FILE REFERENCE: 1794.0030004
; CURRENT APPLICATION NUMBER: US/09/818,780
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,736
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 93
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Rickettsia prowazekii
US-09-818-780-93

Query Match      67.4%; Score 29; DB 2; Length 269;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLMDRV 9
      |||:|:|:|:
Db      197 NLFLMNR1 205

RESULT 45
US-09-252-991A-30349
; Sequence 30349, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30349
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30349

Query Match      67.4%; Score 29; DB 2; Length 280;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLQLMD 7
      |||:|:|:|:
Db      72 NLQLILD 78

RESULT 46
US-10-067-443-6
; Sequence 6, Application US/10067443
; Patent No. 6642041
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALLOPROTEASE HIGHLY EXPRESSED
```

```
; TITLE OF INVENTION: SPINAL CORD, MP-1
; FILE REFERENCE: D0073 NP
; CURRENT APPLICATION NUMBER: US/10/067,443
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 60/282,814
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-067-443-6

Query Match      67.4%; Score 29; DB 2; Length 340;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLMDRV 9
      |||:|:|:|:
Db      54 NLPLLLERI 62

RESULT 47
US-09-252-991A-23698
; Sequence 23698, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23698
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23698

Query Match      67.4%; Score 29; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 QLMDR 8
      |||:|:|:|:
Db      258 QLMDR 263

RESULT 48
US-09-252-991A-30109
; Sequence 30109, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30109
```



```
RESULT 39
US-09-270-767-38268
; Sequence 38268, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38268
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-38268

Query Match          67.4%; Score 29; DB 2; Length 133;
Best Local Similarity 62.5%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLQLLMDR 8
      |:|:|:|:|
Db      13 NVRLLLDR 20

RESULT 40
US-09-270-767-53485
; Sequence 53485, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53485
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53485

Query Match          67.4%; Score 29; DB 2; Length 133;
Best Local Similarity 62.5%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLQLLMDR 8
      |:|:|:|:|
Db      13 NVRLLLDR 20

RESULT 41
US-09-902-540-15069
; Sequence 15069, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
```

```
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15069
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15069

Query Match          67.4%; Score 29; DB 2; Length 160;
Best Local Similarity 75.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LQLLMDRV 9
      |:|:|:|:|
Db      144 LQALLDRV 151

RESULT 42
US-09-134-001C-4694
; Sequence 4694, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4694
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4694

Query Match          67.4%; Score 29; DB 2; Length 228;
Best Local Similarity 62.5%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLLMDR 8
      |:|:|:|:|
Db      40 NIQLLFDK 47

RESULT 43
US-09-134-001C-5495
; Sequence 5495, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5495
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5495

Query Match          67.4%; Score 29; DB 2; Length 228;
Best Local Similarity 62.5%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLOQLMDR 8
Db 444 NLQALMER 451

RESULT 35
US-09-949-016-8283
; Sequence 8283, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8283
; LENGTH: 1813
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8283

Query Match 69.8%; Score 30; DB 2; Length 1813;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLOQLMDR 8
Db 450 NLQALMER 457

RESULT 36
US-09-949-016-8284
; Sequence 8284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8284
; LENGTH: 1813
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8284

Query Match 69.8%; Score 30; DB 2; Length 1813;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLOQLMDR 8
Db 444 NLQALMER 451

RESULT 37
US-09-949-016-8285
; Sequence 8285, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8285
; LENGTH: 1813
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8285

Query Match 69.8%; Score 30; DB 2; Length 1813;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLOQLMDR 8
Db 450 NLQALMER 457

RESULT 38
US-09-438-185A-602
; Sequence 602, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 602
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0600
US-09-438-185A-602

Query Match 67.4%; Score 29; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLOQLMDR 9
Db 36 NLQQLKQDRL 44
```

US-09-949-016-8282  
; Sequence 8282, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8282  
; LENGTH: 1769  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8282

Query Match 69.8%; Score 30; DB 2; Length 1769;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NQLQMDR 8  
||| |||  
Db 450 NQLQALMER 457

RESULT 33  
US-09-040-738-2  
; Sequence 2, Application US/09040738  
; Patent No. 6207374  
; GENERAL INFORMATION:  
; APPLICANT: Sampson et al.  
; TITLE OF INVENTION: Tubercous Sclerosis 2 Gene and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff,  
; ADDRESSEE: Ltd.  
; STREET: One Financial Center  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 6.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/040,738  
; FILING DATE: Concurrently herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB9326470.3  
; FILING DATE: 24-December-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB9411900.5  
; FILING DATE: 14-June-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB94/02823  
; FILING DATE: 23-December-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/652,426  
; FILING DATE: 30-May-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Kathleen M.

; REGISTRATION NUMBER: 34,380  
; REFERENCE/DOCKET NUMBER: 3265/73963  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-9100  
; TELEFAX: 617-345-9111  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1784 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-040-738-2

Query Match 69.8%; Score 30; DB 2; Length 1784;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NQLQMDR 8  
||| |||  
Db 444 NQLQALMER 451

RESULT 34  
US-08-652-426A-2  
; Sequence 2, Application US/08652426A  
; Patent No. 6232452  
; GENERAL INFORMATION:  
; APPLICANT: Sampson et al.  
; TITLE OF INVENTION: Tubercous Sclerosis 2 Gene and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff,  
; ADDRESSEE: Ltd.  
; STREET: One Financial Center  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 6.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,426A  
; FILING DATE: 01-October-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB9326470.3  
; FILING DATE: 12/24/93  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB9411900.5  
; FILING DATE: 06/14/94  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB94/02823  
; FILING DATE: 12/23/94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Kathleen M.  
; REGISTRATION NUMBER: 34,380  
; REFERENCE/DOCKET NUMBER: 96,738  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-9100  
; TELEFAX: 617-345-9111  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1784 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-652-426A-2

Query Match 69.8%; Score 30; DB 2; Length 1784;

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 5094

LENGTH: 1116

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-583-110-5094

Query Match

Best Local Similarity 69.8%; Score 30; DB 2; Length 1116;

Pred. No. 8.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMDR 8

Db 320 LQLVMDR 326

RESULT 29

US-09-107-433-3602

Sequence 3602, Application US/09107433

Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3602:

SEQUENCE CHARACTERISTICS:

LENGTH: 1120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...1120

SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

US-09-107-433-3602

Query Match

Best Local Similarity 69.8%; Score 30; DB 2; Length 1120;

Pred. No. 8.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMDR 8

Db 324 LQLVMDR 330

RESULT 30

US-09-949-016-8280

Sequence 8280, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8280

LENGTH: 1769

TYPE: PRT

ORGANISM: Human

US-09-949-016-8280

Query Match

Best Local Similarity 69.8%; Score 30; DB 2; Length 1769;

Pred. No. 1.4e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDR 8

Db 450 NLQALMER 457

RESULT 31

US-09-949-016-8281

Sequence 8281, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8281

LENGTH: 1769

TYPE: PRT

ORGANISM: Human

US-09-949-016-8281

Query Match

Best Local Similarity 69.8%; Score 30; DB 2; Length 1769;

Pred. No. 1.4e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDR 8

Db 450 NLQALMER 457

RESULT 32

Best Local Similarity 55.6%; Pred. No. 1.4e+02; Mismatches 3; Indels 0; Gaps 0;  
Matches 5; Conservative 1;  
QY 1 NLQLLMDRV 9  
Db 149 NLQSIVDRI 157

RESULT 24  
US-09-134-000C-6666  
; Sequence 6666, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6666  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-6666

Query Match 69.8%; Score 30; DB 2; Length 412;  
Best Local Similarity 62.5%; Pred. No. 2.7e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMDRV 9  
Db 375 IQVIMDRV 382

RESULT 25  
US-09-252-991A-29575  
; Sequence 29575, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29575  
; LENGTH: 656  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29575

Query Match 69.8%; Score 30; DB 2; Length 656;  
Best Local Similarity 55.6%; Pred. No. 4.5e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
Db 444 NLNVILDRV 452

RESULT 26  
US-09-134-001C-4480  
; Sequence 4480, Application US/09134001C  
; Patent No. 6380370

; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4480  
; LENGTH: 673  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4480

Query Match 69.8%; Score 30; DB 2; Length 673;  
Best Local Similarity 66.7%; Pred. No. 4.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
Db 473 NOQLMDRI 481

RESULT 27  
US-09-489-039A-11547  
; Sequence 11547, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 11547  
; LENGTH: 808  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11547

Query Match 69.8%; Score 30; DB 2; Length 808;  
Best Local Similarity 55.6%; Pred. No. 5.7e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLLMDRV 9  
Db 409 NFKLLMDQI 417

RESULT 28  
US-09-583-110-5094  
; Sequence 5094, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02

```
; ORGANISM: Homo sapiens
US-10-104-047-2471

Query Match          69.8%; Score 30; DB 2; Length 132;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLQLMDR 8
   |||: |||
Db 74 NLQMNDR 81

RESULT 20
US-09-270-767-33712
; Sequence 33712, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33712
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33712

Query Match          69.8%; Score 30; DB 2; Length 168;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMDRV 9
   |:|:|:|:
Db 84 LELLDRI 91

RESULT 21
US-09-270-767-48929
; Sequence 48929, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48929
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48929

Query Match          69.8%; Score 30; DB 2; Length 168;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMDRV 9
   |:|:|:|:
Db 84 LELLDRI 91

RESULT 22
US-09-107-433-5177
; Sequence 5177, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
```

```
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5177:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...175
SEQUENCE DESCRIPTION: SEQ ID NO: 5177:
US-09-107-433-5177

Query Match          69.8%; Score 30; DB 2; Length 175;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLMDRV 9
   |||||:|
Db 21 LQLMDLV 28

RESULT 23
US-09-540-236-2077
; Sequence 2077, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAT.
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2077
; LENGTH: 231
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2077

Query Match          69.8%; Score 30; DB 2; Length 231;
```

```
US-09-248-796A-16129
; Sequence 16129, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16129
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16129

Query Match          72.1%; Score 31; DB 2; Length 640;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
Db      12 NLKLLIDKI 20

RESULT 16
US-09-438-185A-464
; Sequence 464, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-00041105
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 464
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0462
US-09-438-185A-464

Query Match          72.1%; Score 31; DB 2; Length 696;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
Db      531 NLQLASDRI 539

RESULT 17
US-09-248-796A-18667
; Sequence 18667, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18667
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18667

Query Match          72.1%; Score 31; DB 2; Length 855;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
Db      493 NLRLLDHV 501

RESULT 18
US-09-252-991A-25165
; Sequence 25165, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25165
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25165

Query Match          69.8%; Score 30; DB 2; Length 67;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 QLLMDRV 9
Db      47 QLVMDRV 53

RESULT 19
US-10-104-047-2471
; Sequence 2471, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2471
; LENGTH: 132
; TYPE: PRT
```

```

, PRIOR APPLICATION NUMBER: DE 19932230.0
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 19932927.3
, PRIOR FILING DATE: 1999-07-14
, PRIOR APPLICATION NUMBER: DE 19933005.0
, PRIOR FILING DATE: 1999-07-14
, PRIOR APPLICATION NUMBER: DE 19933006.9
, PRIOR FILING DATE: 1999-07-14
, PRIOR APPLICATION NUMBER: DE 19940764.9
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940765.7
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940766.5
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940830.0
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940831.9
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940832.7
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940833.5
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19941378.9
, PRIOR FILING DATE: 1999-08-31
, PRIOR APPLICATION NUMBER: DE 19941379.7
, PRIOR FILING DATE: 1999-08-31
, PRIOR APPLICATION NUMBER: DE 19941395.9
, PRIOR FILING DATE: 1999-08-31
, PRIOR APPLICATION NUMBER: DE 19942077.7
, PRIOR FILING DATE: 1999-09-03
, PRIOR APPLICATION NUMBER: DE 19942078.5
, PRIOR FILING DATE: 1999-09-03
, PRIOR APPLICATION NUMBER: DE 19942079.3
, PRIOR FILING DATE: 1999-09-03
, PRIOR APPLICATION NUMBER: DE 19942088.2
, PRIOR FILING DATE: 1999-09-03
, NUMBER OF SEQ ID NOS: 678
, SEQ ID NO 676
, LENGTH: 270
, TYPE: PR1
, ORGANISM: Corynebacterium glutamicum
US-09-602-787A-676

```

```

Query Match          72.18; Score 31; DB 2; Length 270;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NLQLMDRV 9
        |||::|||
Db      22 NLPLIDRV 30

RESULT 12
US-09-252-991A-18006
; Sequence 18006, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18006
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:

```

```

; NAME/KEY: UNSURE
; LOCATION: (53)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-18006

```

Query Match	72.1%;	Score 31;	DB 2;	Length 276;
Best Local Similarity	66.7%;	Pred. No. 1.1e+02;		
Matches 6;	Conservative	3;	Mismatches 0;	Indels 0; Gaps 0;
Y	1	NEQLLMDRV	9	
		:	:	:
b	60	HLELLVDRV	68	

```

Query Match          72.1%; Score 11; DB 2; Length 529;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels

y      2 LQLMDRV 9
      |||||
b      48 LQTMDMI 55

```

```

Query Match      72.1%; Score 31; DB 2; Length 542;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels

Y      1 NLQLLMDRV 9
      |||||
b      531 NLQLASDRI 539

RESULT 15

```



```
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5027
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5027

Query Match          72.1%; Score 31; DB 2; Length 152;
Best Local Similarity 55.6%; Pred. No. 56;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9
Db 132 NLQILLSRI 140

RESULT 9
US-09-248-796A-27510
; Sequence 27510, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27510
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Candida albicans
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-27510

Query Match          72.1%; Score 31; DB 2; Length 159;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9
Db 19 NLQILKQDV 27

RESULT 10
US-09-248-796A-19441
; Sequence 19441, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
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; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19441
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19441

Query Match          72.1%; Score 31; DB 2; Length 189;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLQLLMDRV 9
Db 28 NLQILKQDV 36

RESULT 11
US-09-602-787A-676
; Sequence 676, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Mark
; APPLICANT: Kruger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
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/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 20334
/ LENGTH: 90
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-09-248-796A-20334

Query Match          76.7%; Score 33; DB 2; Length 90;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY      1 NLQLLMDRV 9
      ||||| :
Db      74 NLQLFMDHI 82

RESULT 5
US-10-163-214-13
/ Sequence 13, Application US/10163214
/ Patent No. 6849781
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Stephen M.
/ APPLICANT: Broglie, Karen E.
/ APPLICANT: Butler, Karlene H.
/ APPLICANT: Thorpe, Catherine J.
/ TITLE OF INVENTION: Starch Synthase Isoform V
/ FILE REFERENCE: BB1520 US NA
/ CURRENT APPLICATION NUMBER: US/10/163,214
/ CURRENT FILING DATE: 2002-06-05
/ PRIOR APPLICATION NUMBER: 60/297,099
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 13
/ LENGTH: 874
/ TYPE: PRT
/ ORGANISM: Vigna unguiculata
US-10-163-214-13

Query Match          76.7%; Score 33; DB 2; Length 874;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLQLMDR 8
      ||||| :
Db      195 NLQLLDK 202

RESULT 6
US-09-107-433-2880
/ Sequence 2880, Application US/09107433
/ Patent No. 6800744
/ GENERAL INFORMATION:
/ APPLICANT: Lynn A. Doucette-Stamm and David Bush
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
/ SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS
/ NUMBER OF SEQUENCES: 5206
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: GENOME THERAPEUTICS CORPORATION
/ STREET: 100 Beaver Street
/ CITY: Waltham
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02354
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: CD-ROM ISO9660
/ COMPUTER: <Unknown>
/ OPERATING SYSTEM: <Unknown>
/ SOFTWARE: <Unknown>
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/107,433
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/ FILING DATE: 30-Jun-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/ 085131
/ FILING DATE: May 12, 1998
/ APPLICATION NUMBER: 60/051553
/ FILING DATE: July 2, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ariniello, Pamela Deneke
/ REGISTRATION NUMBER: 40,489
/ REFERENCE/DOCKET NUMBER: GTC-011
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (781)893-5007
/ TELEFAX: (781)893-8277
/ INFORMATION FOR SEQ ID NO: 2880:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 250 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Streptococcus pneumoniae
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (B) LOCATION 1...250
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2880:
US-09-107-433-2880

Query Match          74.4%; Score 32; DB 2; Length 250;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
      ||||| :
Db      196 NLPLLDRI 204

RESULT 7
US-09-583-110-3146
/ Sequence 3146, Application US/09583110
/ Patent No. 6699703
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al.
/ TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
/ FILE REFERENCE: PATH00-07A
/ CURRENT APPLICATION NUMBER: US/09/583,110
/ CURRENT FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/107,433
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/085,131
/ PRIOR FILING DATE: 1998-05-12
/ PRIOR APPLICATION NUMBER: US 60/051,553
/ PRIOR FILING DATE: 1997-07-02
/ NUMBER OF SEQ ID NOS: 5322
/ SEQ ID NO 3146
/ LENGTH: 283
/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
US-09-583-110-3146

Query Match          74.4%; Score 32; DB 2; Length 283;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NLQLLMDRV 9
      ||||| :
Db      172 NLPLLDRI 180

RESULT 8
US-09-583-110-5027
/ Sequence 5027, Application US/09583110
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977 25 58.1 376 2 US-09-404-296B-32 Sequence 32, Appl  
978 25 58.1 384 2 US-09-328-352-5251 Sequence 5251, Ap  
979 25 58.1 397 2 US-09-489-039A-8962 Sequence 8962, Ap  
980 25 58.1 397 2 US-09-489-039A-13498 Sequence 13498, A  
981 25 58.1 399 2 US-09-538-092-361 Sequence 361, App  
982 25 58.1 400 2 US-08-961-083-190 Sequence 190, App  
983 25 58.1 400 2 US-09-536-784-190 Sequence 190, App  
984 25 58.1 400 2 US-09-765-271-190 Sequence 190, App  
985 25 58.1 400 2 US-09-765-272A-190 Sequence 190, App  
986 25 58.1 403 2 US-09-252-991A-29349 Sequence 29349, A  
987 25 58.1 405 2 US-09-355-912A-3 Sequence 3, Appli  
988 25 58.1 405 2 US-10-202-428-3 Sequence 3, Appli  
989 25 58.1 407 2 US-09-949-016-6248 Sequence 6248, Ap  
990 25 58.1 409 1 US-08-924-254-2 Sequence 2, Appli  
991 25 58.1 409 2 US-09-120-249-2 Sequence 2, Appli  
992 25 58.1 412 2 US-09-252-991A-25954 Sequence 25954, A  
993 25 58.1 413 2 US-09-949-016-11721 Sequence 11721, A  
994 25 58.1 414 2 US-09-902-540-15902 Sequence 15902, A  
995 25 58.1 417 1 US-09-099-677A-6 Sequence 6, Appli  
996 25 58.1 417 2 US-09-261-471-6 Sequence 6, Appli  
997 25 58.1 419 2 US-09-489-039A-13188 Sequence 13188, A  
998 25 58.1 420 2 US-09-252-991A-29353 Sequence 29353, A  
999 25 58.1 421 2 US-09-710-279-144 Sequence 144, App  
1000 25 58.1 423 2 US-09-270-767-46381 Sequence 46381, A

ALIGNMENTS

RESULT 1  
US-09-949-016-7333  
; Sequence 7333, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ For Windows Version 4.0  
; SEQ ID NO 7333  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7333

Query Match 100.0%; Score 43; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLQLMDRV 9  
| | | | | | | | | |  
DB 147 NQLQLMDRV 155

RESULT 2  
US-09-621-976-5972  
; Sequence 5972, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5972  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 75  
; OTHER INFORMATION: Xaa = \*, Glu, Lys, Gln  
US-09-621-976-5972

Query Match 81.4%; Score 35; DB 2; Length 113;  
Best Local Similarity 87.5%; Pred. No. 6;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLQLMDR 8  
| | | | | | | | | |  
DB 23 NQLQLVDR 30

RESULT 3  
US-09-513-999C-5230  
; Sequence 5230, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5230  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 80  
; OTHER INFORMATION: Xaa=Lys or Gln or Arg  
US-09-513-999C-5230

Query Match 81.4%; Score 35; DB 2; Length 152;  
Best Local Similarity 87.5%; Pred. No. 8.3;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQLQLMDR 8  
| | | | | | | | | |  
DB 23 NQLQLVDR 30

RESULT 4  
US-09-248-796A-20334  
; Sequence 20334, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409

831	25	58.1	169	2	US-09-270-767-61958	Sequence 61958, A	904	25	58.1	261	2	US-10-015-393A-402	Sequence 402, App
832	25	58.1	173	2	US-09-543-681A-7869	Sequence 7869, Ap	905	25	58.1	261	2	US-10-011-833A-402	Sequence 402, App
833	25	58.1	176	2	US-09-313-458-2	Sequence 2, Appli	906	25	58.1	261	2	US-10-006-041A-402	Sequence 402, App
834	25	58.1	176	2	US-09-746-359A-1	Sequence 1, Appli	907	25	58.1	261	2	US-10-012-064A-402	Sequence 402, App
835	25	58.1	176	2	US-10-101-464A-580	Sequence 580, App	908	25	58.1	263	2	US-09-248-796A-20702	Sequence 20702, A
836	25	58.1	182	2	US-09-489-039A-11493	Sequence 11493, A	909	25	58.1	264	2	US-09-107-532A-5034	Sequence 5034, Ap
837	25	58.1	184	2	US-09-270-767-40139	Sequence 40139, A	910	25	58.1	265	2	US-09-270-767-45969	Sequence 45969, A
838	25	58.1	184	2	US-09-770-767-55355	Sequence 55355, A	911	25	58.1	271	2	US-09-248-796A-27391	Sequence 27391, A
839	25	58.1	187	2	US-09-917-265A-102	Sequence 102, App	912	25	58.1	273	2	US-09-248-796A-18001	Sequence 18001, A
840	25	58.1	190	2	US-09-571-024B-10	Sequence 10, Appl	913	25	58.1	273	2	US-09-248-796A-19918	Sequence 19918, A
841	25	58.1	190	2	US-09-571-024B-11	Sequence 11, Appl	914	25	58.1	273	2	US-09-949-016-8333	Sequence 8333, Ap
842	25	58.1	190	2	US-09-571-024B-12	Sequence 12, Appl	915	25	58.1	274	1	US-08-177-109A-58	Sequence 58, Appl
843	25	58.1	190	2	US-09-571-024B-13	Sequence 13, Appl	916	25	58.1	274	1	US-08-687-706-58	Sequence 58, Appl
844	25	58.1	191	2	US-09-571-024B-9	Sequence 9, Appli	917	25	58.1	283	2	US-09-198-452A-424	Sequence 424, App
845	25	58.1	193	2	US-09-248-796A-27869	Sequence 27869, A	918	25	58.1	283	2	US-09-438-185A-407	Sequence 407, App
846	25	58.1	194	2	US-09-270-767-38140	Sequence 38140, A	919	25	58.1	284	2	US-09-252-991A-29913	Sequence 29913, A
847	25	58.1	195	2	US-09-270-767-53357	Sequence 53357, A	920	25	58.1	287	2	US-09-328-352-5395	Sequence 5395, Ap
848	25	58.1	195	2	US-09-270-767-61506	Sequence 61506, A	921	25	58.1	287	2	US-09-107-532A-4780	Sequence 4780, Ap
849	25	58.1	196	2	US-09-107-532A-3812	Sequence 3812, Ap	922	25	58.1	288	2	US-09-902-540-10024	Sequence 10024, A
850	25	58.1	197	2	US-09-011-143-4	Sequence 4, Appli	923	25	58.1	288	2	US-09-583-110-4529	Sequence 4529, Ap
851	25	58.1	197	2	US-09-302-495-4	Sequence 4, Appli	924	25	58.1	291	2	US-10-083-624-2	Sequence 2, Appli
852	25	58.1	197	2	US-10-079-616-4	Sequence 4, Appli	925	25	58.1	291	2	US-09-248-796A-19473	Sequence 19473, A
853	25	58.1	197	2	US-09-917-265A-36	Sequence 36, Appl	926	25	58.1	292	2	US-09-134-000C-3776	Sequence 3776, Ap
854	25	58.1	197	2	US-09-917-265A-50	Sequence 50, Appl	927	25	58.1	294	2	US-09-489-039A-10933	Sequence 10933, A
855	25	58.1	203	2	US-09-583-110-3736	Sequence 3736, Ap	928	25	58.1	296	2	US-09-489-039A-7531	Sequence 7531, Ap
856	25	58.1	203	2	US-09-248-796A-19170	Sequence 19170, A	929	25	58.1	297	2	US-09-252-991A-28075	Sequence 28075, A
857	25	58.1	207	1	US-08-177-109A-60	Sequence 60, Appl	930	25	58.1	297	2	US-09-270-767-45371	Sequence 45371, A
858	25	58.1	207	1	US-08-687-706-60	Sequence 60, Appl	931	25	58.1	298	2	US-09-582-934-2	Sequence 2, Appli
859	25	58.1	209	2	US-09-328-352-7180	Sequence 7180, Ap	932	25	58.1	299	2	US-09-648-004-22	Sequence 22, Appl
860	25	58.1	211	2	US-09-445-774-24	Sequence 24, Appl	933	25	58.1	299	2	US-10-272-419-22	Sequence 22, Appl
861	25	58.1	213	2	US-09-543-681A-5686	Sequence 5686, Ap	934	25	58.1	300	2	US-09-328-352-7367	Sequence 7367, Ap
862	25	58.1	214	2	US-09-214-278-1	Sequence 1, Appli	935	25	58.1	301	2	US-09-582-934-1	Sequence 1, Appli
863	25	58.1	214	2	US-09-855-722-1	Sequence 1, Appli	936	25	58.1	303	2	US-09-252-991A-17756	Sequence 17756, A
864	25	58.1	214	2	US-09-538-092-204	Sequence 204, App	937	25	58.1	306	2	US-09-489-039A-10306	Sequence 10306, A
865	25	58.1	214	2	US-09-107-433-3882	Sequence 3882, Ap	938	25	58.1	307	2	US-09-107-433-2651	Sequence 2651, Ap
866	25	58.1	215	1	US-08-935-396-10	Sequence 10, Appl	939	25	58.1	310	2	US-09-543-681A-5247	Sequence 5247, Ap
867	25	58.1	216	2	US-09-370-767-32737	Sequence 32737, A	940	25	58.1	313	2	US-09-248-796A-15080	Sequence 15080, A
868	25	58.1	216	2	US-09-270-767-47954	Sequence 47954, A	941	25	58.1	315	1	US-08-378-761A-73	Sequence 73, Appl
869	25	58.1	217	2	US-08-311-731A-67	Sequence 67, Appl	942	25	58.1	315	1	US-08-485-286-73	Sequence 73, Appl
870	25	58.1	218	2	US-08-311-731A-197	Sequence 197, App	943	25	58.1	315	2	US-08-816-977-2	Sequence 2, Appli
871	25	58.1	219	1	US-08-186-529-4	Sequence 4, Appli	944	25	58.1	315	2	US-09-334-477-2	Sequence 2, Appli
872	25	58.1	219	1	US-08-640-386A-4	Sequence 4, Appli	945	25	58.1	316	2	US-09-543-681A-5023	Sequence 5023, Ap
873	25	58.1	219	1	US-08-751-767A-2	Sequence 2, Appli	946	25	58.1	318	2	US-08-729-594A-38	Sequence 38, Appl
874	25	58.1	219	2	US-09-069-023-18	Sequence 18, Appl	947	25	58.1	318	2	US-08-937-993-38	Sequence 38, Appl
875	25	58.1	219	2	US-09-462-941-18	Sequence 18, Appl	948	25	58.1	318	2	US-09-583-110-2976	Sequence 2976, Ap
876	25	58.1	219	2	US-09-949-016-6001	Sequence 6001, Ap	949	25	58.1	319	2	US-09-134-000C-6061	Sequence 6061, Ap
877	25	58.1	219	2	US-10-165-800-14	Sequence 14, Appl	950	25	58.1	319	2	US-09-248-796A-14137	Sequence 14137, A
878	25	58.1	222	2	US-09-011-143-3	Sequence 3, Appli	951	25	58.1	320	2	US-09-325-932A-190	Sequence 190, App
879	25	58.1	222	2	US-09-302-495-3	Sequence 3, Appli	952	25	58.1	320	2	US-09-252-991A-30676	Sequence 30676, A
880	25	58.1	222	2	US-10-079-616-3	Sequence 3, Appli	953	25	58.1	321	2	US-09-270-767-42413	Sequence 42413, A
881	25	58.1	222	2	US-09-917-265A-33	Sequence 12, Appl	954	25	58.1	321	2	US-08-816-977-21	Sequence 21, Appl
882	25	58.1	222	2	US-09-917-265A-47	Sequence 16, Appl	955	25	58.1	323	2	US-09-543-681A-7304	Sequence 7304, Ap
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579	26	60.5	839	2	US-09-758-282B-73	Sequence 73, Appl	652	26	60.5	839	2	US-09-577-304A-153	Sequence 153, App
580	26	60.5	839	2	US-09-758-282B-75	Sequence 75, Appl	653	26	60.5	839	2	US-09-577-304A-169	Sequence 169, App
581	26	60.5	839	2	US-09-758-282B-79	Sequence 79, Appl	654	26	60.5	839	2	US-09-577-304A-172	Sequence 172, App
582	26	60.5	839	2	US-09-758-282B-81	Sequence 81, Appl	655	26	60.5	839	2	US-09-577-304A-175	Sequence 175, App
583	26	60.5	839	2	US-09-758-282B-83	Sequence 83, Appl	656	26	60.5	839	2	US-09-577-304A-178	Sequence 178, App
584	26	60.5	839	2	US-09-758-282B-85	Sequence 85, Appl	657	26	60.5	839	2	US-09-577-304A-181	Sequence 181, App
585	26	60.5	839	2	US-09-758-282B-87	Sequence 87, Appl	658	26	60.5	839	2	US-09-577-304A-184	Sequence 184, App
586	26	60.5	839	2	US-09-758-282B-89	Sequence 89, Appl	659	26	60.5	839	2	US-09-577-304A-187	Sequence 187, App
587	26	60.5	839	2	US-09-758-282B-103	Sequence 103, App	660	26	60.5	839	2	US-09-577-304A-190	Sequence 190, App
588	26	60.5	839	2	US-09-758-282B-106	Sequence 106, App	661	26	60.5	839	2	US-09-577-304A-200	Sequence 200, App
589	26	60.5	839	2	US-09-758-282B-109	Sequence 109, App	662	26	60.5	839	2	US-09-577-304A-202	Sequence 202, App
590	26	60.5	839	2	US-09-758-282B-112	Sequence 112, App	663	26	60.5	839	2	US-09-577-304A-204	Sequence 204, App
591	26	60.5	839	2	US-09-758-282B-115	Sequence 115, App	664	26	60.5	839	2	US-09-577-304A-206	Sequence 206, App
592	26	60.5	839	2	US-09-758-282B-118	Sequence 118, App	665	26	60.5	839	2	US-09-577-304A-218	Sequence 218, App
593	26	60.5	839	2	US-09-758-282B-121	Sequence 121, App	666	26	60.5	839	2	US-09-577-304A-221	Sequence 221, App
594	26	60.5	839	2	US-09-758-282B-124	Sequence 124, App	667	26	60.5	839	2	US-09-577-304A-226	Sequence 226, App
595	26	60.5	839	2	US-09-758-282B-127	Sequence 127, App	668	26	60.5	839	2	US-09-577-304A-228	Sequence 228, App
596	26	60.5	839	2	US-09-758-282B-130	Sequence 130, App	669	26	60.5	839	2	US-09-577-304A-230	Sequence 230, App
597	26	60.5	839	2	US-09-758-282B-133	Sequence 133, App	670	26	60.5	839	2	US-09-577-304A-232	Sequence 232, App
598	26	60.5	839	2	US-09-758-282B-136	Sequence 136, App	671	26	60.5	839	2	US-09-577-304A-234	Sequence 234, App
599	26	60.5	839	2	US-09-758-282B-139	Sequence 139, App	672	26	60.5	839	2	US-09-577-304A-236	Sequence 236, App
600	26	60.5	839	2	US-09-758-282B-142	Sequence 142, App	673	26	60.5	839	2	US-09-577-304A-239	Sequence 239, App
601	26	60.5	839	2	US-09-758-282B-145	Sequence 145, App	674	26	60.5	840	2	US-09-758-282B-280	Sequence 280, App
602	26	60.5	839	2	US-09-758-282B-148	Sequence 148, App	675	26	60.5	846	1	US-08-357-598-12	Sequence 12, Appl
603	26	60.5	839	2	US-09-758-282B-150	Sequence 150, App	676	26	60.5	846	1	US-09-003-289-12	Sequence 12, Appl
604	26	60.5	839	2	US-09-758-282B-153	Sequence 153, App	677	26	60.5	846	4	PCT-US95-16435-12	Sequence 12, Appl
605	26	60.5	839	2	US-09-758-282B-169	Sequence 169, App	678	26	60.5	865	1	US-07-803-633A-13	Sequence 13, Appl
606	26	60.5	839	2	US-09-758-282B-172	Sequence 172, App	679	26	60.5	867	2	US-09-540-236-3193	Sequence 3193, Ap
607	26	60.5	839	2	US-09-758-282B-175	Sequence 175, App	680	26	60.5	870	1	US-08-732-192A-2	Sequence 2, Appli
608	26	60.5	839	2	US-09-758-282B-178	Sequence 178, App	681	26	60.5	870	2	US-09-102-339-8	Sequence 8, Appli
609	26	60.5	839	2	US-09-758-282B-181	Sequence 181, App	682	26	60.5	890	2	US-10-171-464A-958	Sequence 958, App
610	26	60.5	839	2	US-09-758-282B-184	Sequence 184, App	683	26	60.5	896	2	US-09-543-681A-5439	Sequence 5439, Ap
611	26	60.5	839	2	US-09-758-282B-187	Sequence 187, App	684	26	60.5	908	2	US-09-623-326-9	Sequence 9, Appli

393	26	60.5	543	2	US-09-181-336-13	Sequence 13, Appl	466	26	60.5	808	2	US-09-565-909-2	Sequence 2, Appl
394	26	60.5	543	2	US-09-260-0388-2	Sequence 2, Appl	467	26	60.5	810	2	US-09-587-856-2	Sequence 2, Appl
395	26	60.5	543	2	US-09-635-923-2	Sequence 2, Appl	468	26	60.5	810	2	US-09-777-537-2	Sequence 2, Appl
396	26	60.5	543	2	US-09-487-716A-2	Sequence 2, Appl	469	26	60.5	810	2	US-09-777-538-2	Sequence 2, Appl
397	26	60.5	543	2	US-09-322-977A-2	Sequence 2, Appl	470	26	60.5	812	2	US-09-538-092-643	Sequence 643, App
398	26	60.5	543	2	US-09-186-200-1	Sequence 1, Appl	471	26	60.5	830	1	US-07-977-434-6	Sequence 6, Appl
399	26	60.5	543	2	US-09-435-739-10	Sequence 10, Appl	472	26	60.5	830	4	PCT-US91-07035-6	Sequence 6, Appl
400	26	60.5	543	2	US-09-930-218-3	Sequence 3, Appl	473	26	60.5	830	4	PCT-US91-07035-6	Sequence 6, Appl
401	26	60.5	543	2	US-09-704-772A-2	Sequence 2, Appl	474	26	60.5	832	1	US-07-977-434-2	Sequence 2, Appl
402	26	60.5	543	2	US-09-988-113-10	Sequence 10, Appl	475	26	60.5	832	1	US-08-156-020-2	Sequence 2, Appl
403	26	60.5	543	2	US-09-944-602-2	Sequence 2, Appl	476	26	60.5	832	1	US-08-156-020-4	Sequence 4, Appl
404	26	60.5	543	2	US-09-927-738-2	Sequence 2, Appl	477	26	60.5	832	1	US-08-156-020-6	Sequence 6, Appl
405	26	60.5	543	2	US-10-368-044A-1	Sequence 1, Appl	478	26	60.5	832	1	US-08-156-020-8	Sequence 8, Appl
406	26	60.5	543	2	US-10-384-450A-10	Sequence 10, Appl	479	26	60.5	832	1	US-08-156-020-10	Sequence 10, Appl
407	26	60.5	545	2	US-09-899-440-18	Sequence 18, Appl	480	26	60.5	832	1	US-08-073-384C-4	Sequence 4, Appl
408	26	60.5	548	1	US-08-484-956-86	Sequence 86, Appl	481	26	60.5	832	1	US-08-254-359A-4	Sequence 4, Appl
409	26	60.5	548	1	US-08-757-653-86	Sequence 86, Appl	482	26	60.5	832	1	US-08-483-043-4	Sequence 4, Appl
410	26	60.5	548	2	US-08-520-946-86	Sequence 86, Appl	483	26	60.5	832	1	US-08-483-043-4	Sequence 4, Appl
411	26	60.5	548	2	US-08-520-946-86	Sequence 86, Appl	484	26	60.5	832	1	US-08-483-043-4	Sequence 4, Appl
412	26	60.5	552	2	US-09-120-365-5	Sequence 5, Appl	485	26	60.5	832	1	US-08-481-238-4	Sequence 4, Appl
413	26	60.5	552	2	US-09-515-039-5	Sequence 5, Appl	486	26	60.5	832	1	US-08-484-956-4	Sequence 4, Appl
414	26	60.5	555	2	US-09-107-532A-4722	Sequence 4722, Ap	487	26	60.5	832	1	US-08-757-653-4	Sequence 4, Appl
415	26	60.5	562	2	US-09-252-991A-23543	Sequence 23543, A	488	26	60.5	832	1	US-08-599-431-4	Sequence 4, Appl
416	26	60.5	567	2	US-09-583-110-3836	Sequence 3836, Ap	489	26	60.5	832	1	US-08-756-386-4	Sequence 4, Appl
417	26	60.5	568	2	US-09-134-001C-3768	Sequence 3768, Ap	490	26	60.5	832	1	US-08-823-516-4	Sequence 4, Appl
418	26	60.5	569	2	US-09-949-016-10633	Sequence 10633, A	491	26	60.5	832	2	US-08-682-853A-4	Sequence 4, Appl
419	26	60.5	571	2	US-09-107-433-3917	Sequence 3917, Ap	492	26	60.5	832	2	US-08-759-038-4	Sequence 4, Appl
420	26	60.5	572	2	US-10-104-047-3907	Sequence 3907, Ap	493	26	60.5	832	2	US-08-758-314-4	Sequence 4, Appl
421	26	60.5	572	2	US-09-882-274-4	Sequence 4, Appl	494	26	60.5	832	2	US-08-350-309-4	Sequence 4, Appl
422	26	60.5	586	2	US-10-176-884-12	Sequence 12, Appl	495	26	60.5	832	2	US-08-520-946-4	Sequence 4, Appl
423	26	60.5	588	2	US-09-601-777-2	Sequence 2, Appl	496	26	60.5	832	2	US-08-978-806-2	Sequence 2, Appl
424	26	60.5	592	2	US-09-435-739-14	Sequence 14, Appl	497	26	60.5	832	2	US-09-684-938-4	Sequence 4, Appl
425	26	60.5	592	2	US-09-988-113-14	Sequence 14, Appl	498	26	60.5	832	2	US-09-308-825A-4	Sequence 4, Appl
426	26	60.5	592	2	US-10-384-450A-14	Sequence 14, Appl	499	26	60.5	832	2	US-09-758-282B-4	Sequence 4, Appl
427	26	60.5	597	2	US-09-902-540-14203	Sequence 14203, A	500	26	60.5	832	2	US-09-655-378A-4	Sequence 4, Appl
428	26	60.5	601	1	US-08-458-477A-2	Sequence 2, Appl	501	26	60.5	832	2	US-09-940-244-4	Sequence 4, Appl
429	26	60.5	601	1	US-09-033-153-2	Sequence 2, Appl	502	26	60.5	832	2	US-09-333-145-4	Sequence 4, Appl
430	26	60.5	601	2	US-09-325-430B-2	Sequence 2, Appl	503	26	60.5	832	2	US-09-577-304A-4	Sequence 4, Appl
431	26	60.5	603	2	US-09-964-899-29	Sequence 29, Appl	504	26	60.5	832	2	US-09-381-212-4	Sequence 4, Appl
432	26	60.5	604	2	US-09-523-849-35	Sequence 35, Appl	505	26	60.5	832	2	US-10-081-806-4	Sequence 4, Appl
433	26	60.5	625	2	US-09-248-796A-17352	Sequence 17352, A	506	26	60.5	832	2	US-10-190-967-3	Sequence 3, Appl
434	26	60.5	633	1	US-08-458-477A-5	Sequence 5, Appl	507	26	60.5	832	2	US-09-713-601A-4	Sequence 4, Appl
435	26	60.5	633	1	US-09-033-153-5	Sequence 5, Appl	508	26	60.5	833	1	PCT-US91-07035-2	Sequence 2, Appl
436	26	60.5	633	2	US-09-325-430B-5	Sequence 5, Appl	509	26	60.5	833	1	US-08-073-384C-8	Sequence 8, Appl
437	26	60.5	637	2	US-09-252-991A-28952	Sequence 28952, A	510	26	60.5	833	1	US-08-254-359A-8	Sequence 8, Appl
438	26	60.5	659	2	US-09-710-279-1596	Sequence 1596, Ap	511	26	60.5	833	1	US-08-483-043-8	Sequence 8, Appl
439	26	60.5	684	2	US-09-252-991A-28604	Sequence 28604, A	512	26	60.5	833	1	US-08-481-238-8	Sequence 8, Appl
440	26	60.5	688	2	US-09-902-540-14399	Sequence 14399, A	513	26	60.5	833	1	US-08-471-066B-8	Sequence 8, Appl
441	26	60.5	690	2	US-09-134-001C-4938	Sequence 4938, Ap	514	26	60.5	833	1	US-08-484-956-8	Sequence 8, Appl
442	26	60.5	691	2	US-08-946-475-2	Sequence 2, Appl	515	26	60.5	833	1	US-08-484-956-85	Sequence 85, Appl
443	26	60.5	691	2	US-09-340-479-2	Sequence 2, Appl	516	26	60.5	833	1	US-08-757-653-8	Sequence 8, Appl
444	26	60.5	695	1	US-08-484-956-87	Sequence 87, Appl	517	26	60.5	833	1	US-08-757-653-85	Sequence 85, Appl
445	26	60.5	695	1	US-08-757-653-87	Sequence 87, Appl	518	26	60.5	833	1	US-08-757-653-168	Sequence 168, App
446	26	60.5	695	2	US-08-520-946-87	Sequence 87, Appl	519	26	60.5	833	1	US-08-757-653-188	Sequence 188, App
447	26	60.5	695	2	US-09-655-378A-87	Sequence 87, Appl	520	26	60.5	833	1	US-08-757-653-190	Sequence 190, App
448	26	60.5	700	2	US-09-543-681A-4969	Sequence 4969, Ap	521	26	60.5	833	1	US-08-599-491-8	Sequence 8, Appl
449	26	60.5	703	2	US-09-270-767-44732	Sequence 44732, A	522	26	60.5	833	1	US-08-756-386-8	Sequence 8, Appl
450	26	60.5	708	2	US-09-902-540-15537	Sequence 15537, A	523	26	60.5	833	1	US-08-823-516-66	Sequence 66, Appl
451	26	60.5	711	2	US-08-946-475-9	Sequence 9, Appl	524	26	60.5	833	1	US-08-823-516-69	Sequence 69, Appl
452	26	60.5	711	2	US-09-340-479-9	Sequence 9, Appl	525	26	60.5	833	1	US-08-823-516-71	Sequence 71, Appl
453	26	60.5	712	2	US-09-543-681A-8147	Sequence 8147, Ap	526	26	60.5	833	1	US-08-682-853A-8	Sequence 8, Appl
454	26	60.5	717	2	US-09-509-800-2	Sequence 2, Appl	527	26	60.5	833	2	US-08-759-038-8	Sequence 8, Appl
455	26	60.5	718	2	US-09-252-991A-28229	Sequence 28229, A	528	26	60.5	833	2	US-08-759-038-107	Sequence 107, App
456	26	60.5	749	2	US-09-562-737-97	Sequence 97, Appl	529	26	60.5	833	2	US-08-759-038-130	Sequence 130, App
457	26	60.5	758	2	US-09-902-540-16578	Sequence 16578, A	530	26	60.5	833	2	US-08-759-038-132	Sequence 132, App
458	26	60.5	759	2	US-10-258-860-6	Sequence 6, Appl	531	26	60.5	833	2	US-08-758-314-8	Sequence 8, Appl
459	26	60.5	761	2	US-09-328-352-5650	Sequence 5650, Ap	532	26	60.5	833	2	US-08-758-314-107	Sequence 107, App
460	26	60.5	762	2	US-10-258-860-2	Sequence 2, Appl	533	26	60.5	833	2	US-08-758-314-130	Sequence 130, App
461	26	60.5	765	1	US-08-663-112-2	Sequence 2, Appl	534	26	60.5	833	2	US-08-758-314-132	Sequence 132, App
462	26	60.5	765	2	US-09-248-796A-20068	Sequence 20068, A	535	26	60.5	833	2	US-09-350-309-8	Sequence 8, Appl
463	26	60.5	765	2	US-09-538-092-906	Sequence 906, App	536	26	60.5	833	2	US-08-520-946-8	Sequence 8, Appl
464	26	60.5	765	2	US-09-882-274-2	Sequence 2, Appl	537	26	60.5	833	2	US-08-520-946-85	Sequence 85, Appl
465	26	60.5	785	2	US-10-258-860-4	Sequence 4, Appl	538	26	60.5	833	2	US-08-520-946-85	Sequence 85, Appl

247	26	60.5	60	2	US-09-497-491-39	Sequence 39, Appl	320	26	60.5	320	2	US-09-713-601A-61	Sequence 61, Appl
248	26	60.5	64	2	US-09-248-796A-26991	Sequence 26991, A	321	26	60.5	321	2	US-09-758-759-111	Sequence 111, Appl
249	26	60.5	69	2	US-09-270-767-62365	Sequence 62365, A	322	26	60.5	322	1	US-08-484-956-89	Sequence 89, Appl
250	26	60.5	70	2	US-09-497-491-35	Sequence 35, Appl	323	26	60.5	323	1	US-08-757-653-89	Sequence 89, Appl
251	26	60.5	72	2	US-09-513-999C-7082	Sequence 7082, Ap	324	26	60.5	324	2	US-08-520-946-89	Sequence 89, Appl
252	26	60.5	82	1	US-08-248-839C-122	Sequence 122, App	325	26	60.5	325	2	US-09-655-378A-89	Sequence 89, Appl
253	26	60.5	97	2	US-09-902-540-12339	Sequence 12339, A	326	26	60.5	326	2	US-09-107-532A-6263	Sequence 6263, Ap
254	26	60.5	101	2	US-10-004-381-2	Sequence 2, Appli	327	26	60.5	327	2	US-10-152-886-57	Sequence 57, Appl
255	26	60.5	105	2	US-09-248-796A-17804	Sequence 17804, A	328	26	60.5	328	2	US-09-107-532A-6947	Sequence 6947, Ap
256	26	60.5	106	1	US-08-715-554-3	Sequence 3, Appli	329	26	60.5	329	2	US-09-136-073-2	Sequence 2, Appli
257	26	60.5	106	1	US-08-583-118-3	Sequence 3, Appli	330	26	60.5	330	2	US-09-457-024A-2	Sequence 2, Appli
258	26	60.5	106	2	US-09-248-796A-24941	Sequence 24941, A	331	26	60.5	331	2	US-09-602-777A-1148	Sequence 148, App
259	26	60.5	113	2	US-09-107-532A-4396	Sequence 4396, Ap	332	26	60.5	332	2	US-09-094-557-3	Sequence 3, Appli
260	26	60.5	124	2	US-09-270-767-32952	Sequence 32952, A	333	26	60.5	333	2	US-09-438-185A-19	Sequence 19, Appl
261	26	60.5	124	2	US-09-270-767-48169	Sequence 48169, A	334	26	60.5	334	2	US-10-055-364-48	Sequence 48, Appl
262	26	60.5	133	2	US-09-513-999C-5734	Sequence 5734, Ap	335	26	60.5	335	2	US-10-104-047-3298	Sequence 3298, Ap
263	26	60.5	140	2	US-09-248-796A-26871	Sequence 26871, A	336	26	60.5	336	2	US-09-181-336-17	Sequence 17, Appl
264	26	60.5	153	2	US-09-270-767-37297	Sequence 37297, A	337	26	60.5	337	2	US-09-949-016-8340	Sequence 8340, Ap
265	26	60.5	153	2	US-09-270-767-52514	Sequence 52514, A	338	26	60.5	338	2	US-09-328-352-4963	Sequence 4963, Ap
266	26	60.5	166	2	US-09-134-000C-6070	Sequence 6070, Ap	339	26	60.5	339	2	US-09-252-991A-26429	Sequence 26429, A
267	26	60.5	172	2	US-09-270-767-37433	Sequence 37433, A	340	26	60.5	340	2	US-09-285-055-2	Sequence 2, Appli
268	26	60.5	172	2	US-09-270-767-52850	Sequence 52850, A	341	26	60.5	341	2	US-09-407-062-7	Sequence 7, Appli
269	26	60.5	175	2	US-09-395-689-4	Sequence 4, Appli	342	26	60.5	342	2	US-10-045-063A-2	Sequence 2, Appli
270	26	60.5	176	2	US-09-248-796A-19985	Sequence 19985, A	343	26	60.5	343	2	US-09-921-870-109	Sequence 109, App
271	26	60.5	187	2	US-09-710-279-2714	Sequence 2714, Ap	344	26	60.5	344	2	US-09-721-870-109	Sequence 109, App
272	26	60.5	188	2	US-09-489-847-314	Sequence 314, App	345	26	60.5	345	2	US-08-631-607-6	Sequence 6, Appli
273	26	60.5	188	2	US-09-540-236-3769	Sequence 3769, Ap	346	26	60.5	346	2	US-09-098-358B-6	Sequence 6, Appli
274	26	60.5	195	2	US-09-489-039A-12028	Sequence 12028, A	347	26	60.5	347	2	US-09-182-816-28	Sequence 28, Appl
275	26	60.5	208	2	US-09-270-767-36367	Sequence 36367, A	348	26	60.5	348	2	US-09-471-528-28	Sequence 28, Appl
276	26	60.5	208	2	US-09-270-767-51584	Sequence 51584, A	349	26	60.5	349	2	US-09-634-530-28	Sequence 28, Appl
277	26	60.5	210	2	US-09-248-796A-15869	Sequence 15869, A	350	26	60.5	350	2	US-09-902-540-15995	Sequence 15995, A
278	26	60.5	212	2	US-09-270-767-32729	Sequence 32729, A	351	26	60.5	351	2	US-09-182-816-23	Sequence 23, Appl
279	26	60.5	212	2	US-09-270-767-47946	Sequence 47946, A	352	26	60.5	352	2	US-09-471-528-23	Sequence 23, Appl
280	26	60.5	214	2	US-09-902-540-10588	Sequence 10588, A	353	26	60.5	353	2	US-09-634-530-23	Sequence 23, Appl
281	26	60.5	214	2	US-09-893-737-80	Sequence 80, Appl	354	26	60.5	354	2	US-09-248-796A-25017	Sequence 25017, A
282	26	60.5	222	2	US-09-270-767-60188	Sequence 60188, A	355	26	60.5	355	2	US-09-592-054-6	Sequence 6, Appli
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287	26	60.5	255	2	US-09-370-838-183	Sequence 183, App	360	26	60.5	360	2	US-10-332-795-9	Sequence 9, Appli
288	26	60.5	255	2	US-09-854-133-183	Sequence 183, App	361	26	60.5	361	2	US-09-489-039A-10153	Sequence 10153, A
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296	26	60.5	287	2	US-09-105-697-7	Sequence 7, Appli	369	26	60.5	369	2	US-08-757-653-90	Sequence 90, Appl
297	26	60.5	287	2	US-09-105-697-8	Sequence 8, Appli	370	26	60.5	370	2	US-08-520-946-90	Sequence 90, Appl
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106	28	65.1	365	2	US-09-489-847-332	Sequence 322, App	179	27	62.8	330	2	US-09-134-001C-3811	Sequence 3811, Ap
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117	28	65.1	507	2	US-09-107-532A-4386	Sequence 4386, Ap	190	27	62.8	423	2	US-09-540-236-2183	Sequence 2183, Ap
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136	28	65.1	939	2	US-09-252-991A-19109	Sequence 19109, A	209	27	62.8	725	2	US-09-252-991A-29340	Sequence 29340, A
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146	28	62.8	82	2	US-09-407-956-4	Sequence 4, Appli	219	27	62.8	1147	1	US-08-735-893-3	Sequence 3, Appli
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161	27	62.8	216	2	US-09-270-767-55637	Sequence 55637, A	234	27	62.8	1227	2	US-09-328-352-7046	Sequence 7046, Ap
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163	27	62.8	228	2	US-08-976-063E-14	Sequence 14, Appl	236	27	62.8	1976	2	US-08-328-254-6	Sequence 6, Appli
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151	27	61.4	802	11	US-11-264-096-888	Sequence 888, App	224	26	59.1	407	11	US-11-188-298-17827	Sequence 17827, A
152	27	61.4	803	11	US-11-098-686-10842	Sequence 10842, A	225	26	59.1	407	11	US-11-188-298-19883	Sequence 19883, A
153	27	61.4	876	11	US-11-031-206-206	Sequence 206, App	226	26	59.1	408	11	US-11-188-298-18795	Sequence 18795, A
154	27	61.4	884	9	US-10-995-561-786	Sequence 786, App	227	26	59.1	413	7	US-09-978-360A-710	Sequence 710, App
155	27	61.4	904	11	US-11-079-463-6397	Sequence 6397, Ap	228	26	59.1	420	11	US-11-188-298-10248	Sequence 10248, A
156	27	61.4	1828	11	US-11-126-022-23	Sequence 23, Appl	229	26	59.1	421	11	US-11-188-298-7320	Sequence 7320, Ap
157	27	61.4	1852	11	US-11-126-022-21	Sequence 21, Appl	230	26	59.1	426	9	US-10-873-528-34	Sequence 34, Appl
158	27	61.4	1863	11	US-11-126-022-2	Sequence 2, Appli	231	26	59.1	427	11	US-11-087-099-8459	Sequence 8459, Ap
159	27	61.4	1863	11	US-11-126-022-9	Sequence 9, Appli	232	26	59.1	428	11	US-11-096-568A-9065	Sequence 9065, Ap
160	27	61.4	1863	11	US-11-126-022-10	Sequence 10, Appl	233	26	59.1	430	11	US-11-072-512-2204	Sequence 2204, Ap
161	27	61.4	1863	11	US-11-126-022-11	Sequence 11, Appl	234	26	59.1	430	11	US-11-096-568A-9064	Sequence 9064, Ap
162	27	61.4	1863	11	US-11-126-022-12	Sequence 12, Appl	235	26	59.1	432	11	US-11-087-099-2319	Sequence 2319, Ap
163	27	61.4	1863	11	US-11-126-022-13	Sequence 13, Appl	236	26	59.1	432	11	US-11-096-568A-9063	Sequence 9063, Ap
164	27	61.4	1863	11	US-11-126-022-14	Sequence 14, Appl	237	26	59.1	432	11	US-11-096-568A-9066	Sequence 9066, Ap
165	27	61.4	1863	11	US-11-126-022-15	Sequence 15, Appl	238	26	59.1	441	11	US-11-188-298-12933	Sequence 12933, A
166	27	61.4	1863	11	US-11-126-022-16	Sequence 16, Appl	239	26	59.1	442	8	US-10-505-928-525	Sequence 525, App
167	27	61.4	1863	11	US-11-126-022-17	Sequence 17, Appl	240	26	59.1	452	11	US-11-098-686-10222	Sequence 10222, A

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243	26	59.1	456	11	US-11-098-686-10877	Sequence 10877, A	316	1218	11	US-11-188-298-1733	Sequence 1733, Ap
244	26	59.1	467	11	US-11-188-298-20828	Sequence 20828, A	317	1394	11	US-11-188-298-13354	Sequence 13354, A
245	26	59.1	468	11	US-11-188-298-9902	Sequence 9902, Ap	318	1531	9	US-10-330-773-142	Sequence 142, App
246	26	59.1	473	11	US-11-188-298-4172	Sequence 4172, Ap	319	1897	11	US-11-096-568A-28325	Sequence 28325, A
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251	26	59.1	481	9	US-10-858-144-3	Sequence 3, Appli	324	3113	8	US-10-505-928-325	Sequence 325, App
252	26	59.1	481	11	US-11-096-568A-19237	Sequence 19237, A	325	29	11	US-11-264-096-1029	Sequence 1029, Ap
253	26	59.1	484	11	US-11-096-568A-23730	Sequence 23730, A	326	38	11	US-11-141-725-58	Sequence 58, Appl
254	26	59.1	485	11	US-11-112-824-2	Sequence 2, Appli	327	42	11	US-11-264-096-1030	Sequence 1030, Ap
255	26	59.1	485	11	US-11-112-824-28	Sequence 28, Appl	328	51	11	US-11-141-725-62	Sequence 62, Appl
256	26	59.1	485	11	US-11-096-568A-23729	Sequence 23729, A	329	56.8	11	US-11-096-568A-1551	Sequence 1551, Ap
257	26	59.1	485	11	US-11-172-740-2332	Sequence 2332, Ap	330	72	9	US-10-467-657-3006	Sequence 3006, Ap
258	26	59.1	488	11	US-11-169-041-197	Sequence 197, App	331	83	7	US-09-978-360A-418	Sequence 418, App
259	26	59.1	489	11	US-11-242-111-31	Sequence 31, Appl	332	83	8	US-10-511-937-2615	Sequence 2615, Ap
260	26	59.1	491	11	US-11-188-298-4903	Sequence 4903, Ap	333	83	9	US-10-821-234-1346	Sequence 1346, Ap
261	26	59.1	492	11	US-11-188-298-13302	Sequence 13302, A	334	98	9	US-10-506-454-885	Sequence 885, App
262	26	59.1	504	9	US-10-784-004-427	Sequence 427, App	335	106	11	US-11-144-947-553	Sequence 553, App
263	26	59.1	504	9	US-10-784-004-948	Sequence 948, App	336	110	9	US-10-793-626-2152	Sequence 2152, Ap
264	26	59.1	504	11	US-11-188-298-9057	Sequence 9057, Ap	337	126	11	US-11-087-099-2512	Sequence 2512, Ap
265	26	59.1	511	11	US-11-188-298-23047	Sequence 23047, A	338	132	11	US-11-096-568A-19178	Sequence 19178, A
266	26	59.1	520	9	US-10-995-561-532	Sequence 532, App	339	135	11	US-11-087-099-7211	Sequence 7211, Ap
267	26	59.1	520	9	US-10-194-487-332	Sequence 332, App	340	139	11	US-11-072-512-2633	Sequence 2633, Ap
268	26	59.1	520	9	US-10-195-883-332	Sequence 332, App	341	143	9	US-10-821-234-1205	Sequence 1205, Ap
269	26	59.1	520	9	US-10-195-888-332	Sequence 332, App	342	149	11	US-11-087-099-584	Sequence 584, App
270	26	59.1	520	9	US-10-195-889-332	Sequence 332, App	343	149	11	US-11-087-099-777	Sequence 777, App
271	26	59.1	524	9	US-10-216-161A-614	Sequence 614, App	344	149	11	US-11-087-099-875	Sequence 875, App
272	26	59.1	526	9	US-10-467-657-6754	Sequence 6754, App	345	149	11	US-11-087-099-4170	Sequence 4170, Ap
273	26	59.1	543	11	US-11-096-568A-23728	Sequence 23728, A	346	149	11	US-11-087-099-10310	Sequence 10310, A
274	26	59.1	561	9	US-10-943-015-4	Sequence 4, Appli	347	152	8	US-10-511-937-2442	Sequence 2442, Ap
275	26	59.1	567	11	US-11-188-298-4549	Sequence 4549, Ap	348	152	9	US-10-928-828-25	Sequence 25, Appl
276	26	59.1	582	11	US-11-079-463-9255	Sequence 9255, Ap	349	158	9	US-10-506-454-529	Sequence 529, App
277	26	59.1	604	9	US-10-942-072-4	Sequence 4, Appli	350	159	11	US-11-188-298-14070	Sequence 14070, A
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280	26	59.1	633	9	US-10-943-015-10	Sequence 10, Appl	353	186	11	US-11-144-947-394	Sequence 394, App
281	26	59.1	633	11	US-11-188-298-18462	Sequence 18462, A	354	188	11	US-11-045-004-749	Sequence 749, App
282	26	59.1	650	11	US-11-045-004-2433	Sequence 2433, Ap	355	192	11	US-11-087-099-2141	Sequence 2141, Ap
283	26	59.1	662	9	US-10-455-772-1096	Sequence 1096, Ap	356	194	9	US-10-980-388-104	Sequence 104, App
284	26	59.1	671	11	US-11-087-099-8628	Sequence 8628, Ap	357	199	9	US-10-194-487-588	Sequence 588, App
285	26	59.1	683	11	US-11-087-099-7461	Sequence 7461, Ap	358	199	9	US-10-195-883-588	Sequence 588, App
286	26	59.1	683	11	US-11-188-298-17476	Sequence 17476, A	359	199	9	US-10-195-888-588	Sequence 588, App
287	26	59.1	706	11	US-11-087-099-4237	Sequence 4237, Ap	360	199	9	US-10-195-889-588	Sequence 588, App
288	26	59.1	729	9	US-10-523-328-13	Sequence 13, Appl	361	199	11	US-11-019-711-102	Sequence 102, App
289	26	59.1	729	11	US-11-099-691-3	Sequence 3, Appli	362	200	9	US-10-506-454-1508	Sequence 1508, Ap
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291	26	59.1	761	9	US-10-204-639-19	Sequence 19, Appl	364	205	11	US-11-079-463-8194	Sequence 8194, Ap
292	26	59.1	765	11	US-11-087-099-905	Sequence 905, App	365	206	11	US-11-087-099-5654	Sequence 5654, Ap
293	26	59.1	777	11	US-11-087-099-5818	Sequence 5818, Ap	366	213	11	US-11-087-099-7298	Sequence 7298, Ap
294	26	59.1	870	11	US-11-031-206-188	Sequence 188, App	367	216	9	US-10-467-657-1284	Sequence 1284, Ap
295	26	59.1	875	11	US-11-045-004-126	Sequence 126, App	368	216	9	US-10-467-657-5532	Sequence 5532, Ap
296	26	59.1	880	11	US-11-087-099-950	Sequence 950, App	369	216	9	US-10-467-657-7492	Sequence 7492, Ap
297	26	59.1	898	11	US-11-079-463-7619	Sequence 7619, Ap	370	216	9	US-10-467-657-8232	Sequence 8232, Ap
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299	26	59.1	932	9	US-10-511-989-20	Sequence 20, Appl	372	218	9	US-10-506-454-357	Sequence 357, App
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304	26	59.1	1058	11	US-11-124-367A-386	Sequence 386, App	377	227	11	US-11-206-746-3	Sequence 3, Appli
305	26	59.1	1082	11	US-11-124-367A-387	Sequence 387, App	378	234	11	US-11-087-099-10254	Sequence 10254, A
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308	26	59.1	1095	11	US-11-079-463-8973	Sequence 8973, Ap	381	239	11	US-11-188-298-7616	Sequence 7616, Ap
309	26	59.1	1125	9	US-10-821-234-1444	Sequence 1444, Ap	382	242	9	US-10-821-234-1073	Sequence 1073, Ap
310	26	59.1	1154	9	US-10-511-989-22	Sequence 22, Appl	383	242	11	US-11-211-401-4	Sequence 4, Appli
311	26	59.1	1162	10	US-11-106-014-94	Sequence 94, Appl	384	244	11	US-11-045-004-1690	Sequence 1690, Ap
312	26	59.1	1167	9	US-10-942-072-6	Sequence 6, Appli	385	250	9	US-10-821-234-1297	Sequence 1297, Ap
313	26	59.1	1167	9	US-10-942-072-13	Sequence 13, Appl	386	250	11	US-11-211-401-1	Sequence 1, Appli

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388	25	56.8	251	9	US-10-195-883-2	Sequence 2, Appli	461	25	56.8	373	11	US-11-096-568A-10605	Sequence 10605, A
389	25	56.8	251	9	US-10-195-888-2	Sequence 2, Appli	462	25	56.8	378	11	US-11-096-568A-18777	Sequence 18777, A
390	25	56.8	251	9	US-10-195-889-2	Sequence 2, Appli	463	25	56.8	381	11	US-11-079-463-6324	Sequence 6324, Ap
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396	25	56.8	263	11	US-11-096-568A-6706	Sequence 6707, Ap	469	25	56.8	393	11	US-11-096-568A-2147	Sequence 2147, Ap
397	25	56.8	264	11	US-11-096-568A-6706	Sequence 6706, Ap	470	25	56.8	395	7	US-09-978-360A-769	Sequence 769, App
398	25	56.8	264	11	US-11-096-568A-17016	Sequence 17016, A	471	25	56.8	395	9	US-10-467-657-3516	Sequence 3516, Ap
399	25	56.8	266	11	US-11-096-568A-20944	Sequence 20944, A	472	25	56.8	395	11	US-11-072-175-235	Sequence 235, App
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402	25	56.8	274	11	US-11-096-568A-2149	Sequence 2149, Ap	475	25	56.8	396	11	US-11-087-099-12242	Sequence 12242, A
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404	25	56.8	285	11	US-11-264-096-101	Sequence 101, App	477	25	56.8	397	11	US-11-188-298-11451	Sequence 11451, A
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423	25	56.8	323	11	US-11-264-096-1402	Sequence 1402, Ap	496	25	56.8	410	9	US-10-467-657-7680	Sequence 7680, Ap
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433	25	56.8	342	11	US-11-172-740-1768	Sequence 1768, Ap	506	25	56.8	417	11	US-11-079-463-8014	Sequence 8014, Ap
434	25	56.8	342	11	US-11-172-740-1770	Sequence 1770, Ap	507	25	56.8	419	11	US-11-188-298-10420	Sequence 10420, A
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576	25	56.8	580	11	US-11-072-512-2876	Sequence 2876, Ap	649	25	56.8	1298	8	US-10-505-928-857	Sequence 857, App
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ALIGNMENTS

RESULT 1  
US-10-793-626-1264  
; Sequence 1264, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; PRIOR FILING DATE: 2004-03-04  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1264  
; LENGTH: 305  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1264

Query Match 75.0%; Score 33; DB 9; Length 305;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 138 FQLQINWP 145

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US-10-878-556A-55  
; Sequence 55, Application US/10878556A  
; Publication No. US20050266399A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffmann La-Roche Inc.

; TITLE OF INVENTION: HCV regulated protein expression  
; FILE REFERENCE: 21762  
; CURRENT APPLICATION NUMBER: US/10/878,556A  
; CURRENT FILING DATE: 2004-06-28  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
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; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: sw hum/r23b\_human  
; DATABASE ENTRY DATE: 1996-10-01  
US-10-878-556A-55  
  
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; Sequence 4699, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
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; Sequence 4698, Application US/11096568A  
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; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
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RESULT 5  
US-11-096-568A-4697  
; Sequence 4697, Application US/11096568A  
; Publication No. US2006048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 4697  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(360)  
; OTHER INFORMATION: Ceres Seq. ID no. 14303472  
US-11-096-568A-4697

Query Match 72.7%; Score 32; DB 11; Length 360;  
Best Local Similarity 87.5%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLLMEPV 9  
||| |||  
Db 132 LQLLTEPV 139

RESULT 6  
US-11-078-991-1  
; Sequence 1, Application US/11078991  
; Publication No. US20050260727A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer CropScience AG  
; TITLE OF INVENTION: Crystal structure of mitochondrial  
; FILE REFERENCE: BCS 03-3112  
; CURRENT APPLICATION NUMBER: US/11/078,991  
; CURRENT FILING DATE: 2005-03-11  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Nicotiana tabacum  
; FEATURE:  
; NAME/KEY: PRT  
; LOCATION: (1)..(503)  
US-11-078-991-1

Query Match 72.7%; Score 32; DB 11; Length 503;  
Best Local Similarity 62.5%; Pred. No. 55;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMEPV 9  
||| |||  
Db 127 LQMLLEPI 134

## RESULT 7

US-11-188-298-21803  
; Sequence 21803, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 21803  
; LENGTH: 1106  
; TYPE: PRT  
; ORGANISM: Neurospora crassa  
US-11-188-298-21803

Query Match 72.7%; Score 32; DB 11; Length 1106;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEP 8  
||| ||| :  
Db 21 FLQLLQDP 28

## RESULT 8

US-11-051-267-18  
; Sequence 18, Application US/11051267  
; Publication No. US20050257278A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,  
; FILE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME  
; FILE REFERENCE: JHU1470-2  
; CURRENT APPLICATION NUMBER: US/11/051,267  
; CURRENT FILING DATE: 2005-02-03  
; PRIOR APPLICATION NUMBER: US/09/841,730  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: 09/626,896  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 09/485,046  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: PCT/US98/15598  
; PRIOR FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 60/054,461  
; PRIOR FILING DATE: 1997-08-01  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Meleagris gallopavo  
US-11-051-267-18

Query Match 70.5%; Score 31; DB 11; Length 375;  
Best Local Similarity 55.6%; Pred. No. 65;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
||| ||| :  
Db 13 FMQILVHPV 21

## RESULT 9

US-10-922-232B-57  
; Sequence 57, Application US/1092232B  
; Publication No. US20060024668A1

; GENERAL INFORMATION:  
; APPLICANT: van der Hoek, Cornelia  
; TITLE OF INVENTION: Coronavirus, nucleic acid, protein, and methods for the generation  
; FILE REFERENCE: 294-226  
; CURRENT APPLICATION NUMBER: US/10/922,232B  
; CURRENT FILING DATE: 2004-08-18  
; PRIOR APPLICATION NUMBER: US 60/535,002  
; PRIOR FILING DATE: 2004-01-07  
; PRIOR APPLICATION NUMBER: EP 03077602.5  
; PRIOR FILING DATE: 2003-08-18  
; PRIOR APPLICATION NUMBER: EP 04075050.7  
; PRIOR FILING DATE: 2004-01-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 57  
; LENGTH: 2250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence. ORF 1ab, replicase polyprotein of HCoV\_NL63.  
US-10-922-232B-57

; GENERAL INFORMATION:  
; APPLICANT: van der Hoek, Cornelia  
; TITLE OF INVENTION: Coronavirus, nucleic acid, protein, and methods for the generation  
; FILE REFERENCE: 294-226  
; CURRENT APPLICATION NUMBER: US/10/922,232B  
; CURRENT FILING DATE: 2004-08-18  
; PRIOR APPLICATION NUMBER: US 60/535,002  
; PRIOR FILING DATE: 2004-01-07  
; PRIOR APPLICATION NUMBER: EP 03077602.5  
; PRIOR FILING DATE: 2003-08-18  
; PRIOR APPLICATION NUMBER: EP 04075050.7  
; PRIOR FILING DATE: 2004-01-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 56  
; LENGTH: 6738  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence. ORF 1ab, replicase polyprotein of HCoV\_NL63  
US-10-922-232B-56

Query Match 70.5%; Score 31; DB 9; Length 2250;  
Best Local Similarity 66.7%; Pred. No. 4.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Query Match 70.5%; Score 31; DB 9; Length 6738;  
Best Local Similarity 66.7%; Pred. No. 1.6e+03;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
| | | | |  
Db 1594 FSQLLCEPI 1602

QY 1 FLQLLMEPV 9  
| | | | |  
Db 2283 FSQLLCEPI 2291

RESULT 10  
US-10-922-232B-55  
; Sequence 55, Application US/10922232B  
; Publication No. US20060024668A1  
; GENERAL INFORMATION:  
; APPLICANT: van der Hoek, Cornelia  
; TITLE OF INVENTION: Coronavirus, nucleic acid, protein, and methods for the generation  
; FILE REFERENCE: 294-226  
; CURRENT APPLICATION NUMBER: US/10/922,232B  
; CURRENT FILING DATE: 2004-08-18  
; PRIOR APPLICATION NUMBER: US 60/535,002  
; PRIOR FILING DATE: 2004-01-07  
; PRIOR APPLICATION NUMBER: EP 03077602.5  
; PRIOR FILING DATE: 2003-08-18  
; PRIOR APPLICATION NUMBER: EP 04075050.7  
; PRIOR FILING DATE: 2004-01-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 55  
; LENGTH: 4060  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence. ORF 1a, replicase enzyme complex of HCoV\_NL63  
US-10-922-232B-55

RESULT 12  
US-11-212-443-38  
; Sequence 38, Application US/11212443  
; Publication No. US20050287165A1  
; GENERAL INFORMATION:  
; APPLICANT: Scalato, Enzo  
; APPLICANT: Masignani, Rino  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Meningococcal Antigens  
; FILE REFERENCE: CHIR0159  
; CURRENT APPLICATION NUMBER: US/11/212,443  
; CURRENT FILING DATE: 2005-08-24  
; PRIOR APPLICATION NUMBER: US/09/302,626  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: PCT/IB99/00103  
; PRIOR FILING DATE: 1999-01-14  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-11-212-443-38

Query Match 70.5%; Score 31; DB 9; Length 4060;  
Best Local Similarity 66.7%; Pred. No. 9.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Query Match 68.2%; Score 30; DB 11; Length 103;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
| | | | |  
Db 2283 FSQLLCEPI 2291

QY 1 FLQLLMEPV 9  
| | | | |  
Db 26 FLTLLNPV 34

RESULT 11  
US-10-922-232B-56  
; Sequence 56, Application US/1092232B  
; Publication No. US20060024668A1

RESULT 13  
US-11-098-686-10960  
; Sequence 10960, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.

; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; FILE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: US 60/416,395  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 10960  
; LENGTH: 321  
; TYPE: PRT  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-10960

Query Match 68.2%; Score 30; DB 11; Length 321;  
Best Local Similarity 33.3%; Pred. No. 89;  
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
Db 2 YIELMQPI 10

RESULT 14  
US-11-188-298-3421  
; Sequence 3421, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 3421  
; LENGTH: 408  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-11-188-298-3421

Query Match 68.2%; Score 30; DB 11; Length 408;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLLMEPV 9  
Db 18 LQLLMEPV 25

RESULT 15  
US-11-010-239-95  
; Sequence 95, Application US/11010239  
; Publication No. US20060015970A1  
; GENERAL INFORMATION:  
; APPLICANT: ROGER PENNELL  
; APPLICANT: JACK OKAMURO  
; APPLICANT: RICHARD SCHNEEBERGER  
; APPLICANT: YIWEI FANG  
; APPLICANT: SHING KWOK  
; APPLICANT: DIANE JOFUKU  
; APPLICANT: EDWARD A. KIEGLE  
; APPLICANT: JONATHAN DONSON  
; APPLICANT: NESTOR APUYA  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR  
; MODIFYING PLANT CHARACTERISTICS

; FILE REFERENCE: 2750-1585F052  
; CURRENT APPLICATION NUMBER: US/11/010,239  
; CURRENT FILING DATE: 2004-12-09

; PRIOR APPLICATION NUMBER: US 60/529,352  
; PRIOR FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 95  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; NAME/KEY: misc feature  
; LOCATION: (1)..(541)  
; OTHER INFORMATION: 13647840\_protein\_ID\_13647841  
US-11-010-239-95

Query Match 68.2%; Score 30; DB 11; Length 541;  
Best Local Similarity 44.4%; Pred. No. 1.6e+02;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
Db 291 FMEMLQPV 299

RESULT 16  
US-10-784-004-340  
; Sequence 340, Application US/10784004  
; Publication No. US20060084066A1  
; GENERAL INFORMATION:  
; APPLICANT: Biogen Idec  
; TITLE OF INVENTION: Surrogate Markers of Pain  
; FILE REFERENCE: 08201.6029-00000  
; CURRENT APPLICATION NUMBER: US/10/784,004  
; CURRENT FILING DATE: 2004-02-20  
; NUMBER OF SEQ ID NOS: 1251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 340  
; LENGTH: 857  
; TYPE: PRT  
; ORGANISM: rat  
US-10-784-004-340

Query Match 68.2%; Score 30; DB 9; Length 857;  
Best Local Similarity 44.4%; Pred. No. 2.7e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9  
Db 288 FCQLILDPI 296

RESULT 17  
US-10-784-004-658  
; Sequence 658, Application US/10784004  
; Publication No. US20060084066A1  
; GENERAL INFORMATION:  
; APPLICANT: Biogen Idec  
; TITLE OF INVENTION: Surrogate Markers of Pain  
; FILE REFERENCE: 08201.6029-00000  
; CURRENT APPLICATION NUMBER: US/10/784,004  
; CURRENT FILING DATE: 2004-02-20  
; NUMBER OF SEQ ID NOS: 1251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 658  
; LENGTH: 857  
; TYPE: PRT  
; ORGANISM: human  
US-10-784-004-658

Query Match 68.2%; Score 30; DB 9; Length 857;  
Best Local Similarity 44.4%; Pred. No. 2.7e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLLMEPV 9

```
Db      288 FCQLILDPI 296
| | | | |
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
; LENGTH: 1450
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-152

Query Match      68.2%; Score 30; DB 9; Length 1450;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLQLLMEP 8
Db      246 FLSLAMEP 253
| | | | |

RESULT 21
US-10-793-626-2850
; Sequence 2850, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2850
; LENGTH: 1501
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2850

Query Match      68.2%; Score 30; DB 9; Length 1501;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FLQLLMEP 8
Db      297 FLSLAMEP 304
| | | | |

RESULT 22
US-11-045-004-995
; Sequence 995, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA

Db      288 FCQLILDPI 296
| | | | |
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
; LENGTH: 1450
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-152

Query Match      68.2%; Score 30; DB 9; Length 857;
Best Local Similarity 44.4%; Pred. No. 2.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLLMEPV 9
Db      288 FCQLILDPI 296
| | | | |

RESULT 19
US-10-784-004-1057
; Sequence 1057, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1057
; LENGTH: 857
; TYPE: PRT
; ORGANISM: human
US-10-784-004-1057

Query Match      68.2%; Score 30; DB 9; Length 857;
Best Local Similarity 44.4%; Pred. No. 2.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLQLLMEPV 9
Db      288 FCQLILDPI 296
| | | | |

RESULT 20
US-10-485-517-152
; Sequence 152, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
```

; APPLICANT: VAZQUEZ-BOLAND, ANTONIO  
 ; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO  
 ; APPLICANT: GARRIDO-GARCIA, PATRICIA  
 ; APPLICANT: TIERREZ-MARTINEZ, ALBERTO  
 ; APPLICANT: AMEND, ALEXANDRA  
 ; APPLICANT: CHAKRABORTY, TRINAD  
 ; APPLICANT: DOMANN, EUGEN  
 ; APPLICANT: HAIN, THORSTEN  
 ; APPLICANT: BERCHE, PATRICK  
 ; APPLICANT: CHARBIT, ALAIN  
 ; APPLICANT: DURANT, LIONEL  
 ; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO  
 ; APPLICANT: BAQUERO, FERNANDO  
 ; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO  
 ; APPLICANT: GOMEZ-LOPEZ, NURIA  
 ; APPLICANT: MADUENIO, ENCARNIA  
 ; APPLICANT: PABLOS, BETRIZ DE  
 ; APPLICANT: WEHLAND, JURGEN  
 ; APPLICANT: KARST, UWE  
 ; APPLICANT: ENTIAN, KARL-DIETER  
 ; APPLICANT: HAUF, JORG  
 ; APPLICANT: ROSE, MATTHIAS  
 ; APPLICANT: VOSS, HAMUT  
 ; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES  
 ; FILE REFERENCE: 05394.0018-02  
 ; CURRENT APPLICATION NUMBER: US/11/045.004  
 ; CURRENT FILING DATE: 2005-01-28  
 ; PRIOR APPLICATION NUMBER: 10/637,657  
 ; PRIOR FILING DATE: 2003-08-11  
 ; PRIOR APPLICATION NUMBER: 10/257,023  
 ; PRIOR FILING DATE: 2002-10-08  
 ; PRIOR APPLICATION NUMBER: PCT/FR01/01118  
 ; PRIOR FILING DATE: 2001-04-11  
 ; PRIOR APPLICATION NUMBER: FR 00/04,629  
 ; PRIOR FILING DATE: 2000-04-11  
 ; NUMBER OF SEQ ID NOS: 2854  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 995  
 ; LENGTH: 93  
 ; TYPE: PRT  
 ; ORGANISM: Listeria monocytogenes  
 US-11-045-004-995

Query Match 65.9%; Score 29; DB 11; Length 93;  
 Best Local Similarity 71.4%; Pred. No. 36;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQILMEP 8  
 Db 5 LQILLEP 11

RESULT 23  
 US-11-087-099-4627  
 ; Sequence 4627, Application US/11087099  
 ; Publication No. US20060041961A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abad, Mark S. et al.  
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
 ; FILE REFERENCE: 38-21(53450)B EP  
 ; CURRENT APPLICATION NUMBER: US/11/087,099  
 ; CURRENT FILING DATE: 2005-03-22  
 ; NUMBER OF SEQ ID NOS: 12464  
 ; SEQ ID NO 4627  
 ; LENGTH: 190  
 ; TYPE: PRT  
 ; ORGANISM: Triticum aestivum  
 US-11-087-099-4627

Query Match 65.9%; Score 29; DB 11; Length 190;  
 Best Local Similarity 55.6%; Pred. No. 81;  
 Matches 5; Conservative 2; Mismatches 0; Indels 2; Gaps 0;

Qy 1 FLQILMEPV 9  
 Db 88 FLSELLMQPI 96

RESULT 24  
 US-10-921-286B-10  
 ; Sequence 10, Application US/10921286B  
 ; Publication No. US20060069512A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rzhetsky, Andrey  
 ; APPLICANT: Kalachikov, Sergey  
 ; APPLICANT: Krauthammer, Michael  
 ; APPLICANT: Friedman, Carol  
 ; APPLICANT: Kra, Pauline  
 ; TITLE OF INVENTION: GENE DISCOVERY THROUGH COMPARISONS OF  
 ; NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG  
 ; GENES AND PROTEINS  
 ; TITLE OF INVENTION: GENES AND PROTEINS  
 ; FILE REFERENCE: A31869-A-1  
 ; CURRENT APPLICATION NUMBER: US/10/921,286B  
 ; CURRENT FILING DATE: 2004-08-18  
 ; PRIOR APPLICATION NUMBER: US 09/549,827  
 ; PRIOR FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: US 09/327,983  
 ; PRIOR FILING DATE: 1999-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/129,469  
 ; PRIOR FILING DATE: 1999-04-15  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 218  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-921-286B-10

Query Match 65.9%; Score 29; DB 9; Length 218;  
 Best Local Similarity 75.0%; Pred. No. 95;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQILMEPV 9  
 Db 15 LELLKEPV 22

RESULT 25  
 US-10-242-586-102  
 ; Sequence 102, Application US/10242586  
 ; Publication No. US20060073548A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Baton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Phillippe  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Fong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3630RIC21  
 ; CURRENT APPLICATION NUMBER: US/10/242,586  
 ; CURRENT FILING DATE: 2002-09-11  
 ; PRIOR APPLICATION NUMBER: 10/197942  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/059114  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/063046  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/065027

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; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-586-102

Query Match      65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQQLLMEP 8
Db      154 WLELLEP 161

RESULT 26
US-10-242-902-102
; Sequence 102, Application US/10242902
; Publication No. US20060073549A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C54
; CURRENT APPLICATION NUMBER: US/10/242,902
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-586-102
```

```
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-902-102

Query Match      65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQQLLMEP 8
Db      154 WLELLEP 161

RESULT 27
US-10-243-116-102
; Sequence 102, Application US/10243116
; Publication No. US20060073550A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C58
; CURRENT APPLICATION NUMBER: US/10/243,116
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-116-102

Query Match      65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQQLLMEP 8
Db      154 WLELLEP 161
```



```
RESULT 28
US-10-243-136-102
; Sequence 102, Application US/10243136
; Publication No. US20060074228A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C32
; CURRENT APPLICATION NUMBER: US/10/243,136
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-136-102

Query Match      65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTQLLMPEP 8
        :|:|:|:|
Db      154 WLELLLEP 161

RESULT 30
US-10-243-215-102
; Sequence 102, Application US/10243215
; Publication No. US20060073551A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C27
; CURRENT APPLICATION NUMBER: US/10/243,215
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
```

```
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-215-102
```

```
Query Match 65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FQQLMEP 8
Db 154 WLELLEP 161
:|:|:|:
```

```
RESULT 31
US-10-243-236-102
; Sequence 102, Application US/10243236
; Publication No. US20060073552A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C35
; CURRENT APPLICATION NUMBER: US/10/243,236
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-236-102
```

```
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-236-102
```

```
Query Match 65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FQQLMEP 8
Db 154 WLELLEP 161
:|:|:|:
```

```
RESULT 32
US-10-243-298-102
; Sequence 102, Application US/10243298
; Publication No. US20060073553A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C49
; CURRENT APPLICATION NUMBER: US/10/243,298
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 102
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-298-102
```

```
Query Match 65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 FLOLMEP 8  
:|:|:|  
Db 154 WLELLEP 161

## RESULT 33

US-10-243-304-102  
; Sequence 102, Application US/10243304  
; Publication No. US20060073554A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C42  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US/10/243,304  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 102  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-243-304-102

Query Match 65.9%; Score 29; DB 9; Length 221;  
Best Local Similarity 62.5%; Pred. No. 96;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLOLMEP 8  
:|:|:|  
Db 154 WLELLEP 161

## RESULT 34

US-10-243-338-102  
; Sequence 102, Application US/10243338  
; Publication No. US20060073579A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C33  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 10/197942

; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C52  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US/10/243,338  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 102  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-243-338-102

Query Match 65.9%; Score 29; DB 9; Length 221;  
Best Local Similarity 62.5%; Pred. No. 96;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLOLMEP 8  
:|:|:|  
Db 154 WLELLEP 161

## RESULT 35

US-10-243-345-102  
; Sequence 102, Application US/10243345  
; Publication No. US20060073555A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C33  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 10/197942

```
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 102
/ LENGTH: 221
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-243-345-102
```

```
Query Match 65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FLQLLMEP 8
Db 154 WLELLLEP 161
:|:|:|
```

```
RESULT 36
US-10-243-357-102
/ Sequence 102, Application US/10243357
/ Publication No. US20060073556A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C55
/ CURRENT APPLICATION NUMBER: US/10/243,357
/ CURRENT FILING DATE: 2002-09-13
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 102
/ LENGTH: 221
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-243-345-102
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/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 102
/ LENGTH: 221
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-243-357-102
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Query Match 65.9%; Score 29; DB 9; Length 221;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FLQLLMEP 8
Db 154 WLELLLEP 161
:|:|:|
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RESULT 37
US-10-245-083-102
/ Sequence 102, Application US/10245083
/ Publication No. US20060073557A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C91
/ CURRENT APPLICATION NUMBER: US/10/245,083
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 102
/ LENGTH: 221
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-083-102
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Query Match 65.9%; Score 29; DB 9; Length 221;
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Best Local Similarity 62.5%; Pred. No. 96;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLQLLMEP 8

Db 154 WLELLLEP 161

RESULT 38

US-10-247-015-102  
; Sequence 102, Application US/10247015  
; Publication No. US20060073558A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin  
; APPLICANT: Baton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3630R1C118

; CURRENT APPLICATION NUMBER: US/10/247,015

; CURRENT FILING DATE: 2002-09-18

; PRIOR FILING DATE: 2002-07-18

; PRIOR FILING DATE: 1997-09-17

; PRIOR FILING DATE: 1997-10-24

; PRIOR FILING DATE: 1998-03-27

; PRIOR FILING DATE: 1998-05-22

; PRIOR FILING DATE: 1998-06-18

; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25

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; PRIOR FILING DATE: 1998-06-25

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; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25

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Query Match          65.9%; Score 29; DB 11; Length 418;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLLMEP 8
   |||||
Db 71 LQLLQEP 77

RESULT 42
US-11-188-298-18797
; Sequence 18797, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 18797
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Pinus taeda
US-11-188-298-18797

Query Match          65.9%; Score 29; DB 11; Length 433;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLLMEP 8
   |||||
Db 89 LQLLQEP 95

RESULT 43
US-11-188-298-14185
; Sequence 14185, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14185
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Dactylis glomerata
US-11-188-298-14185

Query Match          65.9%; Score 29; DB 11; Length 452;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLLMEP 8
   |||||
Db 108 LQLLQEP 114

RESULT 44
US-11-264-096-212
; Sequence 212, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46D1

Query Match          65.9%; Score 29; DB 11; Length 418;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQLLMEP 8
   |||||
Db 71 LQLLQEP 77

RESULT 45
US-11-264-096-211
; Sequence 211, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (79)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (321)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-264-096-211

Query Match          65.9%; Score 29; DB 11; Length 489;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLLME 7
   ||:||||
Db 305 FLKLME 311

RESULT 46
US-11-079-463-7846
; Sequence 7846, Application US/11079463
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; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7846
; LENGTH: 547
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-7846

Query Match      65.9%; Score 29; DB 11; Length 547;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 LQLLMEPV 9
DB      460 IKLLLEPV 467

RESULT 47
US-11-152-366-42
; Sequence 42, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
; FILE REFERENCE: P27,880-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-42

Query Match      65.9%; Score 29; DB 11; Length 551;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLLME 7
DB      305 FLKLLME 311

RESULT 48
US-11-127-877-68
; Sequence 68, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877

; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 8199
; LENGTH: 653
; TYPE: PRT
US-11-127-877-68

Query Match      65.9%; Score 29; DB 11; Length 565;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLLME 7
DB      305 FLKLLME 311

RESULT 49
US-11-152-366-41
; Sequence 41, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
; FILE REFERENCE: P27,880-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-41

Query Match      65.9%; Score 29; DB 11; Length 565;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLQLLME 7
DB      305 FLKLLME 311

RESULT 50
US-11-079-463-8199
; Sequence 8199, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 8199
; LENGTH: 653
; TYPE: PRT
US-11-079-463-8199
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! ORGANISM: B.fragilis  
US-11-079-463-8199

Query Match 65.9%; Score 29; DB 11; Length 653;  
Best Local Similarity 62.5%; Pred. NO. 3.2e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLLMEPV 9  
Db ::||:||||  
458 IXLLEPV 465

Search completed: May 9, 2006, 02:36:17  
Job time : 17.8 secs



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 02:06:12 ; Search time 99.6 Seconds  
(without alignments)  
63.753 Million cell updates/sec

Title: US-09-870-216C-3

Perfect score: 44

Sequence: 1 FLOLLMEPV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	84.1	75	2	Q8PYR9_METWA
2	35	79.5	47	2	Q85X02_PINKO
3	35	79.5	329	2	Q8SQ02_CANFA
4	35	79.5	379	2	O03991_DAUCA
5	35	79.5	806	2	Q4M2Q2_THPA
6	35	79.5	846	2	Q4UBW5_THEAN
7	35	79.5	1060	2	Q4IUN8_GIBZE
8	34	77.3	297	1	RNHL_CAEEL
9	34	77.3	318	2	Q8DNJ4_STRR6
10	34	77.3	318	2	Q97NY1_STRPN
11	34	77.3	318	2	Q8ES77_OCEIH
12	34	77.3	357	2	Q5Z0B7_NOCPA
13	34	77.3	471	2	Q8AVC6_XENLA
14	34	77.3	628	2	Q5JM56_ORYSA
15	34	77.3	760	2	Q9NIH0_STYMT
16	34	77.3	1070	2	Q4R221_TETNG
17	34	77.3	1073	2	Q5Z0T5_MAGGR
18	34	77.3	1083	2	Q7SB63_NEUCR
19	34	77.3	1869	2	Q7QUP7_GIALA
20	34	77.3	2785	1	DRIM_HUMAN
21	33	75.0	163	2	Q85FQ9_CVAME
22	33	75.0	226	2	Q87826_STAAU
23	33	75.0	252	2	Q6IRD5_RAT
24	33	75.0	287	2	Q87GX1_VIBPA
25	33	75.0	295	2	Q7NGE4_GLOVI
26	33	75.0	317	2	Q5HOZ5_STAEQ
27	33	75.0	318	2	Q6GB96_STAAS
28	33	75.0	318	2	Q6GIQ7_STAAR
29	33	75.0	318	2	Q5HH76_STAAC
30	33	75.0	318	2	Q7A6S9_STAAN
31	33	75.0	318	2	Q8NXM9_STAAM

32	33	75.0	318	2	Q99VP0_STAAM
33	33	75.0	319	2	Q4L4F7_STAHP
34	33	75.0	319	2	Q8CP29_STAHP
35	33	75.0	320	2	Q4T7D6_TETNG
36	33	75.0	320	2	Q5CZ28_RAT
37	33	75.0	337	2	Q7Z5K8_HUMAN
38	33	75.0	368	1	RD23B_ARATH
39	33	75.0	380	2	Q6TLD0_BRARE
40	33	75.0	382	2	Q6PHE9_BRARE
41	33	75.0	385	2	Q5AZM0_EMENI
42	33	75.0	409	1	RD23B_HUMAN
43	33	75.0	409	2	Q53F10_HUMAN
44	33	75.0	415	2	Q6NVC3_MOUSE
45	33	75.0	415	2	Q4KMA2_RAT
46	33	75.0	416	1	RD23B_MOUSE
47	33	75.0	435	2	Q6FU70_CANGA
48	33	75.0	484	2	Q5BL82_XENTR
49	33	75.0	495	2	Q4XOM6_ASPFU
50	33	75.0	525	2	Q4FP57_9RICK
51	33	75.0	2242	2	Q51VL7_MAGGR
52	33	75.0	2653	2	Q51314_ENTHI
53	33	75.0	2746	2	Q8IMS2_DROME
54	33	75.0	2764	2	Q01399_DROME
55	33	75.0	2764	2	Q59DT9_DROME
56	33	75.0	2788	1	DRIM_MOUSE
57	33	75.0	2802	2	Q01397_DROME
58	33	75.0	2802	2	Q01398_DROME
59	33	75.0	2802	2	Q9VBJ2_DROME
60	33	75.0	4135	2	Q54EQ0_DICDI
61	32	72.7	91	2	Q72R76_LEPDI
62	32	72.7	91	2	Q8FAK0_LEPDI
63	32	72.7	144	2	Q6ZDD7_ORYSA
64	32	72.7	147	2	Q7VCG6_PROMA
65	32	72.7	164	2	Q8XQU0_RALSO
66	32	72.7	236	2	Q55K33_CRYNE
67	32	72.7	236	2	Q5K9G6_CRYNE
68	32	72.7	251	2	Q55UD6_CRYNE
69	32	72.7	251	2	Q5KI09_CRYNE
70	32	72.7	278	2	Q893C5_CLOTE
71	32	72.7	280	2	Q4RGX2_TETNG
72	32	72.7	290	2	Q7PXJ2_ANOGA
73	32	72.7	321	2	Q8Z2H3_ENTFA
74	32	72.7	340	2	Q4XZT3_PLACH
75	32	72.7	342	2	Q4RSY1_MACFA
76	32	72.7	367	2	Q4KEF3_PSEF5
77	32	72.7	372	2	Q4XU41_PLACH
78	32	72.7	382	2	Q03990_DAUCA
79	32	72.7	395	1	SYTB_RAT
80	32	72.7	397	2	Q73GE4_WOLPM
81	32	72.7	408	2	Q4YZH3_PLABE
82	32	72.7	434	1	PXR_HUMAN
83	32	72.7	434	2	Q8SQ01_MACMU
84	32	72.7	449	2	Q51FC8_ENTHI
85	32	72.7	467	2	Q8DDV0_VIBVU
86	32	72.7	470	2	Q7MPX3_VIBVY
87	32	72.7	470	2	Q87TB4_VIBPA
88	32	72.7	473	2	Q9UNW4_HUMAN
89	32	72.7	480	2	Q9KMM0_VIBCH
90	32	72.7	504	1	FPOM_TOBAC
91	32	72.7	510	2	Q4T2X4_TETNG
92	32	72.7	534	2	Q7RFT7_PLAYO
93	32	72.7	536	2	Q9SA99_ARATH
94	32	72.7	592	2	Q5ZDY7_ORYSA
95	32	72.7	643	1	SO2A1_MOUSE
96	32	72.7	643	1	SO2A1_RAT
97	32	72.7	643	2	Q4R830_MACFA
98	32	72.7	644	2	Q5FX75_CANFA
99	32	72.7	644	2	Q8H268_BOVIN
100	32	72.7	659	2	Q53LH1_ORYSA
101	32	72.7	677	2	Q9EYM4_THETH
102	32	72.7	677	2	Q72H92_THETH
103	32	72.7	677	2	Q5SGW2_THETH
104	32	72.7	687	1	TRA_HABIN

Q99VP0	staphylococ
Q4L4F7	staphylococ
Q8CP29	staphylococ
Q4T7D6	tetraodon n
Q5CZ28	rattus norv
Q7Z5K8	homo sapien
Q84132	arabidopsis
Q6TLD0	brachydanio
Q6PHE9	brachydanio
Q5AZM0	aspergillus
P54727	homo sapien
Q53F10	homo sapien
Q6NVC3	mus musculus
Q4KMA2	rattus norv
P54728	mus musculus
Q6FU70	candida gla
Q5BL82	xenopus tro
Q4XOM6	aspergillus
Q4FP57	candidatus
Q51VL7	magnaporthe
Q51314	entamoeba h
Q8IMS2	drosophila
Q01399	drosophila
Q59DT9	drosophila
Q5XG71	mus musculus
Q01397	drosophila
Q01398	drosophila
Q9VBJ2	drosophila
Q54EQ0	dictyosteli
Q72R76	leptospiro
Q8FAK0	leptospiro
Q6ZDD7	oryza sativ
Q7VCG6	prochloroco
Q8XQU0	raistonia s
Q55K33	cryptococcu
Q5K9G6	cryptococcu
Q55UD6	cryptococcu
Q5KI09	cryptococcu
Q893C5	clostridium
Q4RGX2	tetraodon n
Q7PXJ2	anopheles g
Q8Z2H3	enterococcu
Q4XZT3	plasmodium
Q4RSY1	macaca fasc
Q4KEF3	pseudomonas
Q4XU41	plasmodium
Q03990	daucus caro
Q925B4	rattus norv
Q73GE4	wolbachia p
Q4YZH3	plasmodium
Q75469	homo sapien
Q8SQ01	macaca mula
Q51FC8	entamoeba h
Q8DDV0	vibrio vuln
Q7MPX3	vibrio vuln
Q87TB4	vibrio para
Q9UNW4	homo sapien
Q9KMM0	vibrio chol
Q24184	nicotiana t
Q4T2X4	tetraodon n
Q7RFT7	plasmodium
Q9SA99	arabidopsis
Q5ZDY7	oryza sativ
Q9EP55	mus musculus
Q00910	rattus norv
Q4R830	macaca fasc
Q5FX75	canis famil
Q8H268	bos taurus
Q53LH1	oryza sativ
Q9EYM4	thermus the
Q72H92	thermus the
Q5SGW2	thermus the
Q05069	haemophilus

105	32	72.7	729	2	Q6BV32_DEBHA	Q6bv32	debaromyce	178	31	70.5	763	2	Q9FH32_ARATH	Q9fh32	arabidopsis
106	32	72.7	753	2	Q9NDT2_PLAFA	Q9ndt2	plasmodium	179	31	70.5	787	2	Q8I7P3_DICDI	Q8i7p3	dictyosteli
107	32	72.7	772	2	Q5YXP9_NOCFA	Q5yxp9	nocardia fa	180	31	70.5	836	2	Q8SNA3_MOUSE	Q8sna3	mus musculu
108	32	72.7	832	1	EF2_CRYPV	Q23716	cryptospori	181	31	70.5	904	2	Q6ODS9_ORISA	Q6ods9	oryza sativ
109	32	72.7	832	2	Q8IKW5_PLAF7	Q8ikw5	plasmodium	182	31	70.5	905	2	Q57WL3_9TRYP	Q57wl3	trypanosoma
110	32	72.7	832	2	Q7RDR5_PLAYO	Q7rdr5	playosoma	183	31	70.5	915	2	Q57Y20_9TRYP	Q57y20	trypanosoma
111	32	72.7	832	2	Q5CMC8_CRYHO	Q5cmc8	cryptospori	184	31	70.5	920	2	Q4HEB9_CAMPYLO	Q4heeb9	campylobact
112	32	72.7	832	2	Q4ZAS4_PLABE	Q4zas4	plasmodium	185	31	70.5	921	2	Q5HSV0_CAMJR	Q5hsv0	campylobact
113	32	72.7	836	2	Q5CVS6_CRYPV	Q5cvs6	cryptospori	186	31	70.5	921	2	Q9PMI1_CAMJE	Q9pmi1	campylobact
114	32	72.7	839	2	Q54UK7_DICDI	Q54jk7	dictyosteli	187	31	70.5	934	2	Q4QHX9_LEIMAN	Q4qhx9	leishmania
115	32	72.7	850	2	Q89NM3_BRAJA	Q89nm3	bradyrhizob	188	31	70.5	939	2	Q5CUB1_CRYPV	Q5cub1	cryptospori
116	32	72.7	1092	2	Q6OPX8_CAEBR	Q6opx8	caenorhabditi	189	31	70.5	940	2	Q5CI48_CRYHO	Q5ci48	dictyosteli
117	32	72.7	1101	1	YA4G_SCHPO	Q09733	schizosacch	190	31	70.5	957	2	Q54RG4_DICDI	Q54rg4	dictyosteli
118	32	72.7	1106	2	Q7S9I4_NEUCR	Q7s9i4	neurospora	191	31	70.5	970	1	GMIP_HUMAN	GMIP	HUMAN
119	32	72.7	1134	2	Q8MPV7_CABEL	Q8mpv7	caenorhabditi	192	31	70.5	1016	2	Q8NSA4_CORGL	Q8nsa4	corynebacte
120	32	72.7	1138	2	Q8MPV6_CABEL	Q8mpv6	caenorhabditi	193	31	70.5	1029	2	Q5SQ40_HUMAN	Q5sq40	homo sapien
121	31	70.5	21	2	Q5BWA6_SCHJA	Q5bwa6	schistosoma	194	31	70.5	1076	2	Q87V22_PSES	Q87v22	pseudomonas
122	31	70.5	132	2	Q6PFK7_ACTAD	Q6pfk7	actinetobact	195	31	70.5	1077	2	Q5SQ42_HUMAN	Q5sq42	homo sapien
123	31	70.5	142	1	GTH2_CORAU	P48251	coregonus a	196	31	70.5	1078	2	Q5SQ43_HUMAN	Q5sq43	homo sapien
124	31	70.5	142	1	GTH2_ONCKE	P10256	oncorhynch	197	31	70.5	1096	2	Q6MG49_RAT	Q6mg49	rattus norv
125	31	70.5	142	2	Q5GJ78_9TELE	Q5gj78	brachymysta	198	31	70.5	1098	2	Q9WTN8_RAT	Q9wtm8	rattus norv
126	31	70.5	161	2	Q7U7B7_SYNFX	Q7u7b7	synecococc	199	31	70.5	1111	2	Q7M564_FUGRU	Q7m564	fugu rubrip
127	31	70.5	172	2	Q4KJPJ_9CRUS	Q4kjpj1	pseudosquill	200	31	70.5	1126	2	Q5HYL9_HUMAN	Q5hyl9	homo sapien
128	31	70.5	181	2	Q74NI6_NANEQ	Q74ni6	nanoarchaeu	201	31	70.5	1126	2	Q9GSA6_HUMAN	Q9gsa6	homo sapien
129	31	70.5	181	2	Q4ZT15_PSESY	Q4zt15	pseudomonas	202	31	70.5	1126	2	Q9BCN4_HUMAN	Q9bcn4	homo sapien
130	31	70.5	190	2	Q6TNR4_BRARE	Q6tnr4	brachydanio	203	31	70.5	1132	1	BAT3_HUMAN	BAT3	HUMAN
131	31	70.5	203	2	Q9NGT3_CABEL	Q9ngt3	caenorhabditi	204	31	70.5	1132	2	O5STC1_HUMAN	O5stc1	homo sapien
132	31	70.5	207	2	Q4SNH9_TETNG	Q4snh9	tetradodon n	205	31	70.5	1140	2	Q5LRA2_SILPO	Q5lra2	silicibacte
133	31	70.5	240	2	Q6FT23_CANGA	Q6ft23	candida gla	206	31	70.5	1154	2	Q9ZIR2_MOUSE	Q9zir2	mus musculu
134	31	70.5	255	1	YPMR_BACSU	P40766	bacillus su	207	31	70.5	1162	2	Q5SQ39_HUMAN	Q5sq39	homo sapien
135	31	70.5	262	2	Q9Y6N3_HUMAN	Q9y6n3	homo sapien	208	31	70.5	1229	2	O9S874_HUMAN	O9s874	homo sapien
136	31	70.5	262	2	Q5T5J7_HUMAN	Q5t5j7	homo sapien	209	31	70.5	1229	2	O5SQ35_HUMAN	O5sq35	homo sapien
137	31	70.5	281	2	Q8AY27_XENIA	Q8ay27	xenopus lae	210	31	70.5	1380	2	O5SR55_CRYNE	O5sr55	cryptococcu
138	31	70.5	282	2	Q4QCN3_LEIMA	Q4qcn3	leishmania	211	31	70.5	1380	2	O5KF15_CRYNE	O5kf15	cryptococcu
139	31	70.5	317	2	Q4RUC9_TETNG	Q4ruc9	tetradodon n	212	31	70.5	1398	2	Q8RJY0_STIAU	Q8rjy0	stigmatella
140	31	70.5	318	2	Q9L5B3_9RHOB	Q9l5b3	sagittula s	213	31	70.5	1538	2	Q9SMG9_ARATH	Q9smg9	arabidopsis
141	31	70.5	328	2	O5LZS4_STRT1	O5lzs4	streptococc	214	31	70.5	1760	2	Q9SHK6_ARATH	Q9shk6	arabidopsis
142	31	70.5	328	2	Q5M4D5_STRT2	O5m4d5	streptococc	215	31	70.5	1800	2	Q6QW5_CABER	Q6qw5	caenorhabditi
143	31	70.5	339	2	Q6LIER6_CABER	Q6lier6	caenorhabditi	216	31	70.5	1978	2	Q7QE10_ANOGA	Q7qe10	anopheles g
144	31	70.5	342	2	P91421_CABEL	P91421	caenorhabditi	217	31	70.5	3172	2	Q4QAV5_LEIMA	Q4qav5	leishmania
145	31	70.5	345	2	Q95Q44_CABEL	Q95q44	caenorhabditi	218	31	70.5	4055	2	Q6RIL8_9CORO	Q6ril8	human group
146	31	70.5	369	2	Q6ETL3_ORYSA	Q6etl3	oryza sativ	219	31	70.5	6724	2	Q6RIL9_9CORO	Q6ril9	human coron
147	31	70.5	375	1	GDR8_MELGA	Q42221	meleagris g	220	31	70.5	6729	2	Q6QIS3_9CORO	Q6qis3	human coron
148	31	70.5	378	1	RD23D_ARATH	Q84130	arabidopsis	221	31	68.2	96	2	O50176_PSEAE	O50176	pseudomonas
149	31	70.5	382	2	Q5WX99_LEGPL	Q5wx99	legionella	222	31	68.2	103	2	Q8LYL5_9ARAC	Q8lyl5	orsonwelles
150	31	70.5	382	2	Q5X5X7_LEGPA	Q5x5x7	legionella	223	31	68.2	104	2	Q8LYL9_9ARAC	Q8lyl9	orsonwelles
151	31	70.5	387	2	Q5WCC6_BACSK	Q5wcc6	bacillus cl	224	31	68.2	105	1	YJN5_YEAST	YJN5	YEAST
152	31	70.5	388	2	Q4TA23_TETNG	Q4ta23	tetradodon n	225	31	68.2	108	2	Q8LYL0_9ARAC	Q8lyl0	orsonwelles
153	31	70.5	389	2	Q9STA6_LYCHS	Q9sta6	lycopersico	226	31	68.2	116	2	Q8LYK6_9ARAC	Q8lyk6	orsonwelles
154	31	70.5	395	2	Q5ZW95_LEGPH	Q5zw95	legionella	227	31	68.2	117	2	Q8LYL7_9ARAC	Q8lyl7	orsonwelles
155	31	70.5	401	2	O22283_ARATH	O22283	arabidopsis	228	31	68.2	119	2	O8LYK4_9ARAC	O8lyk4	orsonwelles
156	31	70.5	407	2	Q89X79_BRAJA	Q89x79	bradyrhizob	229	31	68.2	121	2	Q8LUAC_9ARAC	Q8lua6	orsonwelles
157	31	70.5	418	1	RD23C_KJULA	Q6cr23	kluveromyc	230	31	68.2	121	2	Q8LYT7_9ARAC	Q8lyt7	orsonwelles
158	31	70.5	419	1	RD23C_ARATH	Q84131	arabidopsis	231	31	68.2	121	2	Q8LYL2_9ARAC	Q8lyl2	orsonwelles
159	31	70.5	428	2	Q71W49_LISMF	Q71w49	listeria mo	232	31	68.2	121	2	Q8LYL3_9ARAC	Q8lyl3	orsonwelles
160	31	70.5	440	2	Q5KZS1_GEOKA	Q5kzs1	geobacillus	233	31	68.2	121	2	Q8LYL4_9ARAC	Q8lyl4	orsonwelles
161	31	70.5	442	2	Q4J7I2_SULAC	Q4j7i2	sulfolobus	234	31	68.2	121	2	O8LYL6_9ARAC	O8lyl6	orsonwelles
162	31	70.5	456	1	SHE9_YEAST	Q04172	saccharomyc	235	31	68.2	121	2	Q8LYL8_9ARAC	Q8lyl8	orsonwelles
163	31	70.5	459	2	Q8A9T2_BACTN	Q8a9t2	bacteroides	236	31	68.2	121	2	Q8LYM0_9ARAC	Q8lym0	orsonwelles
164	31	70.5	487	2	Q4TSI7_9SPHN	Q4tsi7	erythrobact	237	31	68.2	121	2	Q8LYM2_9ARAC	Q8lym2	orsonwelles
165	31	70.5	488	2	Q58OP7_MAYDE	Q58op7	mayetiola d	238	31	68.2	121	2	Q8LYM3_9ARAC	Q8lym3	orsonwelles
166	31	70.5	539	2	Q9SVG3_ARATH	Q9svg3	arabidopsis	239	31	68.2	124	2	Q9UDJ1_HUMAN	Q9udj1	homo sapien
167	31	70.5	554	2	Q5B8S3_EMENI	Q5b8s3	aspergillus	240	31	68.2	126	1	YBG2_YEAST	YBG2	YEAST
168	31	70.5	571	2	Q7T2E4_BRARE	Q7t2e4	brachydanio	241	31	68.2	128	2	Q8LYK3_9ARAC	Q8lyk3	orsonwelles
169	31	70.5	573	2	Q4SUH7_TETNG	Q4suh7	tetradodon n	242	31	68.2	128	2	Q8LYK5_9ARAC	Q8lyk5	orsonwelles
170	31	70.5	610	2	Q8IGS0_DROME	Q8igs0	drosophila	243	31	68.2	128	2	Q8LYK7_9ARAC	Q8lyk7	orsonwelles
171	31	70.5	610	2	Q86NM1_DROME	Q86nw1	drosophila	244	31	68.2	128	2	Q8LYK9_9ARAC	Q8lyk9	orsonwelles
172	31	70.5	626	2	Q6EGR9_BRARE	Q6egr9	brachydanio	245	31	68.2	128	2	O8LYL1_9ARAC	O8lyl1	orsonwelles
173	31	70.5	639	1	ACM3_CHICK	P49578	gallus gall	246	31	68.2	135	2	O8LYM4_9ARAC	O8lym4	orsonwelles
174	31	70.5	643	2	Q6STN6_CTEID	Q6stn6	ctenopharyn	247	31	68.2	136	2	O8LYM8_9ARAC	O8lym8	orsonwelles
175	31	70.5	646	2	Q8IH57_DROSOPH	Q8ih57	drosophila	248	31	68.2	137	2	O8LYM5_9ARAC	O8lym5	orsonwelles
176	31	70.5	730	1	PGL1_CABEL	Q9tzg3	caenorhabditi	249	31	68.2	142	1	GTH2_ONCTS	GTH2	ONCTS
177	31	70.5	752	2	Q5KEB6_CRYNE	Q5keb6	cryptococcu	250	31	68.2	147	2	Q7V1F0_PROMP	Q7v1f0	prochloroco

251	30	68.2	150	2	Q5WDL7_BACSK	Q5wdl7 bacillus cl	324	30	68.2	685	2	Q410E4_GIBZE	Q4i0e4 gibberella
252	30	68.2	155	2	Q8VM41_9ACTO	Q8vm41 streptomyce	325	30	68.2	691	2	Q7XBZ6_ORYSA	Q7xbz6 oryza sativ
253	30	68.2	155	2	Q9F2E3_STRTE	Q9f2e3 streptomyce	326	30	68.2	691	2	Q8S7E8_ORYSA	Q8s7e8 oryza sativ
254	30	68.2	156	2	Q7V7X3_PROWM	Q7v7x3 prochloroco	327	30	68.2	691	2	Q9F0L8_STRAU	Q9f0l8 staphylococ
255	30	68.2	156	2	Q6JH67_AMBTI	Q6jh67 ambystoma t	328	30	68.2	712	2	Q4LQ34_9BURK	Q4lq34 burkholderi
256	30	68.2	179	2	Q9S8G5_JSRV	Q9s8g5 sheep pulmo	329	30	68.2	736	2	Q4RF56_TETNG	Q4rf56 tetraodon n
257	30	68.2	179	2	Q9WR72_USRV	Q9wr72 sheep pulmo	330	30	68.2	737	2	Q6P259_XENTR	Q6p259 xenopus tro
258	30	68.2	199	2	Q7QXT0_GIALA	Q7qxt0 giardia lam	331	30	68.2	737	2	Q6NU15_XENLA	Q6nu15 xenopus lae
259	30	68.2	206	2	Q8HJK2_ASTAM	Q8hjk2 asterias am	332	30	68.2	738	1	PLAK_XENLA	P30998 xenopus lae
260	30	68.2	212	2	Q8R7A6_THETN	Q8r7a6 thermoanaer	333	30	68.2	738	1	Q52L07_XENLA	Q52l07 xenopus lae
261	30	68.2	217	2	Q4TFV6_TETNG	Q4tfv6 tetraodon n	334	30	68.2	740	2	Q8DI25_SYNEL	Q8di25 synechococc
262	30	68.2	218	2	Q557G0_DICDI	Q557g0 dictyostelli	335	30	68.2	752	2	Q5SE40_CRYNE	Q5se40 cryptococcu
263	30	68.2	228	2	Q86JX0_DICDI	Q86jx0 dictyostelli	336	30	68.2	752	2	Q4Z6S0_PLABB	Q4z6s0 plasmodium
264	30	68.2	233	2	Q4Y988_PLACH	Q4y988 plasmodium	337	30	68.2	753	2	Q4T227_TETNG	Q4t227 tetraodon n
265	30	68.2	247	2	Q5O9Y7_ENTHI	Q5o9y7 entamoeba h	338	30	68.2	769	2	Q7ZWS3_XENLA	Q7zws3 xenopus lae
266	30	68.2	265	2	Q5GW24_XANOR	Q5gw24 xanthomonas	339	30	68.2	792	2	Q4QF61_LEIMA	Q4qf61 leishmania
267	30	68.2	276	2	Q4T4M2_TETNG	Q4t4m2 tetraodon n	340	30	68.2	793	2	Q4SUZ0_TETNG	Q4su20 tetraodon n
268	30	68.2	304	2	Q41968_GIBZE	Q4i968 gibberella	341	30	68.2	816	1	AMPO_RAT	Pe9527 rattus norv
269	30	68.2	307	2	Q20844_CABEL	Q20844 caenorhabdi	342	30	68.2	826	2	Q6CUP4_KIULA	Q6cup4 kluyveromyc
270	30	68.2	319	2	Q67P06_SYMTH	Q67p06 symbiobacte	343	30	68.2	843	2	Q96S85_HUMAN	Q96s85 homo sapien
271	30	68.2	326	2	Q9V0P7_PYRAB	Q9v0p7 pyrococcus	344	30	68.2	843	2	Q6P3X3_HUMAN	Q6p3x3 homo sapien
272	30	68.2	329	2	Q50121_PYROH	Q50121 pyrococcus	345	30	68.2	843	2	Q5RBM9_PONPY	Q5rbw9 pongo pygma
273	30	68.2	331	2	Q8RGF4_FUSNN	Q8rgf4 fusobacteri	346	30	68.2	843	2	Q6P9L9_MOUSE	Q6p9l9 mus musculu
274	30	68.2	338	2	Q8H4B1_ORYSA	Q8h4b1 oryza sativ	347	30	68.2	849	2	Q91ZE7_RAT	Q91ze7 rattus norv
275	30	68.2	340	2	Q6F6R9_ACIAD	Q6f6r9 acinetobact	348	30	68.2	850	2	Q5U329_RAT	Q5u329 rattus norv
276	30	68.2	344	2	Q7P4X9_FUSNV	Q7p4x9 fusobacteri	349	30	68.2	851	1	CE005_MOUSE	Q8k2h3 mus musculu
277	30	68.2	354	2	Q572U0_9TRYP	Q572u0 trypanosoma	350	30	68.2	852	1	Q5RBP3_PONPY	Q5rbp3 pongo pygma
278	30	68.2	358	2	Q18392_CABEL	Q18392 caenorhabdi	351	30	68.2	852	2	Q6N5S7_RHOA	Q6n5s7 rhodopsuendo
279	30	68.2	371	1	RD23A_ARATH	Q84l33 arabidopsis	352	30	68.2	856	1	K1115_MOUSE	Q7t8l3 mus musculu
280	30	68.2	373	2	Q4KDC0_PSEF5	Q4kdc0 pseudomonas	353	30	68.2	857	1	EF2_CHICK	Q90705 gallus gall
281	30	68.2	379	2	Q6WNY7_DASSA	Q6wny7 dasyatis sa	354	30	68.2	857	1	EF2_CRIGR	P09445 cricetus
282	30	68.2	380	2	Q919F0_SQUAC	Q919f0 squallus aca	355	30	68.2	857	1	EF2_HUMAN	P13639 homo sapien
283	30	68.2	395	2	Q57CZ0_BRUAB	Q57cz0 brucella ab	356	30	68.2	857	1	EF2_MESAU	P05086 mesocricetu
284	30	68.2	395	2	Q8G0B6_BRUSU	Q8g0b6 brucella eu	357	30	68.2	857	1	EF2_MOUSE	P58252 mus musculu
285	30	68.2	395	2	Q8YHG6_ERUME	Q8yhg6 brucella me	358	30	68.2	857	1	EF2_RAT	P05197 rattus norv
286	30	68.2	396	2	Q7ZVC3_ERARE	Q7zvc3 brachydanio	359	30	68.2	858	2	Q5R086_HUMAN	Q5rj86 homo sapien
287	30	68.2	401	2	Q4HSY6_9DEIO	Q4hsy6 deinococcus	360	30	68.2	858	2	Q5R823_PONPY	Q5r823 pongo pygma
288	30	68.2	402	2	Q54QP6_DICDI	Q54qp6 dictyosteli	361	30	68.2	858	2	Q5RBA6_PONPY	Q5rba6 pongo pygma
289	30	68.2	402	2	Q4U9U4_THEAN	Q4u9u4 theileria a	362	30	68.2	858	2	Q60423_CRIGR	Q60423 cricetus
290	30	68.2	412	2	Q758C3_ASHGO	Q758c3 ashbya goss	363	30	68.2	858	2	Q8C153_MOUSE	Q8c153 mus musculu
291	30	68.2	412	2	Q7ZT10_XENLA	Q7zt10 xenopus lae	364	30	68.2	858	2	Q544E4_MOUSE	Q544e4 m 0 day neo
292	30	68.2	416	2	Q5BKM5_XENTR	Q5bkm5 xenopus tro	365	30	68.2	858	2	Q7ZAP8_XENLA	Q7zap8 xenopus lae
293	30	68.2	419	2	Q505M5_XENLA	Q505m5 xenopus lae	366	30	68.2	858	2	Q7ZVM3_BRARE	Q7zvm3 brachydanio
294	30	68.2	427	2	Q4N212_THEPA	Q4n212 theileria p	367	30	68.2	858	2	Q52MA1_XENLA	Q52ma1 xenopus lae
295	30	68.2	431	2	Q8JHX4_DASSA	Q8jhx4 dasyatis sa	368	30	68.2	858	2	Q6P3J5_BRARE	Q6p3j5 brachydanio
296	30	68.2	442	1	DCTA2_RHILO	Q986r8 rhizobium l	369	30	68.2	865	1	GLND_BORR	Q7wj96 bordetella
297	30	68.2	452	2	Q8EYJ0_LEPIN	Q8eyj0 leptospira	370	30	68.2	865	1	GLND_BORPA	Q7wa82 bordetella
298	30	68.2	452	2	Q72M16_LEPIC	Q72m16 leptospira	371	30	68.2	865	1	GLND_BORPE	Q7vyd2 bordetella
299	30	68.2	476	2	Q9SXF2_SCUBA	Q9sxf2 scutellaria	372	30	68.2	872	1	PSAB_GLOVI	Q7nft5 gloeobacter
300	30	68.2	488	2	Q6MP68_BDEBA	Q6mp68 bdellovibri	373	30	68.2	881	1	K1115_HUMAN	Q9upr7 homo sapien
301	30	68.2	495	2	Q51GT5_ENTHI	Q51gt5 entamoeba h	374	30	68.2	892	2	Q4P344_USTMA	Q4p344 ustilago ma
302	30	68.2	501	2	Q6D853_ERWCT	Q6d853 erwina car	375	30	68.2	898	2	Q61623_ORYSA	Q61623 oryza sativ
303	30	68.2	504	2	Q7UX14_RHOBA	Q7ux14 rhodospirell	376	30	68.2	910	2	Q5CR41_CRIPV	Q5cr41 cryptospori
304	30	68.2	510	2	Q8UYB5_9GAWA	Q8jybd5 porcine lym	377	30	68.2	911	1	B3AT_HUMAN	P02730 homo sapien
305	30	68.2	532	2	Q562K2_ARATH	Q562k2 arabidopsis	378	30	68.2	911	2	Q4KKW9_HUMAN	Q4kkw9 homo sapien
306	30	68.2	541	2	Q9S745_ARATH	Q9s745 arabidopsis	379	30	68.2	911	2	Q4VB84_HUMAN	Q4vb84 homo sapien
307	30	68.2	541	2	Q9LPC3_ARATH	Q9lpc3 arabidopsis	380	30	68.2	915	1	CE005_HUMAN	Q9nyf5 homo sapien
308	30	68.2	544	2	Q28548_SHEEP	Q28548 ovis aries	381	30	68.2	920	2	Q4PD22_USTMA	Q4pd22 ustilago ma
309	30	68.2	561	1	RFTI_CANAL	Q5a6n8 candida alb	382	30	68.2	927	1	B3AT_RAT	F23562 rattus norv
310	30	68.2	562	2	Q9GRP8_LEIMA	Q9grp8 leishmania	383	30	68.2	929	1	B3AT_MOUSE	P04919 mus musculu
311	30	68.2	572	2	Q5T3S2_HUMAN	Q5t3s2 homo sapien	384	30	68.2	929	1	Q53ZN9_MOUSE	Q53zn9 mus musculu
312	30	68.2	576	1	CT152_HUMAN	Q96m20 homo sapien	385	30	68.2	975	2	Q4WNK0_ASPFU	Q4wnk0 aspergillus
313	30	68.2	576	1	SYD_CANEP	Q7vnx8 candidatus	386	30	68.2	1004	2	Q4WCL6_ASPFU	Q4wcl6 aspergillus
314	30	68.2	576	2	Q5T3S1_HUMAN	Q5t3s1 homo sapien	387	30	68.2	1005	2	Q5B783_EMENI	Q5b783 aspergillus
315	30	68.2	583	2	Q6PK56_HUMAN	Q6pk56 homo sapien	388	30	68.2	1015	2	Q876Q0_EMENI	Q876q0 emericeila
316	30	68.2	597	2	Q8S7Q9_ORYSA	Q8s7q9 oryza sativ	389	30	68.2	1023	2	Q6AVAS_ORYSA	Q6avas oryza sativ
317	30	68.2	606	2	Q8YZR3_ANASP	Q8yzr3 anabaena sp	390	30	68.2	1030	2	Q9GR73_LEIME	Q9grt3 leishmania
318	30	68.2	616	1	MMP21_CNPY	Q90yc2 cynops pyrr	391	30	68.2	1090	2	Q4QGB0_LEIMA	Q4qgb0 leishmania
319	30	68.2	616	2	Q4RG42_TETNG	Q4rg42 tetraodon n	392	30	68.2	1090	2	Q53JM8_ORYSA	Q53jm8 oryza sativ
320	30	68.2	649	2	Q6MK14_BDEBA	Q6mk14 bdellovibri	393	30	68.2	1229	2	Q5JE24_PYRKO	Q5je24 pyrococcus
321	30	68.2	653	2	Q54IP4_DICDI	Q54ip4 dictyosteli	394	30	68.2	1233	2	Q4FXQ5_LEIMA	Q4fxq5 leishmania
322	30	68.2	678	2	Q41IQ6_GIBZE	Q41iq6 gibberella	395	30	68.2	1264	2	Q7RPM6_PLAYO	Q7rpm6 plasmodium
323	30	68.2	685	1	TOP1_PYRAB	Q9uys8 pyrococcus	396	30	68.2	1271	2	Q911B8_PSEAE	Q911b8 pseudomonas

397	30	68.2	1331	2	Q9KV11_STRCO	Q9kv11 streptomyc	470
398	30	68.2	1486	2	Q6CLO3_KLULA	Q6clq3 klyveromyc	471
399	30	68.2	1498	2	Q8CMR9_STAEP	Q8cmr9 staphylococ	472
400	30	68.2	1499	2	Q6GC17_STAAS	Q6gc17 staphylococ	473
401	30	68.2	1499	2	Q6GJK2_STAAR	Q6gjk2 staphylococ	474
402	30	68.2	1499	2	Q5HIK5_STAAC	Q5hik5 staphylococ	475
403	30	68.2	1499	2	Q7A7D3_STAAN	Q7a7d3 staphylococ	476
404	30	68.2	1499	2	Q8NY14_STAAN	Q8ny14 staphylococ	477
405	30	68.2	1499	2	Q99WD1_STAAM	Q99wd1 staphylococ	478
406	30	68.2	1506	2	Q4L3C8_STAHL	Q4l3c8 staphylococ	479
407	30	68.2	2166	2	Q92NX7_ORYSA	Q92nx7 oryza sativ	480
408	30	68.2	2375	2	Q4SNV4_TETNG	Q4snv4 tetraodon n	481
409	30	68.2	3207	2	Q4QSD6_LEIMA	Q4qsd6 leishmania	482
410	30	68.2	3584	1	NBEA_DROME	Q9w4e2 drosophila	483
411	30	68.2	4981	2	Q77372_PLAPF	Q77372 plasmodium	484
412	30	65.9	68	2	Q72SP2_LEPIC	Q72sp2 leptospira	485
413	29	65.9	69	2	Q64TM9_BACFR	Q64tm9 bacteroides	486
414	29	65.9	93	2	Q71ZU0_LISMF	Q71zu0 listeria mo	487
415	29	65.9	93	2	Q8Y7A8_LISMO	Q8y7a8 listeria mo	488
416	29	65.9	93	2	Q92BX5_LISIN	Q92bx5 listeria in	489
417	29	65.9	95	2	Q42271_ARATH	Q42271 arabidopsis	490
418	29	65.9	102	1	VE7_PAPVE	P11332 european el	491
419	29	65.9	104	2	Q99578_CRAHE	Q99578 cranioleuca	492
420	29	65.9	107	2	Q8BYF7_MOUSE	Q8byf7 mus muscula	493
421	29	65.9	114	1	TF2B_HALVA	Q42198 haloarcula	494
422	29	65.9	116	2	Q8CL10_MOUSE	Q8cl10 mus musculu	495
423	29	65.9	125	1	Q5ULL8_9CAUD	Q5ull8 lactobacill	496
424	29	65.9	138	1	VG06_ICHV1	Q50102 ictalurid h	497
425	29	65.9	140	2	Q54QX0_DICDI	Q54qx0 dictyosteli	498
426	29	65.9	142	2	O15748_DICDI	O15748 dictyosteli	499
427	29	65.9	144	2	Q5JTU2_HUMAN	Q5jtu2 homo sapien	500
428	29	65.9	156	2	Q6AS31_DESPS	Q6as31 desulfotale	501
429	29	65.9	159	2	Q5SU63_THET8	Q5sj63 thermus the	502
430	29	65.9	159	2	P73640_SYNY3	P73640 synecocyt	503
431	29	65.9	160	2	Q61LC3_CABER	Q61lc3 caenorhabdi	504
432	29	65.9	163	2	Q9CV41_MOUSE	Q9cv41 mus musculu	505
433	29	65.9	164	2	Q8BTO8_MOUSE	Q8bto8 mus musculu	506
434	29	65.9	165	2	Q76KY8_STRHA	Q76ky8 streptomyc	507
435	29	65.9	167	2	Q51PG7_MAGGR	Q51pg7 magnaporthe	508
436	29	65.9	171	2	Q4TGY1_TETNG	Q4tgy1 tetraodon n	509
437	29	65.9	173	2	Q8ETL8_OCBIH	Q8etl8 oceanobacil	510
438	29	65.9	176	2	Q8K3C8_MOUSE	Q8k3c8 mus musculu	511
439	29	65.9	177	2	Q7BZP8_ORYSA	Q7bzp8 oryza sativ	512
440	29	65.9	180	2	Q8BZH2_LACPL	Q8bzh2 lactobacill	513
441	29	65.9	181	2	Q9A819_CAUCR	Q9a819 caulobacter	514
442	29	65.9	182	1	ATPD_BACPF	P22479 bacillus ps	515
443	29	65.9	182	1	Q7TPR1_MOUSE	Q7tpr1 mus musculu	516
444	29	65.9	190	2	Q4TA49_TETNG	Q4ta49 tetraodon n	517
445	29	65.9	194	2	Q4WEM2_ASPFU	Q4wem2 aspergillus	518
446	29	65.9	204	1	PYRC_SERMA	Q9s3e1 serratia ma	519
447	29	65.9	204	2	Q7MW11_PORGI	Q7mw11 porphyromon	520
448	29	65.9	205	2	Q8S3K5_ELAL0	Q8s3k5 elaeis olei	521
449	29	65.9	209	2	Q9Y9T5_AERPE	Q9y9t5 aeropyrum p	522
450	29	65.9	213	2	Q8KH3_MOUSE	Q8kh3 mus musculu	523
451	29	65.9	214	2	Q6ZDX0_ORYSA	Q6zdx0 oryza sativ	524
452	29	65.9	216	2	Q5NH99_FRATT	Q5nh99 francisella	525
453	29	65.9	220	1	RECR_DEIRA	Q9zn92 deinococcus	526
454	29	65.9	221	2	Q53FF3_HUMAN	Q53ff3 homo sapien	527
455	29	65.9	221	2	Q9BT30_HUMAN	Q9bt30 homo sapien	528
456	29	65.9	221	2	Q9D942_MOUSE	Q9d942 mus musculu	529
457	29	65.9	221	2	Q9D6Z0_MOUSE	Q9d6z0 mus musculu	530
458	29	65.9	222	2	Q4HA31_9DEIO	Q4ha31 deinococcus	531
459	29	65.9	227	2	Q4TSJ3_TETNG	Q4tsj3 tetraodon n	532
460	29	65.9	232	2	Q6LUF3_PHOPR	Q6luf3 photobacter	533
461	29	65.9	244	2	Q754J9_ASHGO	Q754j9 ashyba goss	534
462	29	65.9	256	1	NIKD_PSEPK	Q88h11 pseudomonas	535
463	29	65.9	260	2	Q7ZV41_BRARE	Q7zv41 brachydanio	536
464	29	65.9	261	1	Y1J3_THEAC	Q9hzu4 thermoplam	537
465	29	65.9	263	2	Q8YTU8_ANASP	Q8ytu8 anabaena sp	538
466	29	65.9	266	2	Q6SH51_9BACT	Q6sh51 uncultured	539
467	29	65.9	266	2	Q9S610_ECOL1	Q9s610 escherichia	540
468	29	65.9	266	2	O51864_ECOL1	O51864 escherichia	541
469	29	65.9	268	2	Q9NSS9_HUMAN	Q9nss9 homo sapien	542

Q10275	schizosacch	269	1	YD3B_SCHPO	Q10275 schizosacch
Q9r088	mus musculu	270	1	KITM_MOUSE	Q9r088 mus musculu
Q8bn51	mus musculu	270	2	Q8BN51_MOUSE	Q8bn51 mus musculu
Q8vcf9	mus musculu	270	2	Q8VCF9_MOUSE	Q8vcf9 mus musculu
Q5bey3	aspergillus	272	2	Q5BEY3_EMENI	Q5bey3 aspergillus
Q6yx25	oryza sativ	272	2	Q6YX25_ORYSA	Q6yx25 oryza sativ
Q489Y4	tetraodon n	273	2	Q489Y4_TETNG	Q489y4 tetraodon n
Q5lwg2	silicibacte	276	2	Q5LWG2_SILPO	Q5lwg2 silicibacte
Q93rz6	streptomyce	277	2	Q93RZ6_STRCO	Q93rz6 streptomyce
Q5qmd0	oryza sativ	279	2	Q5QMD0_ORYSA	Q5qmd0 oryza sativ
Q7u552	synecococc	282	2	Q7U552_SYNPX	Q7u552 synecococc
Q7v640	prochloroco	284	2	Q7V640_PROMM	Q7v640 prochloroco
Q624q7	caenorhabdi	286	2	Q624Q7_CABER	Q624q7 caenorhabdi
Q7XVC4	tritium ae	287	2	Q7XVC4_WHEAT	Q7Xvc4 tritium ae
Q9f5m9	streptococc	292	2	Q9FDS9_STRPY	Q9f5m9 streptococc
Q5xcm9	streptococc	292	2	Q5XCM9_STRP6	Q5xcm9 streptococc
Q7cf82	streptococc	292	2	Q7CF82_STRP3	Q7cf82 streptococc
Q8p1d6	streptococc	292	2	Q8P1D6_STRP8	Q8p1d6 streptococc
Q9eyu8	rhizobium l	293	2	Q9EYU8_RHILO	Q9eyu8 rhizobium l
Q98av9	rhizobium l	293	2	Q98AV9_RHILO	Q98av9 rhizobium l
Q9A098	streptococc	297	2	Q9A098_STRPY	Q9A098 streptococc
Q6p000	xenopus lae	298	2	Q6PB00_XENLA	Q6p000 xenopus lae
Q8g3r7	bifidobacte	299	2	Q8G3R7_BIFLO	Q8g3r7 bifidobacte
Q9v4q2	drosophila	300	2	Q9V4Q2_DROME	Q9v4q2 drosophila
Q67vh2	oryza sativ	303	2	Q67VH2_ORYSA	Q67vh2 oryza sativ
Q8c6q0	mus musculu	306	2	Q8C6Q0_MOUSE	Q8c6q0 mus musculu
Q86fp0	caenorhabdi	312	2	Q86FP0_CABEL	Q86fp0 caenorhabdi
Q8xrb6	raistonias	313	2	Q8XRB6_RALSO	Q8xrb6 raistonias
Q65ne4	bacillus li	314	2	Q65NE4_BACLD	Q65ne4 bacillus li
P94419	bacillus su	315	2	P94419_BACSU	P94419 bacillus su
Y211_AQUAE	haloarcula	318	1	Y211_AQUAE	Y211_AQUAE
Q5V5V1	HALMA	319	2	Q5V5V1_HALMA	Q5V5V1 HALMA
Q86gi7	heliothis z	319	2	Q86GI7_HELZE	Q86gi7 heliothis z
Q5lxv4	magnaporthe	326	2	Q5LXV4_MAGGR	Q5lxv4 magnaporthe
Q6aqt3	desulfotale	326	2	Q6AQT3_DESPA	Q6aqt3 desulfotale
Q15077	homo sapien	328	1	P2RY6_HUMAN	Q15077 homo sapien
Q5x516	pongo pygma	328	2	Q5R5L6_PONPY	Q5x516 pongo pygma
Q61mv7	caenorhabdi	330	2	Q61MV7_CABER	Q61mv7 caenorhabdi
Q8eq00	sus scrofa	330	2	Q8EQ00_PIG	Q8eq00 sus scrofa
Q8hm04	halobacteri	331	2	Q8HM04_HALSA	Q8hm04 halobacteri
Q30365	anabaena sp	332	1	RPSB_ANASP	Q30365 anabaena sp
Q51pw9	magnaporthe	334	2	Q51PW9_MAGGR	Q51pw9 magnaporthe
Q5YQ36	nocardia fa	335	2	Q5YQ36_NOCFA	Q5YQ36 nocardia fa
Q6mc54	parachlamyd	335	2	Q6MC54_PARUM	Q6mc54 parachlamyd
Q4sj85	tetraodon n	335	2	Q4SJS5_TETNG	Q4sj85 tetraodon n
Q6pc00	brachydanio	336	2	Q6PC00_BRARE	Q6pc00 brachydanio
Q8xxd8	methylococc	341	2	Q608N2_METCA	Q8xxd8 methylococc
Q8xxd8	raistonias	343	2	Q8XZD8_RALSO	Q8xxd8 raistonias
Q7ng64	gloeobacter	343	2	Q7NG64_GLOVI	Q7ng64 gloeobacter
Q8wrt3	platynereis	349	2	Q8WRT3_PLADU	Q8wrt3 platynereis
Q7bzj1	xenopus lae	350	2	Q7SZJ1_XENLA	Q7bzj1 xenopus lae
Q6pav9	xenopus lae	350	2	Q6PAV9_XENLA	Q6pav9 xenopus lae
Q8djh5	synecococc	351	2	Q8DJH5_SYNEL	Q8djh5 synecococc
Q5xfx7	rattus norv	351	2	Q5XFX7_RAT	Q5xfx7 rattus norv
Q7vws0	bordetella	353	2	Q7VWS0_BORPE	Q7vws0 bordetella
Q7wam4	bordetella	353	2	Q7WAM4_BORPA	Q7wam4 bordetella
Q7WJ87	bordetella	353	2	Q7WJ87_BORBR	Q7WJ87 bordetella
Q7vcy1	drosophila	356	2	Q7VCY1_DROME	Q7vcy1 drosophila
Q74380	schizosacch	357	2	Q74380_SCHPO	Q74380 schizosacch
Q91k56	arabidopsis	357	2	Q91K56_ARATH	Q91k56 arabidopsis
Q5m7z1	homo sapien	362	2	Q5M7Z1_HUMAN	Q5m7z1 homo sapien
Q9C5S3	arabidopsis	362	2	Q9C5S3_ARATH	Q9C5s3 arabidopsis
Q9M4A2	arabidopsis	362	2	Q9M4A2_ARATH	Q9M4a2 arabidopsis
Q8cap3	mus musculu	362	2	Q8CAP3_MOUSE	Q8cap3 mus musculu
P54725	homo sapien	363	1	RD23A_MOUSE	P54725 homo sapien
Q6b6h4	gordonia al	363	1	RD23A_MOUSE	Q6b6h4 gordonia al
Q6btj5	gordonia sp	365	2	Q6BTJ5_9ACTO	Q6btj5 gordonia sp
Q4VY41	gordonia sp	365	2	Q4VY41_9ACTO	Q4VY41 gordonia sp
Q5wkj7	eschichia cl	367	2	Q5WKJ7_BACSK	Q5wkj7 eschichia cl
P37751	eschichia	372	1	YEFI_ECOLI	P37751 eschichia
Q59E08	homo sapien	379	2	Q59E08_HUMAN	Q59E08 homo sapien
Q6wny5	dasyattis sa	379	2	Q6WNY5_9CHON	Q6wny5 dasyattis sa

543	29	65.9	385	2	Q7LZR8 ICTPU	Q7LZR8 ictalurus p	616	29	65.9	518	2	Q6R653_MOUSE	Q6R653 mus musculus
544	29	65.9	394	2	Q9WOM3_DROME	Q9wom3 drosophila	617	29	65.9	519	2	Q501N0_MOUSE	Q501n0 mus musculus
545	29	65.9	400	2	Q80H41_HPBVO	Q80h41 hepatophila b	618	29	65.9	520	2	Q61091_BACAN	Q61091 bacillus an
546	29	65.9	401	2	Q86NX2_DROME	Q86nx2 drosophila	619	29	65.9	526	2	Q4TAV7_TETNG	Q4tav7 tetraodon n
547	29	65.9	403	2	Q5WFP3_BACSK	Q5wfp3 bacillus cl	620	29	65.9	527	1	RFT1_SCHPO	R94302 schizoeacch
548	29	65.9	405	2	Q8SE11_ARATH	Q8se11 arabidopsis	621	29	65.9	534	2	Q81FI3_BACCR	Q81fi3 bacillus ce
549	29	65.9	405	2	Q87A72_XYLFT	Q87a72 xyella fas	622	29	65.9	538	2	Q86XHO_HUMAN	Q86xho homo sapien
550	29	65.9	405	2	Q9PAE1_XYLFA	Q9pa11 xyella fas	623	29	65.9	539	2	Q7VQU1_CANBF	Q7vqu1 candidatus
551	29	65.9	405	2	Q6GM77_XENLA	Q6gm77 xenopus lae	624	29	65.9	540	2	Q9SVG4_ARATH	Q9svg4 arabidopsis
552	29	65.9	406	1	OR42A_DROME	Q9v912 drosophila	625	29	65.9	542	2	Q4MUR1_BACCE	Q4mur1 bacillus ce
553	29	65.9	406	2	Q98S14_XENLA	Q98s14 xenopus lae	626	29	65.9	542	2	Q6HK85_BACHK	Q6hk85 bacillus th
554	29	65.9	410	2	Q59H60_HUMAN	Q59h60 homo sapien	627	29	65.9	542	2	Q73A32_BACCI	Q73a32 bacillus ce
555	29	65.9	414	2	Q9SST5_PASTR	Q9sst5 matricaria	628	29	65.9	542	2	Q63CT9_BACCC	Q63ct9 bacillus ce
556	29	65.9	418	2	Q9SCD6_PAGSY	Q9scd6 fagus sylvia	629	29	65.9	544	2	Q61L43_CABRN	Q61l43 caenorhabdi
557	29	65.9	419	2	Q94BQ2_ARATH	Q94bq2 arabidopsis	630	29	65.9	544	2	Q5L9M9_BACFN	Q5l9m9 bacteroides
558	29	65.9	420	2	Q9C5U3_ARATH	Q9c5u3 arabidopsis	631	29	65.9	544	2	Q64PX1_BACFR	Q64px1 bacteroides
559	29	65.9	420	1	DYXC1_GORGO	Q863a5 gorilla gor	632	29	65.9	545	2	Q8A651_BACTN	Q8a651 bacteroides
560	29	65.9	420	1	DYXC1_HUMAN	Q8wxu2 homo sapien	633	29	65.9	550	2	Q9HBS2_HUMAN	Q9hbs2 homo sapien
561	29	65.9	420	1	DYXC1_PANPA	Q863a6 pan paniscu	634	29	65.9	551	2	Q5VTX0_HUMAN	Q5vtx0 homo sapien
562	29	65.9	420	1	DYXC1_PANTR	Q863a7 pan troglod	635	29	65.9	554	2	Q80VE7_MOUSE	Q80ve7 mus musculus
563	29	65.9	420	1	DYXC1_PONPY	Q863a4 pongo pygma	636	29	65.9	554	2	Q8G4D6_BIFLO	Q8g4d6 bifidobacte
564	29	65.9	424	2	Q4PGD0_USTWA	Q4pgd0 ustilago ma	637	29	65.9	563	2	Q5B4B4_EMENI	Q5b4b4 aspergillus
565	29	65.9	424	2	Q7GCH3_ORYSA	Q7gch3 oryza sativ	638	29	65.9	565	1	UBP21_HUMAN	Q9uk80 homo sapien
566	29	65.9	424	2	Q9FEB6_ORYSA	Q9feb6 oryza sativ	639	29	65.9	565	2	Q5BKT5_HUMAN	Q5bkt5 homo sapien
567	29	65.9	426	2	Q80XM6_MOUSE	Q80xm6 mus musculus	640	29	65.9	565	2	Q5VTW9_HUMAN	Q5vtw9 homo sapien
568	29	65.9	430	1	ELK4_MOUSE	P41158 mus musculus	641	29	65.9	566	1	UBP21_MOUSE	Q9qz16 mus musculus
569	29	65.9	433	2	Q9M613_PINTA	Q9m613 pinus taeda	642	29	65.9	570	2	Q4WIC6_ASFPF	Q4wic6 aspergillus
570	29	65.9	440	2	Q33671_9STRB	Q33671 streptococ	643	29	65.9	571	2	Q7SHW2_NEUCR	Q7shw2 neurospora
571	29	65.9	441	2	Q815F7_BACCR	Q815f7 bacillus ce	644	29	65.9	575	2	Q9M498_ARATH	Q9m498 arabidopsis
572	29	65.9	441	2	Q81X15_BACAN	Q81x15 bacillus an	645	29	65.9	594	2	Q6ZZI0_ACTTI	Q6zzi0 actinoplane
573	29	65.9	442	2	Q5WBF4_BACSK	Q5wbf4 bacillus cl	646	29	65.9	597	2	Q5CJV0_CRYHO	Q5cjh0 cryptospori
574	29	65.9	447	2	Q5N4W0_SYN6P	Q5n4w0 synchococ	647	29	65.9	598	2	Q70AY2_ACTTI	Q70ay2 actinoplane
575	29	65.9	448	1	FDFT_CANAL	P78589 candida alb	648	29	65.9	622	2	Q5JVP6_HUMAN	Q5jvp6 homo sapien
576	29	65.9	448	1	RMUC_ZYMMO	Q9red3 zymomonas m	649	29	65.9	622	2	Q8C9V4_MOUSE	Q8c9v4 mus musculus
577	29	65.9	448	2	Q59V33_CANAL	Q59v33 candida alb	650	29	65.9	625	2	Q91ZZ6_MOUSE	Q91zz6 mus musculus
578	29	65.9	452	2	Q9FNU8_DACGL	Q9fnu8 dactylis gl	651	29	65.9	625	2	Q92315_RAT	Q92315 rattus norv
579	29	65.9	453	2	Q7QAL6_ANOGA	Q7qal6 anopheles g	652	29	65.9	628	2	Q5N122_FRAIT	Q5n122 francisella
580	29	65.9	459	1	NU4M_CHICK	P18939 gallus gall	653	29	65.9	641	2	Q84ZV0_SOYBN	Q84zv0 glycine max
581	29	65.9	459	1	Q6ZLS4_CHICK	Q6zls4 gallus gall	654	29	65.9	644	2	Q4KJZ8_PSEUDOM	Q4kjz8 pseudomonas
582	29	65.9	459	2	Q7GTU7_CHICK	Q7gtu7 gallus gall	655	29	65.9	645	2	Q6A058_DESPS	Q6a058 desulfotale
583	29	65.9	459	2	Q4GWQ3_CHICK	Q4gwq3 gallus gall	656	29	65.9	646	2	ABUG7_RAT	Q6a058 rattus norv
584	29	65.9	459	2	Q4GWP0_CHICK	Q4gwp0 gallus gall	657	29	65.9	646	2	Q8C750_MOUSE	Q8c750 mus musculus
585	29	65.9	459	2	Q4GWM7_CHICK	Q4gwm7 gallus gall	658	29	65.9	651	2	Q5L8J1_BACFN	Q5l8j1 bacteroides
586	29	65.9	459	2	Q4GWK1_GALILA	Q4gwk1 gallus lafa	659	29	65.9	651	2	Q8A158_BACTN	Q8a158 bacteroides
587	29	65.9	459	2	Q4GWR6_GALSO	Q4gwr6 gallus sonn	660	29	65.9	651	2	Q64NT7_BACFR	Q64nt7 bacteroides
588	29	65.9	462	2	Q6HOV0_BACAN	Q6hov0 bacillus an	661	29	65.9	652	2	Q9VME6_DROME	Q9vme6 drosophila
589	29	65.9	462	2	Q631F3_BACCC	Q631f3 bacillus ce	662	29	65.9	653	2	Q16972_APLCA	Q16972 aplysia cal
590	29	65.9	462	2	Q6HB88_BACHK	Q6hb88 bacillus th	663	29	65.9	653	2	Q08845_APLCA	Q08845 aplysia cal
591	29	65.9	464	2	Q4SCC1_TETNG	Q4sccl tetraodon n	664	29	65.9	655	1	ACADV_HUMAN	Q49748 homo sapien
592	29	65.9	466	2	Q55UZ9_CRYNE	Q55uz9 cryptococcu	665	29	65.9	655	1	ACADV_MACFA	Q8hxy7 macaca fasc
593	29	65.9	466	2	Q5KL83_CRYNE	Q5kl83 cryptococcu	666	29	65.9	655	2	Q53HR2_HUMAN	Q53hr2 homo sapien
594	29	65.9	467	2	Q94000_CANAL	Q94000 candida alb	667	29	65.9	655	2	Q4U9R0_THBAN	Q4u9r0 theileria a
595	29	65.9	467	2	Q5A4N6_CANAL	Q5a4n6 candida alb	668	29	65.9	655	2	Q4R7S5_MACFA	Q4r7s5 macaca fasc
596	29	65.9	467	2	Q6AKJ0_DESPS	Q6akj0 desulfotale	669	29	65.9	660	2	Q16973_APLCA	Q16973 aplysia cal
597	29	65.9	468	1	YG4K_YEAST	P53304 saccharomyc	670	29	65.9	661	1	PSAB_PROHO	P58387 prochloroth
598	29	65.9	468	2	Q67450_AQUAE	Q67450 aquifex aeo	671	29	65.9	662	2	Q69Z26_MOUSE	Q69z26 mus musculus
599	29	65.9	475	2	Q4IAN5_GIBZE	Q4ian5 gibberella	672	29	65.9	673	2	Q4T1K1_TETNG	Q4t1k1 tetraodon n
600	29	65.9	489	2	P74573_SYNY3	P74573 synchocyst	673	29	65.9	675	2	Q5BHV4_DROME	Q5bhv4 drosophila
601	29	65.9	489	2	Q50319_BRARE	Q50319 brachydanio	674	29	65.9	691	2	Q9VML1_DROME	Q9vml1 drosophila
602	29	65.9	491	2	Q7UCR8_SHIFL	Q7ucr8 shigella fl	675	29	65.9	693	2	Q96680_DROME	Q96680 drosophila
603	29	65.9	496	1	TR130_MOUSE	P15533 mus musculus	676	29	65.9	694	1	KTNB1_BRARE	Q7zv22 brachydanio
604	29	65.9	501	2	Q6XW46_ARATH	Q6xw46 arabidopsis	677	29	65.9	696	2	Q5CS83_CRYPV	Q5cs83 cryptospori
605	29	65.9	502	1	CP313_DROME	Q9vhp4 drosophila	678	29	65.9	699	2	Q4KD63_PSBFS	Q4kd63 pseudomonas
606	29	65.9	502	1	YDGA_ECOLI	P77804 escherichia	679	29	65.9	701	2	Q5ISL3_MACFA	Q5isl3 macaca fasc
607	29	65.9	502	2	Q9S108_ARATH	Q9s108 arabidopsis	680	29	65.9	705	1	ABUG7_MOUSE	Q9e928 mus musculus
608	29	65.9	502	2	Q83KZ0_SHIFL	Q83kz0 shigella fl	681	29	65.9	705	2	Q52NKO_RAT	Q52nko rattus norv
609	29	65.9	502	2	Q8X676_ECOS7	Q8x676 escherichia	682	29	65.9	713	2	Q8RWB3_ARATH	Q8rwb3 arabidopsis
610	29	65.9	504	2	Q4RV71_TETNG	Q4rv71 tetraodon n	683	29	65.9	716	2	Q4TBT2_TETNG	Q4tbt2 tetraodon n
611	29	65.9	506	2	Q6XW62_ARATH	Q6xw62 arabidopsis	684	29	65.9	720	2	Q6CXK2_KJULA	Q6cxk2 kluyveromyc
612	29	65.9	506	2	Q6XW35_ARATH	Q6xw35 arabidopsis	685	29	65.9	731	2	Q4WMH2_ASFPF	Q4wmh2 aspergillus
613	29	65.9	506	2	Q6XW40_ARATH	Q6xw40 arabidopsis	686	29	65.9	731	2	Q9FYB8_ARATH	Q9fyb8 arabidopsis
614	29	65.9	509	2	Q872L9_NEUCR	Q872l9 neurospora	687	29	65.9	744	2	Q4QAAL_LEIMA	Q4qaal leishmania
615	29	65.9	515	2	Q6QJF2_APLCA	Q6qjf2 aplysia cal	688	29	65.9	759	2	Q9N1G9_TETPY	Q9n1g9 tetrahymena

689	29	65.9	762	2	Q9G8T2_9CRYP	Q9g8t2 rhodomonas	762	29	65.9	984	2	Q8K2K2_MOUSE	Q8k2k2 mus musculus
690	29	65.9	763	2	Q4IHY8_GIRZE	Q4ihy8 gibberella	763	29	65.9	985	2	Q7SHP3_NEUCR	Q7shp3 neurospora
691	29	65.9	764	2	Q8K4I3_MOUSE	Q8k4i3 mus musculus	764	29	65.9	987	2	Q7LNC5_ATH	Q7lnc5 arabidopsis
692	29	65.9	765	2	Q5XXR3_RAT	Q5xxr3 rattus norvegicus	765	29	65.9	987	2	Q8GZQ4_ATH	Q8gzq4 arabidopsis
693	29	65.9	766	2	Q4R3D3_MACFA	Q4r3d3 macaca fasciata	766	29	65.9	996	2	Q4S0X0_TETNG	Q4s0x0 tetraodon n
694	29	65.9	767	1	ARHG6_HUMAN	Q15052 homo sapien	767	29	65.9	1005	2	Q4S703_BACTM	Q4s703 bacillus th
695	29	65.9	768	2	Q723W1_HUMAN	Q723w1 homo sapien	768	29	65.9	1024	2	Q8AX93_FUGRU	Q8ax93 fugu rubrip
696	29	65.9	769	2	Q5JQ66_HUMAN	Q5jq66 homo sapien	769	29	65.9	1027	2	Q4SMI5_TETNG	Q4smi5 tetraodon n
697	29	65.9	770	2	Q8JID2_BRARE	Q8jid2 brachydanio	770	29	65.9	1031	2	Q8BXS8_MOUSE	Q8bxs8 mus musculus
698	29	65.9	771	2	Q58P69_ATH	Q58p69 arabidopsis	771	29	65.9	1055	2	Q6E2E8_WHEAT	Q6e2e8 triticum ae
699	29	65.9	772	2	Q90424_BRARE	Q90424 brachydanio	772	29	65.9	1056	2	Q5LEB8_BACFN	Q5leeb bacteroides
700	29	65.9	773	2	Q72U14_BRARE	Q72u14 brachydanio	773	29	65.9	1073	2	Q64VK3_BACFR	Q64vk3 bacteroides
701	29	65.9	774	2	Q7T192_CARAU	Q7t192 carassius a	774	29	65.9	1081	2	Q8BZL9_MOUSE	Q8bzl9 mus musculus
702	29	65.9	775	1	CTNB1_HUMAN	P35222 homo sapien	775	29	65.9	1088	1	UN13D_RAT	Q9r189 rattus norv
703	29	65.9	776	1	CTNB1_MOUSE	Q02248 mus musculus	776	29	65.9	1090	1	UN13D_HUMAN	Q70199 homo sapien
704	29	65.9	777	1	CTNB1_RAT	Q09u82 rattus norv	777	29	65.9	1090	1	Q9H0F2_HUMAN	Q9h0f2 homo sapien
705	29	65.9	778	1	CTNB_XENLA	P26233 xenopus lae	778	29	65.9	1092	2	Q9NSV3_CABEL	Q9nsv3 caenorhabdi
706	29	65.9	779	2	Q8WNW4_PIG	Q8wnw4 sus scrofa	779	29	65.9	1099	2	Q518L7_ENTHI	Q518l7 entamoeba h
707	29	65.9	780	2	Q5R5L8_PONPY	Q5r5l8 pongo pygma	780	29	65.9	1102	2	Q4RKE9_TETNG	Q4rke9 tetraodon n
708	29	65.9	781	2	Q76LW0_MERUN	Q76lw0 meriones un	781	29	65.9	1116	2	Q6PA26_XENLA	Q6pa26 xenopus lae
709	29	65.9	782	2	Q42486_CHICK	Q42486 gallus gall	782	29	65.9	1119	2	Q6CWR5_KULULA	Q6cwr5 kluyveromyc
710	29	65.9	783	2	Q72X35_XENLA	Q72x35 xenopus lae	783	29	65.9	1132	2	Q4RTB9_TETNG	Q4rtb9 tetraodon n
711	29	65.9	784	2	Q632T4_XENLA	Q632t4 xenopus lae	784	29	65.9	1135	2	Q9YHD3_XENLA	Q9yhd3 xenopus lae
712	29	65.9	785	2	Q5R2I4_TRISI	Q5r2i4 trionyx sin	785	29	65.9	1154	2	Q9BKQ3_CABEL	Q9bkq3 caenorhabdi
713	29	65.9	786	2	Q419B0_GIRZE	Q4i9b0 gibberella	786	29	65.9	1205	1	PD55_SCHPO	Q9hff5 schizosacch
714	29	65.9	787	2	Q5AKI7_CANAL	Q5aki7 candida alb	787	29	65.9	1210	2	O14251_SCHPO	O14251 schizosacch
715	29	65.9	788	2	Q522Y7_MAGGR	Q522y7 magnaporthe	788	29	65.9	1264	2	Q55L56_CRYNE	Q55l56 cryptococcu
716	29	65.9	789	2	Q4RFE6_TETNG	Q4rfe6 tetraodon n	789	29	65.9	1264	2	Q5KAC5_CRYNE	Q5kak5 cryptococcu
717	29	65.9	790	2	Q62QI5_MOUSE	Q62qi5 mus musculus	790	29	65.9	1273	2	Q4T5J1_TETNG	Q4t5j1 tetraodon n
718	29	65.9	791	2	Q6XPA5_MOUSE	Q6xpa5 mus musculus	791	29	65.9	1292	2	Q8DIH6_SYNEL	Q8dih6 synechococ
719	29	65.9	792	2	Q8WRT5_CHAVR	Q8wrt5 chaetopteru	792	29	65.9	1302	2	Q68DW0_HUMAN	Q68dw0 homo sapien
720	29	65.9	793	1	AMPO_MOUSE	Q8bxq6 mus musculus	793	29	65.9	1309	2	Q5P9W4_ANAMM	Q5p9w4 anaplasma m
721	29	65.9	794	2	Q8GVF1_ATH	Q8gvf1 arabidopsis	794	29	65.9	1325	2	Q4PAW5_USTMA	Q4paw5 ustilago ma
722	29	65.9	795	1	AMPO_HUMAN	Q8bnm6 homo sapien	795	29	65.9	1325	2	Q95TM2_DROME	Q95tm2 drosophila
723	29	65.9	796	1	VP853_YEAST	P47061 saccharomyc	796	29	65.9	1398	2	Q54SJ9_DICDI	Q54sj9 dictyosteli
724	29	65.9	797	2	Q6PC19_XENLA	Q6pci19 xenopus lae	797	29	65.9	1432	2	Q55G34_DICDI	Q55g34 dictyosteli
725	29	65.9	798	2	Q8MU83_TETTH	Q8mu83 tetrahymena	798	29	65.9	1445	2	Q4QAC8_LEIMA	Q4qac8 leishmania
726	29	65.9	799	2	EP2_CHIKE	P28996 chlorella k	799	29	65.9	1447	2	Q4Q7H5_LEIMA	Q4q7h5 leishmania
727	29	65.9	800	2	Q5SP45_CRYNE	Q5sp45 cryptococcu	800	29	65.9	1450	2	Q552Q7_DICDI	Q552q7 dictyosteli
728	29	65.9	801	2	Q5KEB1_CRYNE	Q5keb1 cryptococcu	801	29	65.9	1506	2	Q6NS59_MOUSE	Q6n59 mus musculus
729	29	65.9	802	1	Y343_METJA	Q57789 methanococ	802	29	65.9	1511	2	Q5BH67_EMENI	Q5bh67 aspergillus
730	29	65.9	803	2	Q19070_CABEL	Q19070 caenorhabdi	803	29	65.9	1515	2	Q5JXK1_HUMAN	Q5jxk1 homo sapien
731	29	65.9	804	2	Q9D2J6_MOUSE	Q9d2j6 mus musculus	804	29	65.9	1522	2	Q9P2D6_HUMAN	Q9p2d6 homo sapien
732	29	65.9	805	2	Q6P3N8_XENTR	Q6p3n8 xenopus tro	805	29	65.9	1551	2	Q4WVF2_ASPFU	Q4wvf2 aspergillus
733	29	65.9	806	2	Q5FVX0_XENTR	Q5fvx0 xenopus tro	806	29	65.9	1559	2	Q8WSM2_SCHMA	Q8wsm2 schistosoma
734	29	65.9	807	2	Q51W82_MAGGR	Q51w82 magnaporthe	807	29	65.9	1602	2	Q7DB74_MYCTU	Q7db74 mycobacteri
735	29	65.9	808	1	YKL6_CABEL	P42173 caenorhabdi	808	29	65.9	1602	2	Q65933_MYCTU	Q65933 mycobacteri
736	29	65.9	809	1	CLPB1_SYNPF	P53533 synechococ	809	29	65.9	1636	2	Q7VEV0_MYCBO	Q7vev0 mycobacteri
737	29	65.9	810	2	Q4S9W0_TETNG	Q4s9w0 tetraodon n	810	29	65.9	1636	2	Q4N6X7_THEPA	Q4n6x7 theileria p
738	29	65.9	811	2	Q4Q9N1_LEIMA	Q4q9n1 leishmania	811	29	65.9	1659	2	Q7Q7K8_AMOGA	Q7q7k8 anopheles g
739	29	65.9	812	2	Q6FMH5_CANGA	Q6fmh5 candida gia	812	29	65.9	1663	2	Q54KD0_DICDI	Q54kd0 dictyosteli
740	29	65.9	813	2	Q582T0_9TRYP	Q582t0 trypanosoma	813	29	65.9	1664	2	Q5AX84_EMENI	Q5ax84 aspergillus
741	29	65.9	814	2	Q571J0_MOUSE	Q571j0 mus musculus	814	29	65.9	1724	2	Q4TIK3_TETNG	Q4tik3 tetraodon n
742	29	65.9	815	2	Q504W7_HUMAN	Q504w7 homo sapien	815	29	65.9	1745	2	Q4N6X8_THEPA	Q4n6x8 theileria p
743	29	65.9	816	2	Q4VY09_HUMAN	Q4vy09 homo sapien	816	29	65.9	1755	2	Q4I5Z7_GIBZE	Q4i5z7 gibberella
744	29	65.9	817	2	Q5R9G5_PONPY	Q5r9g5 pongo pygma	817	29	65.9	1776	2	Q17901_CABEL	Q17901 caenorhabdi
745	29	65.9	818	2	Q6FL60_CANGA	Q6fl60 candida gia	818	29	65.9	1782	2	Q9XTJ1_CABEL	Q9xtj1 caenorhabdi
746	29	65.9	819	2	Q6NVF0_MOUSE	Q6nvf0 mus musculus	819	29	65.9	1786	2	Q4GZ48_9TRYP	Q4gz48 trypanosoma
747	29	65.9	820	1	OCRL_HUMAN	Q0N1968 homo sapien	820	29	65.9	1787	2	Q5AFB2_CANAL	Q5afb2 candida alb
748	29	65.9	821	2	Q4VY10_HUMAN	Q4vy10 homo sapien	821	29	65.9	1800	2	Q68T18_CABEL	Q68t18 caenorhabdi
749	29	65.9	822	2	Q6XW48_ATH	Q6xw48 arabidopsis	822	29	65.9	1801	2	Q6BZ13_DEBHA	Q6bz13 debaryomyce
750	29	65.9	823	1	RPF8_ATH	Q8w4j9 arabidopsis	823	29	65.9	1846	2	Q814Z1_PLAF7	Q814z1 plasmodium
751	29	65.9	824	2	Q6C230_YARLI	Q6c230 yarrowia li	824	29	65.9	1869	2	Q6BZT4_YARLI	Q6bzt4 yarrowia li
752	29	65.9	825	2	Q51S73_MAGGR	Q51s73 magnaporthe	825	29	65.9	2028	2	Q6Q891_LEPMC	Q6q891 leprospiraer
753	29	65.9	826	2	Q60U26_CABER	P88954 caenorhabdi	826	29	65.9	2045	2	Q5B9K8_EMENI	Q5b9k8 aspergillus
754	29	65.9	827	2	P88954_HVH7	Q60u26 human herpe	827	29	65.9	2073	1	BIME_EMENI	P24686 emerigella
755	29	65.9	828	2	Q55YT4_CRYNE	Q55yt4 cryptococcu	828	29	65.9	2130	2	Q9GSR1_DROME	Q9gsr1 drosophila
756	29	65.9	829	2	Q5KNS3_CRYNE	Q5kns3 cryptococcu	829	29	65.9	2130	2	Q9GSR2_DROME	Q9gsr2 drosophila
757	29	65.9	830	2	Q9C6W3_ATH	Q9c6w3 arabidopsis	830	29	65.9	2142	2	Q4RNY6_TETNG	Q4rny6 tetraodon n
758	29	65.9	831	2	Q8L7A9_ATH	Q8l7a9 arabidopsis	831	29	65.9	2335	2	Q51M85_MAGGR	Q51m85 magnaporthe
759	29	65.9	832	2	Q5FPT6_GLUOX	Q5fpt6 gluconobact	832	29	65.9	2479	2	Q6RKJ6_BOTCI	Q6rkj6 botrytis ci
760	29	65.9	833	2	Q23463_CABEL	Q23463 caenorhabdi	833	29	65.9	2763	2	Q9YGV2_FUGRU	Q9ygv2 fugu rubrip
761	29	65.9	834	2	Q741L1_LACJO	Q741l1 lactobacill	834	29	65.9	2910	2	Q6BFC5_PARTE	Q6bfc5 paramecium

835	29	55.9	3056	2	Q8I639_PIAF7	Q8I639 plasmodium	908	28	63.6	174	2	Q5N2J8_SYN6	Q5n2j8 synechococ
836	29	65.9	3076	2	Q9X7E2_MYCLE	Q9x7e2 mycobacteri	909	28	63.6	177	2	Q4KJ07_PSEF5	Q4kj07 pseudomonas
837	29	65.9	3094	2	Q6UDW3_PLAFA	Q6udw3 plasmodium	910	28	63.6	179	2	Q83G10_TROWT	Q83g10 tropheryma
838	29	65.9	3258	2	Q4QIZ6_LEIMA	Q4qiz6 leishmania	911	28	63.6	179	2	Q83I55_TROW8	Q83i55 tropheryma
839	29	65.9	3258	2	Q4QIZ6_LEIMA	Q4qiz6 leishmania	912	28	63.6	181	2	Q9P045_HUMAN	Q9p045 homo sapien
840	29	65.9	3989	2	Q7QG81_ANOGA	Q7qg81 anopheles g	913	28	63.6	182	2	Q5WCR8_BACSK	Q5wcr8 bacillus cl
841	29	65.9	4053	2	Q5C243_CABEL	Q5c243 caenorhabdi	914	28	63.6	182	2	Q55446_SYN3K	Q55446 synechocyst
842	29	65.9	4061	2	Q6A4L2_CABEL	Q6a4l2 caenorhabdi	915	28	63.6	183	2	Q8L5G9_HEVBR	Q8l5g9 hevea bras
843	29	65.9	4064	2	Q18667_CABEL	Q18667 caenorhabdi	916	28	63.6	187	2	Q8H029_ORYSA	Q8h029 oryza sativ
844	29	65.9	4085	2	Q62088_CABER	Q62088 caenorhabdi	917	28	63.6	189	2	Q8HTG2_PSEAE	Q8htg2 pseudomonas
845	29	65.9	4674	2	Q4RGA0_TETNG	Q4rga0 tetraodon n	918	28	63.6	189	2	Q7U865_RHOBA	Q7ue65 rhodopirell
846	28	63.6	38	2	Q5NK21_ZYMMO	Q5nk21 zymomonas m	919	28	63.6	189	2	Q9F0H5_PSESM	Q9f0h5 pseudomonas
847	28	63.6	41	2	Q77557_FIG	Q77557 sus scrofa	920	28	63.6	193	2	Q6L4R1_ORYSA	Q6l4r1 oryza sativ
848	28	63.6	85	2	Q33151_METMA	Q33151 methanosarc	921	28	63.6	194	2	Q9RX50_DEIRA	Q9rx50 deinococcus
849	28	63.6	86	2	Q70Jt4_MICAB	Q70jta microcycetis	922	28	63.6	197	2	Q7TBL8_VIRU	Q7tbl8 iranian whe
850	28	63.6	87	2	Q6X518_9CHRO	Q6x518 microcycetis	923	28	63.6	197	2	Q90383_CARPL	Q90383 carcharinu
851	28	63.6	90	2	Q9ZG34_CHLTR	Q9zgz4 chlamydia t	924	28	63.6	199	2	Q8BPM3_MOUSE	Q8bpm3 mus musculu
852	28	63.6	90	2	Q4NX33_9DELT	Q4nx33 anaeromyxob	925	28	63.6	202	2	Q9HPR0_HANSA	Q9hpr0 halobacteri
853	28	63.6	94	2	Q4NS10_THEPA	Q4ns10 thelleria p	926	28	63.6	203	2	Q97ZT6_SULTO	Q97zt6 sulfolobus
854	28	63.6	96	2	Q29595_FIG	Q29595 sus scrofa	927	28	63.6	203	2	Q11439_9VIRU	Q11439 urochloa ho
855	28	63.6	99	2	Q8I021_FELCA	Q8i021 felis silve	928	28	63.6	207	2	Q9LVE4_ARATH	Q9lve4 arabidopsis
856	28	63.6	101	2	Q866A1_HORSE	Q866a1 equus cabal	929	28	63.6	213	2	Q9CRX7_MOUSE	Q9crx7 mus musculu
857	28	63.6	108	2	Q4T7Q3_TETNG	Q4t7q3 tetraodon n	930	28	63.6	214	2	Q50VP6_ENTHI	Q50vp6 entamoeba h
858	28	63.6	111	2	Q9YD37_AERPE	Q9yd37 aeropyrum p	931	28	63.6	216	2	Q4XV29_PLACH	Q4xv29 plasmodium
859	28	63.6	113	2	Q523G3_MAGGR	Q523g3 magnaporthe	932	28	63.6	227	2	Q9GH46_9CHLO	Q9gh46 basichlamys
860	28	63.6	114	2	Q59WA0_CANAL	Q59wa0 candida alb	933	28	63.6	231	2	Q5QVR7_IDILO	Q5qvr7 idiomarina
861	28	63.6	117	2	Q8LY21_9ARAC	Q8ly21 trochosa or	934	28	63.6	232	2	Q7TLN5_NPVCF	Q7tlm5 choriostoneu
862	28	63.6	118	2	Q6GZ70_HUMAN	Q6gz70 homo sapien	935	28	63.6	233	2	Q8DAV2_VIRVU	Q8dav2 vibrio vuln
863	28	63.6	118	2	Q8HDB7_9CHLO	Q8hdb7 carteria ob	936	28	63.6	234	2	Q7NS21_CHRVO	Q7ns21 chromobacte
864	28	63.6	120	2	Q7MKF6_VIBVY	Q7mkf6 vibrio vuln	937	28	63.6	234	2	Q8DE79_VIBVU	Q8de79 vibrio vuln
865	28	63.6	123	2	Q7MKK4_VIBVU	Q7mkk4 vibrio vuln	938	28	63.6	234	2	Q7MPES_VIBVU	Q7mps vibrio vuln
866	28	63.6	123	2	Q6BAAS_CHICK	Q6baas gallus gall	939	28	63.6	235	2	Q8XNY8_CLOPE	Q8xny8 clostridium
867	28	63.6	124	2	Q5TWS1_ANOGA	Q5tws1 anopheles g	940	28	63.6	240	2	Q4USG0_XANCP	Q4usg0 xanthomonas
868	28	63.6	127	2	Q9EVA2_BACCE	Q9eva2 bacillus ce	941	28	63.6	240	2	Q5HIQ9_XANCP	Q5hiq9 xanthomonas
869	28	63.6	130	2	Q6WC55_9ARAC	Q6wec55 orthrus bic	942	28	63.6	240	2	Q8PB49_XANCP	Q8pb49 xanthomonas
870	28	63.6	130	2	Q8NU40_CORGL	Q8nu40 corynebacte	943	28	63.6	240	2	Q8PMU7_XANAC	Q8pmu7 xanthomonas
871	28	63.6	133	2	Q8BQBE_MOUSE	Q8bqbe mus musculu	944	28	63.6	242	2	Q87SX1_VIBPA	Q87sx1 vibrio para
872	28	63.6	137	2	Q800P3_ONCKI	Q800p3 oncorhynch	945	28	63.6	243	2	Q8HDA8_9CHLO	Q8hda8 pteromonas
873	28	63.6	142	2	Q6HNB9_BACHK	Q6hnb9 bacillus th	946	28	63.6	245	2	Q6CJ56_KJULIA	Q6cj56 kluyveromyc
874	28	63.6	142	2	Q6HNB9_BACHK	Q6hnb9 bacillus th	947	28	63.6	245	2	Q4NME4_9MICC	Q4nme4 arthrobacte
875	28	63.6	142	2	Q61V08_BACAN	Q61v08 bacillus an	948	28	63.6	249	2	Q5P874_AZOSE	Q5p874 azoarcus ap
876	28	63.6	143	2	Q63F09_BACCC	Q63f09 bacillus ce	949	28	63.6	250	2	Q88615_MERUN	Q88615 meriones un
877	28	63.6	143	2	Q05849_MYCTU	Q05849 mycobacteri	950	28	63.6	256	2	Q8WV22_HUMAN	Q8wv22 homo sapien
878	28	63.6	145	2	Q8WND8_RABIT	Q8wnd8 corynebacte	951	28	63.6	256	2	Q6V1P1_9ACTO	Q6v1p1 streptomyce
879	28	63.6	145	2	Q4FM34_9RICK	Q4fm34 candidatus	952	28	63.6	258	2	Q7PMJ3_ANOGA	Q7pmj3 anopheles g
880	28	63.6	147	2	Q9P049_HUMAN	Q9p049 homo sapien	953	28	63.6	261	2	Q7MGF6_VIBVY	Q7mgf6 vibrio vuln
881	28	63.6	147	2	Q6GZ72_HUMAN	Q6gz72 homo sapien	954	28	63.6	266	2	Q5RAZ5_PONPY	Q5raz5 pongo pygma
882	28	63.6	147	2	Q6M8P5_CORGL	Q6m8p5 corynebacte	955	28	63.6	266	2	Q9D720_MOUSE	Q9d720 mus muscu
883	28	63.6	148	2	Q4FRP4_9GAMM	Q4frf4 psychrobact	956	28	63.6	268	1	PLSC_MYCGE	Q4y8b2 plasmodium
884	28	63.6	149	2	Q8HT29_9BRYO	Q8ht29 neodolichom	957	28	63.6	268	1	Q4WYF3_ASPPU	Q4wyf3 aspergillus
885	28	63.6	149	2	Q67234_AQUAE	Q67234 aquifex aeo	958	28	63.6	269	2	Q8TK64_METAC	Q8tk64 methanosarc
886	28	63.6	150	2	Q4PMT2_IXOSC	Q4pmt2 ixodes scap	959	28	63.6	271	2	Q5ZCQ9_ORYSA	Q5zcg9 oryza sativ
887	28	63.6	150	2	Q8HT26_9BRYO	Q8ht26 calliargone	960	28	63.6	271	2	Q9ABS8_CAUCR	Q9abs8 caulobacter
888	28	63.6	150	2	Q8HT36_9BRYO	Q8ht36 hypanum tris	961	28	63.6	271	2	Q9SMS6_GROTH	Q9sms6 arabidopsis
889	28	63.6	150	2	Q8HT41_9BRYO	Q8ht41 pylaisia po	962	28	63.6	275	2	Q5L2U8_GEOKA	Q5l2u8 geobacillus
890	28	63.6	150	2	Q609B8_METCA	Q609b8 methylococc	963	28	63.6	276	2	Q74HX5_LACJO	Q74hx5 lactobacill
891	28	63.6	151	2	Q8HT38_9BRYO	Q8ht38 isopterygiu	964	28	63.6	278	2	Q5LUZ1_SILPO	Q5lu21 silicibacte
892	28	63.6	152	2	Q8HT50_9BRYO	Q8ht50 bartramia p	965	28	63.6	279	2	Q8CCH5_MOUSE	Q8cch5 mus musculu
893	28	63.6	155	2	Q9UTN8_SCHFO	Q9utn8 schizosacch	966	28	63.6	280	2	Q5PLS3_AZOSE	Q5pls3 azoarcus sp
894	28	63.6	155	2	Q9TNK2_ANTPU	Q9tnk2 anthoceros	967	28	63.6	280	2	Q8K2B4_MOUSE	Q8k2b4 mus musculu
895	28	63.6	156	2	Q8HT45_9BRYO	Q8ht45 stereophyll	968	28	63.6	280	2	Q9CY20_MOUSE	Q9cy20 mus muscu
896	28	63.6	157	2	Q8HT43_9BRYO	Q8ht43 pylaisia in	969	28	63.6	280	2	ARLY_THENE	Q924g3 thermotoga
897	28	63.6	160	2	Q9UNM7_HUMAN	Q9unm7 homo sapien	970	28	63.6	284	2	Q948P9_HEVBR	Q948p9 hevea bras
898	28	63.6	161	2	Q5XVY4_FUNHE	Q5xv4 fundulus he	971	28	63.6	285	2	Q6VFD3_ANOGA	Q6vfd3 anopheles g
899	28	63.6	163	2	Q8KPUE_SYNPF	Q8kpue synechococ	972	28	63.6	285	2	Q7VMF3_HAEUD	Q7vmf3 haemophilus
900	28	63.6	165	2	Q8BPM8_MOUSE	Q8bpm8 mus musculu	973	28	63.6	288	2	Q7KM16_DROME	Q7km16 drosophila
901	28	63.6	166	2	Q7U5Y6_SYNXP	Q7u5y6 synechococ	974	28	63.6	288	2	Q703K0_BURTH	Q703k0 burkholderi
902	28	63.6	168	2	Q9TNK8_COLNI	Q9tnk8 coleochaete	975	28	63.6	288	2	Q75CF5_ASHGO	Q75cf5 ashbya gos
903	28	63.6	169	2	Q8GT23_9CHLO	Q8gt23 chloromonas	976	28	63.6	289	2	Q88BW8_PSEPK	Q88bw8 pseudomonas
904	28	63.6	169	2	Q8HVA9_9CHLO	Q8hav9 chloromonas	977	28	63.6	289	2	Q8LSZ6_HEVBR	Q8lsz6 hevea bras
905	28	63.6	169	2	Q9TNL3_PHYPA	Q9tnl3 phycomitre	978	28	63.6	290	2	Q8L5H1_HEVBR	Q8l5h1 hevea bras
906	28	63.6	170	2	Q9MOQ6_ARATH	Q9moq6 arabidopsis	979	28	63.6	290	2	Q8L5H1_HEVBR	Q8l5h1 hevea bras
907	28	63.6	173	2	Q9CCH6_MYCLE	Q9cch6 mycobacteri	980	28	63.6	290	2		



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981 28 63.6 290 2 Q8L5B7 HEVBR
982 28 63.6 290 2 Q8L3V1 HEVBR
983 28 63.6 290 2 Q5Q1V2 HEVBR
984 28 63.6 290 2 Q5BMV4 HEVBR
985 28 63.6 290 2 Q74BY0 GEOSL
986 28 63.6 295 2 Q81QP8 BACAN
987 28 63.6 295 2 Q6HJ03 BACHK
988 28 63.6 295 2 Q63BJ6 BACCZ
989 28 63.6 296 2 Q6DGM3 BRACHYDANIO
990 28 63.6 297 2 Q61VP6 CAENOTHABDI
991 28 63.6 297 2 Q4MU44 BACCCE
992 28 63.6 297 2 Q738J3 BACC1
993 28 63.6 297 2 Q81DQ1 BACC1
994 28 63.6 298 2 Q6B8M5 GRATL
995 28 63.6 299 2 Q7U3H4 SYNFX
996 28 63.6 303 2 Q5VR40 ORYSA
997 28 63.6 305 2 Q87967 STREPTOMYCE
998 28 63.6 305 2 Q5WDY2 BACSK
999 28 63.6 308 2 Q8ZAL0 YERPE
1000 28 63.6 308 2 Q8XRG7 RALSONIA S

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## ALIGNMENTS

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RESULT 1
Q8PYR9 METMA PRELIMINARY; PRT; 75 AA.
AC Q8PYR9;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein MM0791.
GN OrderedLocustNames=MM0791;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
RC MEDLINE=22120827; PubMed=12125824;
RA Depkenmeier U., Johann A., Hartsch T., Merkl R.C., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wietzer A., Baumecke M., Steckel S.,
RA Bruggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013304; AAM30487.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 75 AA; 9035 MW; 695543A5C06F505D CRC64;

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Query Match 84.1%; Score 37; DB 2; Length 75;
Best Local Similarity 87.5%; Pred. No. 5.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FLQLLMEP 8
    |||||
Db 40 FLQLLLEP 47

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RESULT 2
Q85X02 PINKO PRELIMINARY; PRT; 47 AA.
AC Q85X02;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ORF47d.
OS Pinus koraiensis (Korean pine).
OG Chloroplast.

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus; Strobilus.
OX NCBI_TaxID=88728;
[1]
RN NUCLEOTIDE SEQUENCE.
RA Noh B.W., Lee J.S., Choi Y.I., Han M.S., Yi Y.S., Han S.U.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY228468; AA074065.1; -; Genomic_DNA.
DR GO; GO:0009507; Chloroplast; IEA.
SQ SEQUENCE 47 AA; 5510 MW; B72C7950F3876DCD CRC64;

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Query Match 79.5%; Score 35; DB 2; Length 47;
Best Local Similarity 87.5%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 FLQLLMEP 8
    |||||
Db 25 FLQLLLEP 32

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RESULT 3
Q8SQ02 CANFA PRELIMINARY; PRT; 329 AA.
AC Q8SQ02;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Pregnane X receptor (Fragment).
GN Name=PX;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21977871; PubMed=11981033; DOI=10.1210/me.16.5.977;
RX Moore L.B., Megllich J.M., McKee D.D., Wisely B., Willson T.M.,
RA Klierer S.A., Lambert M.H., Moore J.T.;
RT "Pregnane X receptor (PXR), constitutive androstane receptor (CAR),
RT and benzoate X receptor (BXR) define three pharmacologically distinct
RT classes of nuclear receptors.";
RL Mol. Endocrinol. 16:977-986(2002).
DR EMBL; AF454670; AAM10632.1; -; mRNA.
DR HSSP; O75469; INRL.
DR SMR; Q8SQ02; 37-327.
DR Ensembl; ENSCAG0000011094; Canis familiaris.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000536; Hrmn recept lig.
DR InterPro; IPR001723; Stdhrm receptor.
DR InterPro; IPR001728; ThyRH_receptor.
DR InterPro; IPR000324; VldR_receptor.
DR Pfam; PF00104; Hormone_recep; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00546; THYROIDHORMR.
DR PRINTS; PR00350; VITAMINDR.
DR SMART; SM00430; HOLI; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 329 AA; 37479 MW; 237F59C90C367474 CRC64;

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Query Match 79.5%; Score 35; DB 2; Length 329;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 FLQLLMEPV 9
    |||||
Db 210 FQQLLEPV 218

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RESULT 4
O03991 DAUCA PRELIMINARY; PRT; 379 AA.
AC O03991;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RAD23 protein, isoform II.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Apiales; Apiaceae; Scandiceae;
OC Daucinae; Daucus.
OX NCBI_TaxID=4039;
RN NCBI_TaxID=4039;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98345997; PubMed=9681019;
RA Sturm A., Leinhardt S.;
RT "Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.";
RL Plant J. 13:815-821(1998).
DR EMBL; Y12014; CAA72742.1; -; mRNA.
DR PIR; T14337; T14337.
DR HSP; P54725; IF41.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0006289; P:nucleotide-excision repair; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR006636; STI1.
DR InterPro; IPR000449; UBA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00627; UBA; 2.
DR PRINTS; PR01839; RAD23PROTEIN.
DR SMART; SM00727; STI1; 1.
DR SMART; SM00165; UBA; 2.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50030; UBA; 2.
DR PROSITE; PS50053; UBIQUITIN 2; 1.
SQ SEQUENCE 379 AA; 40530 MW; B26697B439CC5929 CRC64;

Query Match 79.5%; Score 35; DB 2; Length 379;
Best Local Similarity 77.8%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLMEPV 9
DB 302 FLOLINEPV 310
||||: |||

RESULT 5
Q4WZQ2 THEPA PRELIMINARY; PRT; 806 AA.
AC Q4WZQ2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TP03_0465;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5875;
RN NCBI_TaxID=5875;
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Muguga;
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,

Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
Venter J.C., Fraser C.M., Nene V.;
"Genome sequence of Theileria parva, a bovine pathogen that transforms lymphocytes";
Science 309:134-137(2005).
RN Science 309:134-137(2005).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAK0100005; EAN31209.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 806 AA; 92133 MW; B9DE773590FBF838 CRC64;

Query Match 79.5%; Score 35; DB 2; Length 806;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMEPV 9
DB 225 LQLLEPV 232
||||: |||

RESULT 6
Q4UBW5 THEAN PRELIMINARY; PRT; 846 AA.
AC Q4UBW5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TA04715;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN NCBI_TaxID=5874;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 3 genome sequence of Theileria annulata.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940352; CAI75686.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 846 AA; 98086 MW; 78F163492B5033FC CRC64;

Query Match 79.5%; Score 35; DB 2; Length 846;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLMEPV 9
DB 255 LQLLEPV 262
||||: |||

RESULT 7
Q4IUN8 GIBZE PRELIMINARY; PRT; 1060 AA.
AC Q4IUN8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG02570.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocymycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nubaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramaamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; RACM01000129; EAA68813.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1060 AA; 116785 MW; 589348AF6D66BF04 CRC64;

Query Match 79.5%; Score 35; DB 2; Length 1060;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLMEPV 9
Db 313 FVQLVLEPV 321
|:|:|:|:|

RESULT 8
RNHL CAEEL
ID Q8DNJ4 CAEEL STANDARD; PRT; 297 AA.
AC Q8DNJ4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ribonuclease H1 large subunit (EC 3.1.26.4) (RNase H1 large subunit)
DE (RNase H(35)).
GN Name=rnh-2; Synonyms=rnh2; ORFNames=TI3H5.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Feloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22300325; PubMed=12411600;
RA Arudchandran A.P., Carritelli S.M., Bowen N.J., Chen X., Krause M.W.,
RA Crouch R.J.;
RT "Multiple ribonuclease H-encoding genes in the Caenorhabditis elegans
RT genome contrasts with the two typical ribonuclease H-encoding genes in
RT the human genome.";
RL Mol. Biol. Evol. 19:1910-1919(2002).

[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Bristol N2; PubMed=9851916;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- FUNCTION: Degrades the ribonucleotide moiety on RNA-DNA hybrid
CC molecules. Participates in DNA replication (By similarity).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -!- SIMILARITY: Belongs to the RNase HII family. Eukaryotic subfamily.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF181619; RAF01208.1; -; mRNA.
CC EMBL; Z66524; CAC70103.1; -; Genomic_DNA.
CC HSSP; Q57599; 1RKE.
CC Ensembl; TI3H5.7; Caenorhabditis elegans.
CC WormBase; WBGene0004383; rnh-2.
CC WormPep; TI3H5.7; CE28960.
CC InterPro; IPR001352; RNase_HII/HIII.
CC InterPro; IPR012337; RNaseH_fold.
CC InterPro; IPR004649; RnhII.
CC PANTHER; PTHR10954; RNase_HII/HIII; 1.
CC Pfam; PF01351; RNase_HII; 1.
CC TIGRFAMs; TIGR00729; RnhII; 1.
KW Complete proteome; Endonuclease; Hydrolase; Nuclease.
FT ACT_SITE 27 27 By similarity.
FT ACT_SITE 138 138 By similarity.
FT ACT_SITE 166 166 By similarity.
SQ SEQUENCE 297 AA; 33191 MW; 233C11EDDA47B5B2 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 297;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLMEPV 9
Db 217 FLOLVEPV 225
|:|:|:|:|

RESULT 9
Q8DNJ4 STRR6
ID Q8DNJ4 STRR6 PRELIMINARY; PRT; 318 AA.
AC Q8DNJ4;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ABC transporter membrane-spanning permease-feric iron transport.
GN Name=fatC; OrderedLocNames=spr1685;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC BAA-255 / R6; PubMed=11544234;
RX MEDLINE=21429245; PubMed=19.5709-5717.2001;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Fu D.-J., Fuller W., Geringer C.,
RA DeHoff B.S., Estrem S.T., Fritz L., Kraft A.R., Lagace R.E.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAdams S.M., McHenry M., Mcleaster K., Mundy C.W., Niclas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,

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RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AE008534; AAL00488.1; -; Genomic_DNA.
DR PIR; C98082; C98082.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005222; FecD.
DR Pfam; PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 318 AA; 36296 MW; 9C1894E4F57C3210 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 318;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQQLMEPV 8
DB 152 FLQVLMDP 159

RESULT 10
Q97NY1_STRPN
ID Q97NY1_STRPN PRELIMINARY; PRT; 318 AA.
AC Q97NY1;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Iron-compound ABC transporter, permease protein.
GN OrderedLocNames=SPI870;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]

NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Unayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL; AE007478; AAK75942.1; -; Genomic_DNA.
DR PIR; E95218; E95218.
DR TIGR; SPI870; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000522; FecD.
DR Pfam; PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 318 AA; 36234 MW; 72BB0DC3DC0BFD13 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 318;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQQLMEPV 8
DB 152 FLQVLMDP 159

RESULT 11
Q8ESS7_OCEIH
ID Q8ESS7_OCEIH PRELIMINARY; PRT; 318 AA.

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AC Q8ESS7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferrichrome ABC transporter permease.
DE OrderedLocNames=OB0540;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]

NUCLEOTIDE SEQUENCE.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; HAC12496.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000522; FecD.
DR Pfam; PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 318 AA; 35775 MW; 3A53578580A52E71 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 318;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQQLMEPV 9
DB 150 FLQVLMDP 158

RESULT 12
Q5Z0B7_NOCFA
ID Q5Z0B7_NOCFA PRELIMINARY; PRT; 357 AA.
AC Q5Z0B7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative esterase.
GN OrderedLocNames=nfal2790;
OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]

NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD56124.1; -; Genomic_DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000379; Ser_estr.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 357 AA; 37664 MW; 9ED5372BD38E516E CRC64;

Query Match 77.3%; Score 34; DB 2; Length 357;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQQLMEPV 9
DB 224 FLQVLMDP 232

RESULT 13

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Q8AVC6 XENLA  
 ID Q8AVC6\_XENLA PRELIMINARY; PRT; 471 AA.  
 AC Q8AVC6;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE MGS2635 protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 TX TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC041717; AAH41717.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005215; F:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR011701; MFS\_1.  
 DR Pfam; PF07690; MFS 1; 1.  
 DR PROSITE; PS50850; MFS; 1.  
 SQ SEQUENCE 471 AA; 51058 MW; 1504C5B99AA70B01 CRC64;  
 Query Match 77.3%; Score 34; DB 2; Length 471;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLQLLMEPV 9  
 DB 121 FLQLLVNPI 129  
 RESULT 14  
 Q5JM56 ORYSA  
 ID Q5JM56\_ORYSA PRELIMINARY; PRT; 628 AA.  
 AC Q5JM56;

DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
 DE Copi protein-like.  
 GN Name=P0042A10.14;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaeae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
 RA Okamoto M., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
 RA Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Zhong H., Iwana H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
 RA Yano M., Jiang J., Gojobori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
 DR EMBL; AP003343; BAD87451.1; -; Genomic\_DNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004672; F:protein kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR Pfam; PF00400; WD40; 3.  
 DR PRINTS; PR00320; GPROTEINBRPT.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000018; WD40; 1.  
 DR SMART; SM00320; WD40; 3.  
 DR PROSITE; PS0011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 1.  
 DR PROSITE; PS0082; WD\_REPEATS\_2; 1.  
 DR PROSITE; PS00294; WD\_REPEATS\_REGION; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding; Repeat; Transferase;  
 WD repeat.  
 SQ SEQUENCE 628 AA; 69231 MW; F851CE723C4B4405 CRC64;  
 Query Match 77.3%; Score 34; DB 2; Length 628;  
 Best Local Similarity 77.8%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FLQLLMEPV 9  
 DB 237 FCQLLMHPV 245  
 RESULT 15  
 Q9NIH0 STYMT  
 ID Q9NIH0\_STYMT PRELIMINARY; PRT; 760 AA.  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Elongation factor 2 (Fragment).  
 GN Name=EF2;  
 OS Stylonychia mytilus.  
 OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;  
 OC Stichotrichida; Oxytrichidae; Stylonychia.  
 OX NCBI\_TaxID=5950;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20269356; PubMed=10811219; DOI=10.1038/35011054;

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RA Moreira D., Le Guyader H., Phillippe H.;
RT "The origin of red algae and the evolution of chloroplasts.";
RL Nucleotide sequence; AF213664; AAF711707.1; -; Genomic_DNA.
DR HSPB; P32324; INOV.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003746; P:translation elongation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000795; ProtSyn.GTPbind.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNCT.
DR TIGRfams; TIGR00231; small_GTP; 1.
DR PROSITE; PS00301; EFACTOR_GTP; 1.
KW Elongation factor; GTP-binding; Nucleotide-binding;
KW Protein biosynthesis.
FT NON_TER 1 1
FT SEQUENCE 760 760
SQ SEQUENCE 760 AA; 84711 MW; 6CD14EE3F1E6590D CRC64;

Query Match 77.3%; Score 34; DB 2; Length 760;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9
DB 237 FVQFIMEPI 245

RESULT 16
Q4RZ21.TETNG
ID Q4RZ21.TETNG PRELIMINARY; PRT; 1070 AA.
AC Q4RZ21;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 16 SCAF14974, whole genome shotgun sequence.
OS Tetraodon lineatus.
GN Tetraodon lineatus (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaut S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bremond C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier C., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier P., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAEE01014974; CAG06361.1; -; Genomic_DNA.
FT NON_TER 1 1
FT SEQUENCE 1070 1070
SQ SEQUENCE 1070 AA; 118772 MW; 8EAC61F6D1D37511B CRC64;

Query Match 77.3%; Score 34; DB 2; Length 1070;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLQLMEPV 9
DB 623 FVELLMKPV 631

RESULT 17
Q520T5.MAGGR
ID Q520T5.MAGGR PRELIMINARY; PRT; 1073 AA.
AC Q520T5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Magnaporthe oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshstein B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseelis M., Karlsson E.,
RA Kellis C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Maraballa R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Meneus L.,
RA Mesirov J., Mhalev A., Mihova T., Mikkelson T., Mieng V., Moru K.,
RA Mozes J., Mulran L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osmann S., Parker S., Perrin D., Phunkhang P., Piquani B.,
RA Purcell S., Rachupka T., Ramasamy U., Raneau R., Ray V., Raymond C.,
RA Retka R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov N., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-Thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tensing P., Tsafaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towse S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe oryzae.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=70-15;
RA	Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RA	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RL	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=70-15;
RA	Zhu H., Blackmon B.;
RA	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RL	-1- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC	preliminary data.
CC	-1- FUNCTION: This protein promotes the GTP-dependent translocation of
CC	the nascent protein chain from the A-site to the P-site of the
CC	ribosome (By similarity).
CC	-1- SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
CC	chain (By similarity).
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR	EMBL; AACU01000806; EAA52573.1; -; Genomic_DNA.
DR	InterPro; IPR000640; EFG_C.
DR	InterPro; IPR004161; EFTU_D2.
DR	InterPro; IPR000795; ProtSyn_GTP_bd.
DR	Pfam; PF00679; EFG_C; 1.
DR	Pfam; PF00009; GTP_EFTU; 1.
DR	Pfam; PF03144; GTP_EFTU_D2; 1.
DR	PRINTS; PR00315; ELONGATNFCT.
KW	GTP-binding; Hypothetical protein; Initiation factor;
KW	Nucleotide-binding; Protein biosynthesis.
SQ	SEQUENCE 1073 AA; 116727 MW; BE92CD85766768A3 CRC64;
	Query Match 77.3%; Score 34; DB 2; Length 1073;
	Best Local Similarity 55.6%; Pred. No. 4.2e+02;
	Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy	1 FLQLMEPV 9
	: : : :
Db	313 FVQLVLEPI 321
RESULT 18	
ID	Q7SB63_NEUCR PRELIMINARY; PRT; 1083 AA.
AC	Q7SB63;
DT	01-MAR-2004 (TrEMBLrel. 26, Created)
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein.
OS	Name=NCU06278.1;
GN	Neurospora crassa.
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX	NCBI_TaxId=5141;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=OR74E;
RA	Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA	Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA	Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA	Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA	Selittrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA	Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA	Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA	Kamal M., Kamyselis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA	Krystofova S., Rasmussen C., Metzenberg R.B., Perkins D.D., Kroken S.,
RA	Cogoni C., Macino G., Catshide D., Li W., Pratt R.J., Osmani S.A.,
RA	DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA	Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA	Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA	Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT	"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL	Nature 0:0-0(2003).
CC	-1- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.  
RA MEDLINE=98338066; PubMed=9673349;  
RA Schwirzke M., Gnirke A., Bork P., Tarin D., Weidle U.H.;  
RT "Differential gene expression in mammary carcinoma cell lines:  
RT identification of DRIM, a new gene down-regulated in metastasis.";  
RT Anticancer Res. 18:1409-1421(1998).  
RN [2]  
RN NUCLEOTIDE SEQUENCE [MRNA] OF 1883-2785.  
RA Ke Y., Hagiwara K., Zhao H., Ning T., Su X.L., Mcmenamin H., Lu G.R.,  
RA Wang B., Harris C.C.;  
RT "Key-1A6.";  
RN [3]  
RN SUBMITTED (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN IDENTIFICATION BY MASS SPECTROMETRY, AND SUBCELLULAR LOCATION.  
RP MEDLINE=21650333; PubMed=11790298; DOI=10.1016/S0960-9822(01)00650-9;  
RA Andersen J.S., Lyon C.E., Fox A.H., Leung A.K.L., Lam Y.W., Steen H.,  
RA Mann M., Lamond A.I.;  
RT "Directed proteomic analysis of the human nucleolus.";  
RN [4]  
RN Curr. Biol. 12:11-11(2002).  
RN [5]  
RN PHOSPHORYLATION SITES THR-1741 AND SER-2637.  
RP PubMed=15302935; DOI=10.1073/pnas.0404720101;  
RA Beauvoile S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,  
RA Li J., Cohn M.A., Cantley L.C., Gygi S.P.;  
RT "Large-scale characterization of HeLa cell nuclear phosphoproteins.";  
RA Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).  
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolus.  
CC -1- TISSUE SPECIFICITY: Expressed in appendix, brain, colon, fetal  
CC liver, heart, ovary, pancreas, placenta, prostate, skeletal  
CC muscle, small intestine, spleen, testis and thymus.  
CC -1- SIMILARITY: Contains 2 HEAT repeats.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; AJ006778; CAA07243.1; -; mRNA.  
DR EMBL; AF072718; AAG35208.1; ALT\_INIT; mRNA.  
DR SWISS-2DPAGE; O75691; HUMAN.  
DR Ensembl; ENSG00000120800; Homo sapiens.  
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
DR InterPro; IPR011989; ARM-like.  
DR InterPro; IPR011430; DRIM.  
DR InterPro; IPR000357; HEAT.  
DR Pfam; PF07539; DRIM; 1.  
DR Pfam; PF02985; HEAT; 1.  
DR PROSITE; PS50077; HEAT\_REPEAT; FALSE NEG.  
KW Coiled coil; Nuclear protein; Phosphorylation; Polymorphism; Repeat.  
FT REPEAT 165 202 HEAT 1.  
FT REPEAT 1841 1878 HEAT 2.  
FT COILED 2688 2765 Potential.  
FT COMPIAS 1319 1324 Poly-Lys.  
FT MOD\_RES 1741 1741 Phosphothreonine.  
FT MOD\_RES 2637 2637 Phosphoserine.  
FT VARIANT 502 502 S -> C (in dbSNP:4764643).  
FT VARIANT 2612 2612 E -> Q (in dbSNP:1061436).  
FT FTID=VAR 022162.  
FT FTID=VAR 022163.  
SQ SEQUENCE 2785 AA; 318426 MW; 6A2BBE9B2ADB983 CRC64;  
Query Match 77.3%; Score 34; DB 1; Length 2785;  
Best Local Similarity 77.8%; Pred. No. 1.1e+03;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FLOLLMEPV 9  
DB 1056 FLDLLPEPV 1064  
RESULT 21  
Q85FQ9 CYAME  
ID Q85FQ9 CYAME PRELIMINARY; PRT; 163 AA.  
AC Q85FQ9;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE ATP synthase CF1 delta chain.  
GN Name=atpD;  
OS Cyanidioschyzon merolae (Red alga).  
OG Chloroplast.  
OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;  
OC Cyanidioschyzon.  
OX NCBI\_TaxID=45157;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=102;  
RX MEDLINE=22539682; PubMed=12755171;  
RA Ohta N., Matsuzaki M., Misumi O., Miyagishima S.-Y., Nozaki H.,  
RA Tanaka K., Shin-i T., Kohara Y., Kuroiwa T.;  
RT "Complete sequence and analysis of the plastid genome of the  
RT unicellular red alga Cyanidioschyzon merolae.";  
RL DNA Res. 10:67-77(2003).  
DR EMBL; AB002583; BAC76286.1; -; Genomic DNA.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
DR GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.  
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.  
DR InterPro; IPR000711; ATPsynth\_OSCP.  
DR Pfam; PF00133; OSCP; 1.  
DR PRINTS; PR00125; ATPASEDELTA.  
DR TIGRFAMs; TIGR01145; ATP\_synt\_delta; 1.  
KW Chloroplast.  
SQ SEQUENCE 163 AA; 19233 MW; 448F2P9548FC51D1 CRC64;  
Query Match 75.0%; Score 33; DB 2; Length 163;  
Best Local Similarity 75.0%; Pred. No. 95;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLOLLMEPV 8  
DB 34 FMOQLMNP 41  
RESULT 22  
O87826 STAAU  
ID O87826 STAAU PRELIMINARY; PRT; 226 AA.  
AC O87826;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Membrane protein.  
GN Name=sstB;  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BB;  
RX MEDLINE=20249235; PubMed=10785640; DOI=10.1016/S0966-842X(00)01728-5;  
RA Modun B., Morrissey J.A., Williams P.;  
RT "The staphylococcal transferrin receptor: a glycolytic enzyme with  
RT novel functions.";  
RL Trends Microbiol. 8:231-237(2000).  
DR EMBL; AJ005352; CAA06498.1; -; Genomic DNA.

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DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000522; FecD.
DR Pfam; PF01032; FecCD; 1.
SQ SEQUENCE 226 AA; 25261 MW; 335430D799F5F18B CRC64;

Query Match 75.0%; Score 33; DB 2; Length 226;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLMPEP 8
Db 78 FQQLMPEP 85
|:|:|:|:|

RESULT 23
Q6IRDS5 RAT PRELIMINARY; PRT; 252 AA.
AC Q6IRDS5_2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE LOC298012 protein (Fragment).
GN Name=LOC298012;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070960; AAH70960.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0006289; P:nucleotide-excision repair; IEA.
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR006636; STI1.
DR InterPro; IPR000449; UBA.
DR Pfam; PF00627; UBA; 2.
DR PRINTS; PR01839; RAD23PROTEIN.
DR SMART; SM00727; STI1.1.
DR SMART; SM00165; UBA; 2.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS00303; UBA; 2.
FT NON TER 1
SQ SEQUENCE 252 AA; 26669 MW; F68AC957DD42445E CRC64;

Query Match 75.0%; Score 33; DB 2; Length 252;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLMPEV 9
Db 161 FQQLMPEV 169
|:|:|:|:|

RESULT 24
Q87GX1 VIBPA PRELIMINARY; PRT; 287 AA.
AC Q87GX1_2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE Hypothetical protein VPA1194.
GN OrderedLocusNames=VPA1194;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OC NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:K6.
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nijima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; BA000032; BAC62537.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 287 AA; 34348 MW; 36799EAB97630E6 CRC64;

Query Match 75.0%; Score 33; DB 2; Length 287;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLMPEP 8
Db 226 FQQLMPEP 233
|:|:|:|:|

RESULT 25
Q7NGE4 GLOVI PRELIMINARY; PRT; 295 AA.
AC Q7NGE4_2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE G113227 protein.
GN OrderedLocusNames=g113227;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacteriales; Gloeobacter.
OC NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpō S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
DR EMBL; BA000045; BAC91168.1; -; Genomic DNA.
DR HSSP; P27292; IDSJ.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.

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DR GO: 0006355; P: regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003313; AraC bd.  
 DR InterPro: IPR012287; Homeodomain-rel.  
 DR InterPro: IPR000005; HTHARAC.  
 DR Pfam: PF00165; HTH\_AraC; 2.  
 DR PRINTS: PR00032; HTHARAC  
 DR PROSITE: PS00041; HTH\_ARAC\_FAMILY\_1; 2.  
 DR PROSITE: PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
 KW Activator; Complete proteome; DNA-binding; Transcription;  
 KW Transcription regulation.  
 SQ SEQUENCE 295 AA; 33473 MW; 77E3D14A5FB3B337 CRC64;  
 Query Match 75.0%; Score 33; DB 2; Length 295;  
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLQLLMEPV 9  
 Db 103 FLQLYLEPM 111  
 RESULT 26  
 Q5HQZ5 STAEQ  
 ID Q5HQZ5 STAEQ PRELIMINARY; PRT; 317 AA.  
 AC Q5HQZ5;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Iron compound ABC transporter, permease protein.  
 DE OrderedLocNames=SERP0401;  
 GN Staphylococcus epidermidis (strain ATCC 35984 / RP62A).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=176279;  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]  
 RP PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;  
 RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,  
 RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,  
 RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,  
 RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,  
 RA Dmitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,  
 RA Hance I.R., Nelson K.E., Fraser C.M.;  
 RT "Insights on evolution of virulence and resistance from the complete  
 RT genome analysis of an early methicillin-resistant Staphylococcus  
 RT aureus strain and a biofilm-producing methicillin-resistant  
 RT Staphylococcus epidermidis strain."  
 RL J. Bacteriol. 187:2426-2438(2005).  
 DR EMBL: CP000029; AAWS3790.1; -; Genomic\_DNA.  
 DR TIGR: SERP0401; -;  
 DR GO: 0005215; F: transporter activity; IEA.  
 DR GO: 0005215; F: transporter; IEA.  
 DR GO: 0006810; P: transport; IEA.  
 DR InterPro: IPR000522; FecD.  
 DR Pfam: PF01032; FecCD; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 317 AA; 35630 MW; 11481D8D1A31083F CRC64;  
 Query Match 75.0%; Score 33; DB 2; Length 317;  
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLQLLMEP 8  
 Db 150 FLQLINWP 157  
 RESULT 27  
 Q6GB96 STAA  
 ID Q6GB96 STAA PRELIMINARY; PRT; 318 AA.  
 AC Q6GB96;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE FecD transport family protein.  
 GN OrderedLocNames=SAS0699;  
 OS Staphylococcus aureus (strain MSSA476).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=282459;  
 RN NUCLEOTIDE SEQUENCE.  
 RP PubMed=15213324; DOI=10.1073/pnas.0402521101;  
 RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,  
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,  
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,  
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,  
 RA Feitwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,  
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,  
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,  
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,  
 RA Spratt B.G., Parkhill J.;  
 RT "Complete genomes of two clinical Staphylococcus aureus strains:  
 RT evidence for the rapid evolution of virulence and drug resistance.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).  
 DR EMBL: BX571857; CAG42475.1; -; Genomic\_DNA.  
 DR GO: 0016020; C: membrane; IEA.  
 DR GO: 0005215; F: transporter activity; IEA.  
 DR GO: 0006810; P: transport; IEA.  
 DR InterPro: IPR000522; FecD.  
 DR Pfam: PF01032; FecCD; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 318 AA; 35789 MW; 1B931B882739BE3B CRC64;  
 Query Match 75.0%; Score 33; DB 2; Length 318;  
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLQLLMEP 8  
 Db 151 FLQLIMDP 158  
 RESULT 28  
 Q6GIQ7 STAA  
 ID Q6GIQ7 STAA PRELIMINARY; PRT; 318 AA.  
 AC Q6GIQ7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE FecD transport family protein.  
 GN Name=stB; OrderedLocNames=SAR0788;  
 OS Staphylococcus aureus (strain MRSA252).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=282458;  
 RN NUCLEOTIDE SEQUENCE.  
 RP PubMed=15213324; DOI=10.1073/pnas.0402521101;  
 RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,  
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,  
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,  
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,  
 RA Feitwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,  
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,  
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,  
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,  
 RA Spratt B.G., Parkhill J.;  
 RT "Complete genomes of two clinical Staphylococcus aureus strains:  
 RT evidence for the rapid evolution of virulence and drug resistance.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).  
 DR EMBL: BX571856; CAG39798.1; -; Genomic\_DNA.  
 DR GO: 0016020; C: membrane; IEA.  
 DR GO: 0005215; F: transporter activity; IEA.  
 DR GO: 0006810; P: transport; IEA.  
 DR InterPro: IPR000522; FecD.  
 DR Pfam: PF01032; FecCD; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 318 AA; 35831 MW; C1B5A3BF19728ED6 CRC64;

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Query Match          75.0%; Score 33; DB 2; Length 318;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQIQLMEP 8
Db 151 FQIQLMDP 158

RESULT 29
QSHHT6 STAAAC
ID Q5HHT6_STAAC PRELIMINARY; PRT; 318 AA.
AC Q5HHT6_
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Iron compound ABC transporter, permease protein.
GN OrderedLocusNames=SACOL0797;
OS Staphylococcus aureus (strain COL)
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Uterback T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RA "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
DR EMBL; CP000046; AAW37852.1; -; Genomic_DNA.
DR TIGR; SACOL0797; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000522; FecD.
DR Pfam; PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 318 AA; 35777 MW; 21ACE8A20E39BE21 CRC64;

Query Match          75.0%; Score 33; DB 2; Length 318;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQIQLMEP 8
Db 151 FQIQLMDP 158

RESULT 30
Q7A6S9 STAAAC
ID Q7A6S9_STAAN PRELIMINARY; PRT; 318 AA.
AC Q7A6S9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SA0689 protein.
GN OrderedLocusNames=SA0689;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

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RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Ogasawara A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Yagashita N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000018; BAB41922.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000522; FecD.
DR Pfam; PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 318 AA; 35777 MW; 21ACE8A20E39BE21 CRC64;

Query Match          75.0%; Score 33; DB 2; Length 318;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQIQLMEP 8
Db 151 FQIQLMDP 158

RESULT 31
Q8NXM9 STAAAC
ID Q8NXM9_STAAM PRELIMINARY; PRT; 318 AA.
AC Q8NXM9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 25, Last annotation update)
DE MW0696 protein.
GN OrderedLocusNames=MM0696;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; BA000033; BAB94561.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000522; FecD.
DR Pfam; PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 318 AA; 35789 MW; 1B931B882739BE3B CRC64;

Query Match          75.0%; Score 33; DB 2; Length 318;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQIQLMEP 8
Db 151 FQIQLMDP 158

RESULT 32
Q99VP0 STAAAC
ID Q99VP0_STAAM PRELIMINARY; PRT; 318 AA.
AC Q99VP0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to ferrichrome ABC transporter permease.
GN OrderedLocusNames=SAV0734;

```

OS Staphylococcus aureus (strain Mu50 / ATCC 700699).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

NCBI\_TaxID=158878;  
 [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]  
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;  
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,  
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,  
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,  
 RA Kanehisa M., Yamashita A., Ohnita K., Furuya K., Yoshino C., Shiba T.,  
 RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;  
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
 RT aureus";

RL Lancet 357:1225-1240(2001).

DR EMBL; BA000017; BAB56896.1; -; Genomic\_DNA.

DR PIR; G89845; G89845.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR000522; FecD.

DR Pfam; PF01032; FecCD; 1.

KW Complete proteome.

SQ SEQUENCE 318 AA; 35777 MW; 21ACE8A20E39BE21 CRC64;

Query Match 75.0%; Score 33; DB 2; Length 318;

Best Local Similarity 62.5%; Pred. No. 1.9e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLMPEP 8

||:|:|:|

Db 151 FLOLMIMP 158

RESULT 33

Q4L4F7\_STAHP

ID Q4L4F7\_STAHP PRELIMINARY; PRT; 319 AA.

AC Q4L4F7;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Similar to ferrichrome ABC transporter permease.

GN ORFNames=SH2159;

OS Staphylococcus haemolyticus (strain JCS1435).

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

NCBI\_TaxID=279808;

[1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=JCS1435;

RA Takeuchi F., Watanabe S., Baba T., Yuzawa H., Ito T., Cui L.,

RA Morimoto Y., Kuroda M., Takahashi M., Anka A., Baba S., Fukui S.,

RA Lee J.C., Hiramoto K.;

RT "Whole genome sequencing of Staphylococcus haemolyticus uncovers

RT extreme plasticity of its genome and dynamism in the evolution of

RT human-colonizing staphylococcal species";

RT Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP006716; BAE05468.1; -; Genomic DNA.

SQ SEQUENCE 319 AA; 35555 MW; 4A296179F63A12DA CRC64;

Query Match 75.0%; Score 33; DB 2; Length 319;

Best Local Similarity 62.5%; Pred. No. 1.9e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLOLMPEP 8

||:|:|:|

Db 152 FLOLMIMP 159

RESULT 34

Q8CFZ9\_STAEP

ID Q8CFZ9\_STAEP PRELIMINARY; PRT; 319 AA.

AC Q8CFZ9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Ferrichrome ABC transporter permease.

GN OrderedLocusNames=SE0516;

OS Staphylococcus epidermidis.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

NCBI\_TaxID=1282;

[1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=ATCC 12228;

RX PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;

RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;

RT "Genome-based analysis of virulence genes in a non-biofilm-forming

RT Staphylococcus epidermidis strain (ATCC 12228).";

RL Mol. Microbiol. 49:1577-1593(2003).

DR EMBL; AS016745; AAC04113.1; -; Genomic\_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR000522; FecD.

DR Pfam; PF01032; FecCD; 1.

KW Complete proteome.

SQ SEQUENCE 319 AA; 35889 MW; 2C4EDA99D1CA4F88 CRC64;

Query Match 75.0%; Score 33; DB 2; Length 319;

Best Local Similarity 75.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLMPEP 8

||:|:|:|

Db 152 FLOLMIMP 159

RESULT 35

Q4T7D6\_TETNG

ID Q4T7D6\_TETNG PRELIMINARY; PRT; 320 AA.

AC Q4T7D6;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Chromosome undetermined SCF8128, whole genome shotgun sequence.

GN ORFNames=GSTENG0005778001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

NCBI\_TaxID=99883;

[1]

RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Nicada S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,

RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,

RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,

RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;

RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

RT the early vertebrate proto-karyotype.";

RL Nature 431:946-957(2004).

[2]

RP NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAE01008128; CAF91196.1; -; Genomic\_DNA.  
FT NON\_TER 320 320  
SQ SEQUENCE 320 AA; 35069 MW; 1FB68A9932B5F94D CRC64;

Query Match 75.0%; Score 33; DB 2; Length 320;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
|:|:|  
Db 244 FIQMLNEPV 252

RESULT 36  
Q5CZ28 RAT PRELIMINARY; PRT; 333 AA.  
AC Q5CZ28;  
DT 10-MAY-2005 (TremBLrel. 30, Created)  
DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)  
DE LOC298012 protein (Fragment).  
GN Name=LOC298012;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RG NIH MGC Project;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC090351; RAH90351.1; -; mRNA.  
DR InterPro; IPR004806; Rad23.  
DR InterPro; IPR006636; STI1.  
DR Pfam; PF00627; UBA; 2.  
DR PRINTS; PR01839; RAD23PROTEIN.  
DR SMART; SM00165; UBA; 2.  
DR TIGRFAMs; TIGR00601; rad23; 1.  
DR PROSITE; PS50030; UBA; 2.  
SQ SEQUENCE 333 AA; 34314 MW; 6148C1434FB81A1 CRC64;

Query Match 75.0%; Score 33; DB 2; Length 333;

Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
|:|:|  
Db 242 FIQMLNEPV 250

RESULT 37  
Q7Z5K8 HUMAN PRELIMINARY; PRT; 337 AA.  
AC Q7Z5K8;  
DT 01-OCT-2003 (TremBLrel. 25, Created)  
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE RAD23-like protein B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RX PubMed=15064313;  
RA Huang X., Wang H., Xu M., Lu L., Xu Z., Li J., Zhou Z., Sha J.;  
RT "Expression of a Novel RAD23B mRNA Splice Variant in the Human  
Testis.";  
RL J. Androl. 25:363-368 (2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RA Sha J.H., Zhou Z.M., Li J.M.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY313777; AAP81008.1; -; mRNA.  
DR HSP; P54725; 1QZE.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0006289; P:nucleotide-excision repair; IEA.  
DR InterPro; IPR004806; Rad23.  
DR InterPro; IPR006636; STI1.  
DR Pfam; PF00627; UBA; 2.  
DR PRINTS; PR01839; RAD23PROTEIN.  
DR SMART; SM00727; STI1; 1.  
DR SMART; SM00165; UBA; 2.  
DR TIGRFAMs; TIGR00601; rad23; 1.  
DR PROSITE; PS50030; UBA; 2.  
SQ SEQUENCE 337 AA; 35033 MW; E9338A403D821FB8 CRC64;

Query Match 75.0%; Score 33; DB 2; Length 337;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLOLLMEPV 9  
|:|:|  
Db 252 FIQMLNEPV 260

RESULT 38  
RD23B ARATH STANDARD; PRT; 368 AA.  
AC Q84L32; Q9S9L8; Q9SA20;  
DT 01-FEB-2005 (Rel. 46, Created)  
DT 13-SEP-2005 (Rel. 48, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Putative DNA repair protein RAD23-2 (RAD23-like protein 2) (AtRAD23-2).  
GN Name=RAD23-2; Synonyms=RAD23; OrderedLocusNames=Atlg16190;  
GN ORFNames=FS09.1;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

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OX NCBI_TaxID=3702;
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RP TISSUE=Flower buds;
RA Ishikawa Y., Endo M., Abe K., Osakabe K., Nakajima N., Saji H.,
RA Ito Y., Ichikawa H., Kameya T., Toki S.;
RA "Isolation of four RAD23 genes from Arabidopsis thaliana and detection
RT of alternative splicing variants.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altairi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buchler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.B., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Xu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -!- FUNCTION: May be involved in nucleotide excision repair (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q84L32-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q84L32-2; Sequence=VSP_014979;
CC Note=May be due to a competing donor splice site. No
CC experimental confirmation available;
CC -!- SIMILARITY: Belongs to the RAD23 family.
CC -!- SIMILARITY: Contains 2 UBA domains.
CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -!- CAUTION: Ref.2 sequences differ from that shown due to erroneous
CC gene model prediction.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB109195; BAC76391.1; -; mRNA.
CC EMBL; AC006341; RAD34676.1; ALT_SEQ; Genomic DNA.
CC EMBL; AC010924; AAF18513.1; ALT_SEQ; Genomic DNA.
CC PIR; G86296; G86296.
CC PIR; H86296; H86296.
CC HSP; P54725; 11FY.
CC GeneFam; 4551; 453.
CC PROSITE; PS50030; UBA; 2.
CC PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
CC PROSITE; PS50053; UBIQUITIN_2; 1.
KW Alternative splicing; DNA damage; DNA repair; Nuclear protein; Repeat.
FT DOMAIN 1 77 Ubiquitin-like.
FT DOMAIN 142 185 UBA 1.
FT DOMAIN 320 360 UBA 2.
FT VARSPIC 20 21 Missing (in isoform 2).
FT /FTid=VSP_014979.
FT SEQUENCE 368 AA; 39842 MW; BPF4FE75E6C431F CRC64;
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Query Match 75.0%; Score 33; DB 1; Length 368;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 8
Db 289 FLQLMEPV 296

RESULT 39
Q6TLD0 BRARE
ID Q6TLD0 BRARE PRELIMINARY; PRT; 380 AA.
AC Q6TLD0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RAD23 homolog B.
GN Name=rad23b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney marrow;
RX PubMed=15520368; DOI=10.1073/pnas.0407241101;
RA Song H.-D., Sun X.-J., Dang M., Zhang G.-W., Zhou Y., Wu X.-Y.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.-L., Fan H.-Y., Zou L.-I.,
RA Kanki J.P., Liu T.X., Look A.T., Chen Z.;
RA "Hematopoietic gene expression profile in zebrafish kidney marrow.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:16240-16245(2004).
DR EMBL; AY394976; AAQ94603.1; -; mRNA.
DR HSP; O862M4; 1AAR.
DR ZFIN; ZDB-GENE-040426-1487; rad23b.
DR GO; GO:0005834; C:nucleus; IEA.
DR GO; GO:0006289; P:nucleotide-excision repair; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR006636; ST11.
DR InterPro; IPR000449; UBA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00627; UBA; 2.
DR Pfam; PF00240; ubiquitin; 1.
DR PRINTS; PR01839; RAD23PROTEIN.
DR SMART; SM00727; ST11; 1.
DR SMART; SM00165; UBA; 2.
DR SMART; SM00213; UBO; 1.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50030; UBA; 2.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 380 AA; 40107 MW; 5D05919718B28852 CRC64;

Query Match 75.0%; Score 33; DB 2; Length 380;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLQLMEPV 9
Db 300 FLQLMEPV 308

RESULT 40
Q6PHE9 BRARE
ID Q6PHE9 BRARE PRELIMINARY; PRT; 382 AA.
AC Q6PHE9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RAD23 homolog B.
GN Name=rad23b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton K., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Bosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Rohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RX Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 RA EMBL; BC056578; AAH56578.1; -; mRNA.  
 DR HSP; Q862M4; IAA.  
 DR ZFIN; ZDB-GENE-040426-1487; rad23b.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0006289; P:nucleotide-excision repair; IEA.  
 DR GO; GO:0006464; P:protein modification; IEA.  
 DR InterPro; IPR004806; Rad23.  
 DR InterPro; IPR006636; STIL.  
 DR InterPro; IPR000449; UBA.  
 DR InterPro; IPR000626; Ubiquitin.  
 DR Pfam; PF00627; UBA; 2.  
 DR Pfam; PF00240; ubiquitin; 1.  
 DR PRINTS; PR01839; RAD23PROTEIN.  
 DR SMART; SM00727; STIL; 1.  
 DR SMART; SM00165; UBA; 2.  
 DR SMART; SM00213; UBO; 1.  
 DR TIGRfams; TIGR00601; rad23; 1.  
 DR PROSITE; PS50030; UBA; 2.  
 DR PROSITE; PS50053; UBIQUITIN 2; 1.  
 SQ SEQUENCE 382 AA; 40308 MW; 7EBC3D165BEEBC88 CRC64;  
 Query Match 75.0%; Score 33; DB 2; Length 382;  
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLQQLMEPV 9  
 |:|:|:|  
 Db 302 FLQQLMEPV 310  
 RESULT 41  
 Q5AZM0 EMBI PRELIMINARY; PRT; 385 AA.  
 AC Q5AZM0;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DE Hypothetical protein.  
 GN ORFNames=AN6260.2;  
 OS Aspergillus nidulans FGSC A4.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eutotiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=227321;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FGSC A4;  
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,  
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,  
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,  
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,  
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,  
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,  
 RA Hagopian D., Hager S., Graham L., Grand-Pierre N., Hafez N.,  
 RA Gargyala N., Grosse B., Hall J., Horton L., Hulme W., Iliev I.,  
 RA Jaffe C., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
 RA Kellis D., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,  
 RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Meneus L.,  
 RA Mihoiva T., Mlenga T., Murphy T., Naylor J., Nguyen C., Nicol R.,  
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,  
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,  
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,  
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
 RA Lander E.;  
 RT "Genome Sequence of Aspergillus nidulans.";  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; RACD01000107; EAA58644.1; -; Genomic\_DNA.  
 DR Hypothetical protein.  
 KW SEQUENCE 385 AA; 42995 MW; D10ABCA78EAF057C CRC64;  
 Query Match 75.0%; Score 33; DB 2; Length 385;  
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FLQQLMEPV 8  
 |:|:|:|  
 Db 261 FLQQLMEPV 268  
 RESULT 42  
 RD23B HUMAN STANDARD; PRT; 409 AA.  
 ID RD23B HUMAN STANDARD; PRT; 409 AA.  
 AC P54727; Q8WUB0;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE UV excision repair protein RAD23 homolog B (hHR23B) (XP-C repair  
 complementing complex 58 kDa protein) (p58).  
 GN Name=RAD23B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
 RX MEDLINE=94222030; PubMed=8168482;  
 RA Masutani C., Sugawara K., Yanagisawa J., Sonoyama T., Ui M.,  
 RA Nomoto T., Takio K., Tanaka K., van der Spek P.J., Bootsma D.,  
 RA Hoeijmakers J.H.J., Hanaoka F.;  
 RT "Purification and cloning of a nucleotide excision repair complex  
 involving the Xeroderma pigmentosum group C protein and a human  
 homologue of yeast RAD23.";  
 RL EMBO J. 13:1831-1843(1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT VAL-249.  
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,

RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;  
RT "NIH-SNP", environmental genome project, NIH/ES15478, Department  
of Genome Sciences, Seattle, WA [URL: <http://egp.gs.washington.edu>].;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Ramsay H.;  
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RL [4]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT VAL-249.  
RC TISSUE=Uterus;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Involved in DNA excision repair. May play a part in DNA  
damage recognition and/or in altering chromatin structure to allow  
access by damage-processing enzymes.  
CC -1- SUBUNIT: Heterodimer of a 125 kDa subunit (p125) and of a 58 kDa  
subunit (p58). Interacts with MJD.  
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -1- DOMAIN: The ubiquitin-like domain mediates interaction with MJD.  
CC -1- SIMILARITY: Belongs to the RAD23 family.  
CC -1- SIMILARITY: Contains 2 UBA domains.  
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.  
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removed.  
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EMBL; D21090; BAA04652.1; -; mRNA.  
DR EMBL; AL137852; CAD13275.1; -; Genomic DNA.  
DR EMBL; AY165178; AAM47194.1; -; Genomic DNA.  
DR EMBL; BC020973; AAH20973.1; -; mRNA.  
DR PIR; S44346; S44346.  
DR PDB; 1PIA; NMR; A=1-82.  
DR PDB; 1PVE; NMR; A=275-342.  
DR PDB; 1UEI; NMR; A=1-87.  
DR OGP; P54727; -.  
DR Ensembl; ENSG00000119318; Homo sapiens.  
DR HGNC; HGNC:9813; RAD23B.  
DR H-InvDB; HIX0008261; -.  
DR Reactome; P54727; -.  
DR MIM; 600062; -.  
DR GO; GO:0005634; C:nucleus; TAS.  
DR GO; GO:0003697; F:single-stranded DNA binding; TAS.  
DR GO; GO:0006289; P:nucleotide-excision repair; TAS.  
DR InterPro; IPR004806; Rad23.  
DR InterPro; IPR006636; STIL\_HS\_bd.  
DR InterPro; IPR000449; UBA.  
DR InterPro; IPR000626; Ubiquitin.  
DR PANTHER; PTHR10621; Rad23; 1.  
PFam; PF00627; UBA; 2.

DR Pfam; PF00240; ubiquitin; 1.  
DR PRINTS; PRO1839; RAD23PROTEIN.  
DR SMART; SM00727; STI1; 1.  
DR SMART; SM00165; UBA; 2.  
DR SMART; SM00213; UBQ; 1.  
DR TIGRFAMs; TIGR00601; rad23; 1.  
DR PROSITE; PSS0030; UBA; 2.  
DR PROSITE; PSS00299; UBIQUITIN 1; FALSE\_NEG.  
DR PROSITE; PSS0053; UBIQUITIN 2; 1.  
KW 3D-structure; Direct protein sequencing; DNA damage; DNA repair;  
KW Nuclear protein; Polymorphism; Repeat.  
FT DOMAIN 1 79 Ubiquitin-like.  
FT DOMAIN 188 228 UBA 1.  
FT DOMAIN 364 404 UBA 2.  
FT COMPIAS 103 106 Poly-Thr.  
FT COMPIAS 254 260 Poly-Ala.  
FT COMPIAS 261 269 Poly-Thr.  
FT COMPIAS 336 348 Poly-Gly.  
FT VARIANT 249 249 A -> V (in dbSNP:1805329).  
FT /FTID=VAR\_014350.  
SQ SEQUENCE 409 AA; 43171 MW; C026C78273BCB289 CRC64;  
Query Match 75.0%; Score 33; DB 1; Length 409;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLQLMEPV 9  
|:|:|  
DB 324 FQMLNEPV 332  
|:|:|  
RESULT 43  
Q53F10 HUMAN  
ID Q53F10\_HUMAN PRELIMINARY; PRT; 409 AA.  
AC Q53F10; 2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE UV excision repair protein RAD23 homolog B variant (Fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Thymus;  
RA Maruyama K., Sugano S.;  
RT "Oligo-capping: a simple method to replace the cap structure of  
RT eucaryotic mRNAs with oligoribonucleotides.";  
RL Gene 138:171-174(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Thymus;  
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;  
RT "Construction and characterization of a full length-enriched and a 5'-  
RT end-enriched cDNA library.";  
RL Gene 200:149-156(1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Thymus;  
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK223479; BAD97199.1; -; mRNA.  
FT NON\_TER 1  
SQ SEQUENCE 409 AA; 43113 MW; 814E1D4C3E0AAC9A CRC64;  
Query Match 75.0%; Score 33; DB 2; Length 409;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FLQLMEPV 9  
|:|:|

Db 324 FIQMLNEPV 332

## RESULT 44

Q6NVC3 MOUSE PRELIMINARY; PRT; 415 AA.  
AC Q6NVC3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein LOC298012  
GN Name=Rad23b;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshitaki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC068193; AAH68193.1; -; mRNA.  
DR HSSP; Q862M4; 1AAR.  
DR GO; GO:0006974; P:response to DNA damage stimulus; IDA.  
DR GO; GO:0007283; P:spermatogenesis; IMP.  
DR InterPro; IPR004806; Rad23.  
DR InterPro; IPR006636; STIL.  
DR InterPro; IPR000626; Ubiquitin.  
DR Pfam; PF00627; UBA; 2.  
DR PRINTS; PF00240; ubiquitin; 1.  
DR SMART; SM00727; STI1; 1.  
DR SMART; SM00165; UBA; 2.  
DR TIGR; TIGR00601; rad23; 1.  
DR PROSITE; P55003; UBA; 2.  
DR PROSITE; P55003; UBQUITIN 2; 1.  
SQ SEQUENCE 415 AA; 43415 MW; 3C53336BC784786B CRC64;

Query Match 75.0%; Score 33; DB 2; Length 415;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIQMLNEPV 9

Db 323 FIQMLNEPV 331

## RESULT 45

Q4KMA2 RAT PRELIMINARY; PRT; 415 AA.  
AC Q4KMA2;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein LOC298012.  
GN Name=LOC298012;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshitaki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Heart;  
RG NIH MGC Project;  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC098674; AAH98674.1; -; mRNA.  
DR Hypothetical protein.  
SQ SEQUENCE 415 AA; 43497 MW; 221022C803418390 CRC64;

Query Match 75.0%; Score 33; DB 2; Length 415;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIQMLNEPV 9

Db 324 FIQMLNEPV 332

## RESULT 46

RD23B MOUSE  
ID RD23B MOUSE STANDARD; PRT; 416 AA.  
AC P54728;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE UV excision repair protein RAD23 homolog B (mHR23B) (XP-C repair  
complementing complex 58 kDa protein) (p58).  
GN Name=Rad23b; Synonyms=Mhr23b;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]



RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BALB/c; TISSUE=Testis; DOI=10.1006/geno.1996.0004;  
RX MEDLINE=96403997; PubMed=8808275; DOI=10.1073/pnas.242603899;  
RA van der Spek P.J., Visser C.E., Hanaoka F., Smit B., Hagemeijer A.,  
RA Bootsma D., Hoeijmakers J.H.J.;  
RT "Cloning, comparative mapping, and RNA expression of the mouse  
RT homologues of the Saccharomyces cerevisiae nucleotide excision repair  
RL gene RAD23.";  
RL Genomics 31:20-27(1996).  
RN [2]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RP STRAIN=FVB/N; TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -I- FUNCTION: Involved in DNA excision repair. May play a part in DNA  
CC damage recognition and/or in altering chromatin structure to allow  
CC access by damage-processing enzymes.  
CC -I- SUBUNIT: Heterodimer of a 125 kDa subunit (p125) and of a 58 kDa  
CC subunit (p58).  
CC -I- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -I- SIMILARITY: Belongs to the RAD23 family.  
CC -I- SIMILARITY: Contains 2 UBA domains.  
CC -I- SIMILARITY: Contains 1 ubiquitin-like domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; X92411; CAA63146.1; -; mRNA.  
CC EMBL; BC027747; AAH27747.1; -; mRNA.  
CC HSSP; P54725; IDV0.  
CC Ensemble; ENSMUSG0000028426; Mus musculus.  
CC MG1; MG1:105128; Rad23b.  
CC GO; GO:0006974; P:response to DNA damage stimulus; IDA.  
CC GO; GO:0007283; P:spermatogenesis; IMP.  
CC DR InterPro; IPR004806; Rad23  
CC DR InterPro; IPR006636; STI1\_HS\_bd.  
CC DR InterPro; IPR000449; UBA.  
CC DR InterPro; IPR000626; Ubiquitin.  
CC DR PANTHER; PTHR10621; Rad23; 1.  
CC DR Pfam; PF00627; UBA; 2.  
CC DR Pfam; PF00240; ubiquitin; 1.  
CC DR PRINTS; PR01839; RAD23PROTEIN.  
CC DR SMART; SM00727; STI1; 1.  
CC DR SMART; SM00165; UBA; 2.  
CC DR SMART; SM00213; UBO; 1.  
CC DR TIGRfam; TIGR00601; rad23; 1.  
CC DR PROSITE; PSS0030; UBA; 2.  
CC DR PROSITE; PSS0299; UBIQUITIN\_1; FALSE\_NEG.  
CC DR PROSITE; PSS0053; UBIQUITIN\_2; 1.  
CC DR DNA damage; DNA repair; Nuclear protein; Repeat.  
CC DOMAIN 1 79 Ubiquitin-like.

FT DOMAIN 188 228 UBA 1.  
FT DOMAIN 371 411 UBA 2.  
FT COMPBIAS 255 261 Poly-Ala.  
RA COMPBIAS 262 270 Poly-Thr.  
FT COMPBIAS 336 355 Poly-Gly.  
SQ SEQUENCE 416 AA; 43517 MW; 13E0245A6D982205 CRC64;  
  
Query Match 75.0%; Score 33; DB 1; Length 416;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 FLQQLMEPV 9  
DB 324 FLQQLMEPV 332  
|:|:|  
|:|:|  
  
RESULT 47  
Q6FU70\_CANGA PRELIMINARY; PRT; 435 AA.  
ID AC Q6FU70;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Similarities with tr|Q03983|Saccharomyces cerevisiae YDR179wa.  
GN OrderedLocusNames=CAGL0F05819g;  
OS Candida glabrata (Yeast) (Torulopsis glabrata).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5478;  
RN [1]  
RC STRAIN=ATCC 2001 / CBS 138;  
RX PubMed=15229592; DOI=10.1038/nature02579;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
RA Boisrame A., Boyer E., Cattolico L., Confanioleri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Niclaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.-L.;  
RL "Genome evolution in yeasts.";  
RL Nature 430:35-44(2004).  
RC EMBL; CR380952; CAG59148.1; -; Genomic\_DNA.  
KW Complete proteome.  
SQ SEQUENCE 435 AA; 50090 MW; 404285EE38181F47 CRC64;  
  
Query Match 75.0%; Score 33; DB 2; Length 435;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 FLQQLMEPV 9  
DB 418 FLQQLMEPI 426  
|:|:|  
|:|:|  
  
RESULT 48  
Q5BL82\_XENTR PRELIMINARY; PRT; 484 AA.  
ID AC Q5BL82;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus; Silurana.  
 OX NCBI\_TaxID=8364;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Klein S., Gerhardt D.S.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC090568; AAH90568.1; -; mRNA.  
 DR InterPro; IPR012282; Cytochrome\_c\_r.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR011701; MFS.  
 DR InterPro; IPR011993; PH\_type.  
 DR Pfam; PF07690; MFS.1; 1\_type.  
 DR PROSITE; PS00850; MFS; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 484 AA; 52391 MW; CB67FC9810D2F79C CRC64;  
 Query Match 75.0%; Score 33; DB 2; Length 484;  
 Best Local Similarity 66.7%; Pred. No. 3e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FQLLMFV 9  
 Db 128 FQLLMFV 136  
 RESULT 49  
 Q4XOM6 ASPFU PRELIMINARY; PRT; 495 AA.  
 AC Q4XOM6;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=Afu2G12960;  
 OS Aspergillus fumigatus Af293.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 OX NCBI\_TaxID=330879;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Af293;  
 RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,  
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,  
 RA Bowyer P., Chen D., Collins M., Coulson R., Dyer P.S.,  
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,  
 RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,  
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,

RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,  
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,  
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,  
 RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,  
 RA Mouny I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,  
 RA Penvalva M.A., Perteu M., Price C., Pritchard B.L., Quail M.A.,  
 RA Rabinovitch E., Rawlins N., Rajandream M.-A., Reichard U.,  
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,  
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,  
 RA Machida M., Hall N., Barrell B., Denning D.W.;  
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
 RT Aspergillus fumigatus.";  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAHF01000001; EAL93589.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 495 AA; 55147 MW; B945804CB503EB0 CRC64;  
 Query Match 75.0%; Score 33; DB 2; Length 495;  
 Best Local Similarity 87.5%; Pred. No. 3.1e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FQLLMFV 8  
 Db 345 FQLLMFV 352  
 RESULT 50  
 Q4FP57 9RICK PRELIMINARY; PRT; 525 AA.  
 AC Q4FP57;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Lysine-tRNA ligase (EC 6.1.1.6).  
 GN Name=lysS; ORFNames=SAR11\_0210;  
 OS Candidatus Pelagibacter ubique HTCC1062.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC SAR11 cluster; Candidatus Pelagibacter.  
 OX NCBI\_TaxID=335992;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HTCC1062;  
 RA Giovannoni S.J., Tripp H.J., Givan S.A., Podar M., Vergin K.L.,  
 RA Baptista D., Bibbs L., Eads J., Richardson T.H., Noordweir M.,  
 RA Rappe M.S., Short J., Carrington J.C., Mathur E.J.;  
 RT "Genome Streamlining in a Cosmopolitan Oceanic Bacterium.";  
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CP000084; AAZ21032.1; -; Genomic\_DNA.  
 KW Ligase.  
 SQ SEQUENCE 525 AA; 60698 MW; 92D323AE809520E1 CRC64;  
 Query Match 75.0%; Score 33; DB 2; Length 525;  
 Best Local Similarity 87.5%; Pred. No. 3.2e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LQLLMFV 9  
 Db 355 LQLLMFV 362  
 Search completed: May 9, 2006, 02:24:12  
 Job time : 135.6 secs